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OM nucleic - nucleic search, using sw model

Run on: December 14, 2003, 13:24:39 ; Search time 602.28 Seconds  
(Without alignments)  
10059.976 Million cell updates/sec

Title: US-10-027-923-1

Perfect score: 1823  
Sequence: 1 aaatgctctctgtgat.....aaaaaaaaaaaaaaaa 1823

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 2201672 seqs, 1661799599 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4403344

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Published Applications NA:\*  
1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*  
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12: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*  
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17: /cgn2\_6/ptodata/2/pubpna/US01\_PUBCOMB.seq:\*  
18: /cgn2\_6/ptodata/2/pubpna/US00\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1823	100.0	1823	14	US-10-027-923-1
2	1784	97.9	1788	10	US-09-822-830A-61
3	1110	60.9	1110	14	US-10-027-923-3
4	222	12.2	2826	13	US-10-346-241-1
5	222	12.2	3129	13	US-10-346-241-5
6	222	12.2	4518	15	US-10-225-567A-177
7	33	1.8	55	15	US-10-245-988-9
8	33	1.8	111	10	US-09-960-352-7296
9	33	1.8	116	9	US-09-770-696-726
10	33	1.8	166	10	US-09-867-701-9576
11	33	1.8	174	9	US-09-925-299-750
12	33	1.8	174	11	US-09-925-299-750
13	33	1.8	190	10	US-09-867-701-9295
14	33	1.8	200	10	US-09-960-352-4816
15	33	1.8	212	10	US-09-867-701-9190

16	33	1.8	241	9	US-09-604-287A-334	Sequence 334, App
17	33	1.8	241	11	US-09-551-621-334	Sequence 334, App
18	33	1.8	241	13	US-10-124-805-334	Sequence 334, App
19	33	1.8	241	14	US-10-007-805-334	Sequence 334, App
20	33	1.8	241	15	US-10-076-622-334	Sequence 334, App
21	33	1.8	244	10	US-09-867-701-9643	Sequence 9643, App
22	33	1.8	250	10	US-09-867-701-9524	Sequence 9524, App
23	33	1.8	257	10	US-09-983-965-2210	Sequence 2210, App
24	33	1.8	262	15	US-10-102-552-1489	Sequence 1489, App
25	33	1.8	267	13	US-09-814-352-17816	Sequence 17816, App
26	33	1.8	277	10	US-09-960-352-9815	Sequence 9815, App
27	33	1.8	295	10	US-09-867-701-9246	Sequence 9246, App
28	33	1.8	317	10	US-09-960-352-14196	Sequence 14196, App
29	33	1.8	331	10	US-09-880-107-1410	Sequence 1410, App
30	33	1.8	365	10	US-09-960-352-8635	Sequence 8635, App
31	33	1.8	385	10	US-09-960-352-3491	Sequence 3491, App
32	33	1.8	387	10	US-09-960-352-3404	Sequence 3404, App
33	33	1.8	399	11	US-09-918-995-5340	Sequence 5340, App
34	33	1.8	418	11	US-09-918-995-5002	Sequence 5002, App
35	33	1.8	418	11	US-09-918-995-7292	Sequence 7292, App
36	33	1.8	420	15	US-10-074-475-127	Sequence 127, App
37	33	1.8	436	13	US-09-814-352-17851	Sequence 17851, App
38	33	1.8	438	10	US-09-960-352-13952	Sequence 13952, App
39	33	1.8	439	10	US-09-960-352-1009	Sequence 1009, App
40	33	1.8	449	13	US-10-027-632-44327	Sequence 44327, App
41	33	1.8	449	14	US-10-027-632-44327	Sequence 44327, App
42	33	1.8	464	11	US-09-918-995-113312	Sequence 113312, App
43	33	1.8	465	15	US-10-198-846-11931	Sequence 11931, App
44	33	1.8	503	10	US-09-995-494-26	Sequence 26, App
45	33	1.8	515	15	US-10-198-846-9933	Sequence 9933, App

## ALIGNMENTS

RESULT 1  
US-10-027-923-1  
; Sequence 1, Application US/10027923  
; Publication No. US20020142330A1  
; GENERAL INFORMATION:  
; APPLICANT: Brian Galtner Bates  
; APPLICANT: Kamalaka Gulukota  
; APPLICANT: Yuhong Xie  
; TITLE OF INVENTION: NOVEL GLUTAMATE RECEPTOR MODULATORY PROTEINS AND  
; FILE REFERENCE: GNN-024  
; CURRENT APPLICATION NUMBER: US/10/027,923  
; PRIOR FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/257,589  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 1823  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (4)..(1110)  
US-10-027-923-1

Query Match 100.0%; Score 1823; DB 14; Length 1823;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1823; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAATGCTCTCTGTGTTAGCTTCGTCAGCTTACTTTGAAAGAGATGCGTGAGCT 60  
DB 1 AAATGCTCTCTGTGTTAGCTTCGTCAGCTTACTTTGAAAGAGATGCGTGAGCT 60  
QY GCACACTCCAGTGAAGAGAGGAGTGTGCTCACTGCTGGTGCATCATTTATTGAGCT 120  
DB GCACACTCCAGTGAAGAGAGGAGTGTGCTCACTGCTGGTGCATCATTTATTGAGCT 120

QY 121 CTCTTTCTGTGATCAACAGCCCTACGTGGAGAGATTGCAAGAGAGAGTGGGCA 180  
Db 121 CTCTTTCTGTGATCAACAGCCCTACGTGGAGAGATTGCAAGAGAGTGGGCA 180  
QY 181 GTCCGTGAAGATGAGATTCAGAGAGTGGAGGCAATGCTGATACCTTGAAGATC 240  
Db 181 GTCCGTGAAGATGAGATTCAGAGAGTGGAGGCAATGCTGATACCTTGAAGATC 240  
QY 241 AATTGAGACCCACACTCTTGGCCCAATCACTGAGCTGTGAGATTAAGGATTCCTGC 300  
Db 241 AATTGAGACCCACACTCTTGGCCCAATCACTGAGCTGTGAGATTAAGGATTCCTGC 300  
QY 301 TGGGATTCGGCTGGCCCTAGAGACAGATTAAGTCAATTAAGATTCCTCATTTCT 360  
Db 301 TGGGATTCGGCTGGCCCTAGAGACAGATTAAGTCAATTAAGATTCCTCATTTCT 360  
QY 361 TCGGAGAGAGAGAGGCTTGTATGCTGTGTGATGGCTCTCTCTCTCCCTCC 420  
Db 361 TCGGAGAGAGAGAGGCTTGTATGCTGTGTGATGGCTCTCTCTCTCCCTCC 420  
QY 421 AAGAGCCCAATAGAGGAGTCAATTTGAGCTTTCAGATTCAGATTCAGATTCAG 480  
Db 421 AAGAGCCCAATAGAGGAGTCAATTTGAGCTTTCAGATTCAGATTCAGATTCAG 480  
QY 481 AATTGCTCCAGCTTTCAACATCTCAATGCTTACTGAGACCAATCAATGATCTG 540  
Db 481 AATTGCTCCAGCTTTCAACATCTCAATGCTTACTGAGACCAATCAATGATCTG 540  
QY 541 AATTGCTCCAGCTTTCAACATCTCAATGCTTACTGAGACCAATCAATGATCTG 540  
Db 541 AATTGCTCCAGCTTTCAACATCTCAATGCTTACTGAGACCAATCAATGATCTG 540  
QY 541 AGTGAACAAGACTCTGTTCAAAATATTTATGAGAGGTTGCTGAGATTCAGAGCA 600  
Db 541 AGTGAACAAGACTCTGTTCAAAATATTTATGAGAGGTTGCTGAGATTCAGAGCA 600  
QY 601 AGGTCCATGCTGATGATGAGAGGATCACTGACCTATGATGATGATGATGATG 660  
Db 601 AGGTCCATGCTGATGATGAGAGGATCACTGACCTATGATGATGATGATGATG 660  
QY 661 GAGGCAACATGAGAGAGAGGATGAGAGGCTTCAAAAGATTAAGTCAAGAGAGAG 720  
Db 661 GAGGCAACATGAGAGAGAGGATGAGAGGCTTCAAAAGATTAAGTCAAGAGAGAG 720  
QY 721 AATTGATCCGCCCACTCTTCAAAATCTACAGTATGAGAGGAGAGAGGATTTAG 780  
Db 721 AATTGATCCGCCCACTCTTCAAAATCTACAGTATGAGAGGAGAGAGGATTTAG 780  
QY 781 CTGCTGAAGAGCTCAACAGTCACTTGCCTCAAGGCTGCTGCTGCTGCTGCTG 840  
Db 781 CTGCTGAAGAGCTCAACAGTCACTTGCCTCAAGGCTGCTGCTGCTGCTGCTG 840  
QY 841 GGCATGACGGTGAAGAGTCTGCTGATGAGGCTGAGGCTGCTGATGAGAGATTT 900  
Db 841 GGCATGACGGTGAAGAGTCTGCTGATGAGGCTGAGGCTGCTGATGAGAGATTT 900  
QY 901 CTGCTTCTGGGACAGGAGACAGATGCTTATTAAGATCTCAAGAGACAGATCTTA 960  
Db 901 CTGCTTCTGGGACAGGAGACAGATGCTTATTAAGATCTCAAGAGACAGATCTTA 960  
QY 961 TGGGAGACAGAGAGAGAGAGTGGCTTCTTCAAGGCTTTTGGAGACATATTAAC 1020  
Db 961 TGGGAGACAGAGAGAGAGAGTGGCTTCTTCAAGGCTTTTGGAGACATATTAAC 1020  
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QY 1141 AATTGAGACCAACACTGATTAATTTGATGAGATTTGAGAGCAATTTGATGATGAT 1200  
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QY 1201 GACCGTCAAAATGAGCCCATATCACTGCAACACTTCAAGTTTCTTGATGGGCT 1260  
Db 1201 GACCGTCAAAATGAGCCCATATCACTGCAACACTTCAAGTTTCTTGATGGGCT 1260  
QY 1261 CAGACTTCACTCTGCAAGATTAATCTGAGAGTCCATGAGGAGCTCTTGAATGG 1320  
Db 1261 CAGACTTCACTCTGCAAGATTAATCTGAGAGTCCATGAGGAGCTCTTGAATGG 1320  
QY 1321 GCTTGGGCTTGTATTAAGTCTGAGAGAGGAGAGAGAGAGAGAGAGAGAGAG 1380  
Db 1321 GCTTGGGCTTGTATTAAGTCTGAGAGAGGAGAGAGAGAGAGAGAGAGAGAG 1380  
QY 1381 GAGAGGAGACTTGTATTAAGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440  
Db 1381 GAGAGGAGACTTGTATTAAGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440  
QY 1441 ACCCTCCAGTTACACTGAGATGATGCTCCAGAGCTTCAAGACATGATTAATTC 1500  
Db 1441 ACCCTCCAGTTACACTGAGATGATGCTCCAGAGCTTCAAGACATGATTAATTC 1500  
QY 1501 GATTGAGAGCTTGAAGTCTGAGAGTCTGATGATTAATTAAGTCTTCAATTA 1560  
Db 1501 GATTGAGAGCTTGAAGTCTGAGAGTCTGATGATTAATTAAGTCTTCAATTA 1560  
QY 1561 ATCCCTAATGCTCTTCTGACCTCTGAGGCTATCTTGTGATTAATTAATTA 1620  
Db 1561 ATCCCTAATGCTCTTCTGACCTCTGAGGCTATCTTGTGATTAATTAATTA 1620  
QY 1621 CAGAGCAAAATGAGAGAGTGTATTAATGCTGAGAGAGAGAGAGAGAGAGAG 1680  
Db 1621 CAGAGCAAAATGAGAGAGTGTATTAATGCTGAGAGAGAGAGAGAGAGAGAG 1680  
QY 1681 TCTTCTGCTGCTTATCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740  
Db 1681 TCTTCTGCTGCTTATCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740  
QY 1741 CTATGTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1800  
Db 1741 CTATGTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1800  
QY 1801 AAAAAAAAAAAAAAAAAAAAAA 1823  
Db 1801 AAAAAAAAAAAAAAAAAAAAAA 1823  
RESULT 2  
US-09-822-830A-61  
Sequence 61, Application US/09822830A  
Patent No. US20020142952A1  
GENERAL INFORMATION:  
APPLICANT: Genetics Institute, Inc.  
APPLICANT: Wong, Gordon G.  
APPLICANT: Clark, Hilary  
APPLICANT: Fehnel, Kim  
APPLICANT: Agostino, Michael J.  
APPLICANT: Hewes, Steven H.  
APPLICANT: Resnick, Richard J.  
APPLICANT: Gulukota, Kamalakkar  
APPLICANT: Graham, James R.  
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS  
FILE REFERENCE: GIN 6402  
CURRENT APPLICATION NUMBER: US/09/822, 830A  
CURRENT FILING DATE: 2001-03-29  
PRIOR APPLICATION NUMBER: 60/195, 604  
PRIOR FILING DATE: 2000-04-06  
NUMBER OF SEQ ID NOS: 631  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 61  
LENGTH: 1788  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-822-830A-61

Query Match	Similarity	Score	DB	Length
Beet Local	100.0%	Pred. No. 0		
Matches 1784	Conservative	0	Mismatches	0
			Indels	0
			Gaps	0
QY	6	GGTCCCTTCTGTGATCCTGTCAGTCTTACTTTTGAAGAAGATGCGGTGGAGTGCACA	65	
DB	1	GGTCCCTTCTGTGATCCTGTCAGTCTTACTTTTGAAGAAGATGCGGTGGAGTGCACA	60	
QY	66	GTCCAGTGAAGAGGGGTGTGGCTCACATGCTGGGTGACATCATTAATTTGAGCTCTTT	125	
DB	61	GTCCAGTGAAGAGGGGTGTGGCTCACATGCTGGGTGACATCATTAATTTGAGCTCTTT	120	
QY	126	TTTCGTTTATCAACCAAGCTTACTGTGTGAAGAACTTATGAAGAAAGTGTGGGCACTCCG	185	
DB	121	TTTCGTTTATCAACCAAGCTTACTGTGTGAAGAACTTATGAAGAAAGTGTGGGCACTCCG	180	
QY	186	TGAACAGATGGCATTTCAAGAGGTGAGAGGCCATGCTGCATACCCCTGGAAGAAAGATCAATTC	245	
DB	181	TGAACAGATGGCATTTCAAGAGGTGAGAGGCCATGCTGCATACCCCTGGAAGAAAGATCAATTC	240	
QY	246	AGACCCCACTCTTTGCCCAATCACACTGGGCTGTGAGATTAAGGAATTCCTGTGCGA	305	
DB	241	AGACCCCACTCTTTGCCCAATCACACTGGGCTGTGAGATTAAGGAATTCCTGTGCGA	300	
QY	306	TTTCGCTGTGGCCCTTAAGACAGAGCATTTGAATTCATTAAGATTTCCCTCATTTTCTTCCGA	365	
DB	301	TTTCGCTGTGGCCCTTAAGACAGAGCATTTGAATTCATTAAGATTTCCCTCATTTTCTTCCGA	360	
QY	366	AGAGGAAGAGGGCTGTGATGCTGTGTGATGGGCTCTCTTCTTCCGCTCCAGAA	425	
DB	361	AGAGGAAGAGGGCTGTGATGCTGTGTGATGGGCTCTCTTCTTCCGCTCCAGAA	420	
QY	426	GCCCATAGTAGGGGTCAATTTGGGCTGTGTCAGTTCTTTAGGCATTCAGTTCAGAAATTT	485	
DB	421	GCCCATAGTAGGGGTCAATTTGGGCTGTGTCAGTTCTTTAGGCATTCAGTTCAGAAATTT	480	
QY	486	GCTCCAGCTTTTCAACATACCTCAGATTGCTTACTCAGCAACCATCATGATCTGAATGA	545	
DB	481	GCTCCAGCTTTTCAACATACCTCAGATTGCTTACTCAGCAACCATCATGATCTGAATGA	540	
QY	546	CAGAAGCTGTTCAAATATTTCAATAGAGGGTGTGGCTCAGATGCTAGAGGCAAGGTC	605	
DB	541	CAGAAGCTGTTCAAATATTTCAATAGAGGGTGTGGCTCAGATGCTAGAGGCAAGGTC	600	
QY	606	CATGTGACATATGTGAAGAGGTACATGTGACATGTATATCAGCCGTACACAGAAAG	665	
DB	601	CATGTGACATATGTGAAGAGGTACATGTGACATGTATATCAGCCGTACACAGAAAG	660	
QY	666	CAACTATGAGAAAGTGGATGGAAGGCTTCAAGATATGTCAAGGAGAAAGGATTTG	725	
DB	661	CAACTATGAGAAAGTGGATGGAAGGCTTCAAGATATGTCAAGGAGAAAGGATTTG	720	
QY	726	CATGSCCACTCTTAACAATCTACAGTAATGAGAGGAGAGCAAGACTTTGATTAAGCTGCT	785	
DB	721	CATGSCCACTCTTAACAATCTACAGTAATGAGAGGAGAGCAAGACTTTGATTAAGCTGCT	780	
QY	786	GAAAGAGCTCAAAAGTCACTTGGCCCAAGGCCCGGGTGTGGCTACTCTGTGAGGGCAT	845	
DB	781	GAAAGAGCTCAAAAGTCACTTGGCCCAAGGCCCGGGTGTGGCTACTCTGTGAGGGCAT	840	
QY	846	GACGGTGAAGAGTCTGTGATGAGCATGAGGCGCTGGGCTCTAATGTGGAGAAATTTTGCT	905	
DB	841	GACGGTGAAGAGTCTGTGATGAGCATGAGGCGCTGGGCTCTAATGTGGAGAAATTTTGCT	900	
QY	906	TCTGGGCAAGGAAACAGATGGCATTTTATTTGAGATCTCAAGAAACAGATCTTAATGGGA	965	
DB	901	TCTGGGCAAGGAAACAGATGGCATTTTATTTGAGATCTCAAGAAACAGATCTTAATGGGA	960	
QY	966	AGACAGAAAGAAATGCAAGGTGCTTCTTCAAGGTTTGTGAGACATATTTACACAGAG	1025	
DB	961	AGACAGAAAGAAATGCAAGGTGCTTCTTCAAGGTTTGTGAGACATATTTACACAGAG	1020	
QY	1026	TGAGTCCGTGCTGTCACATGCCAGGCTCTGATCTAAGAGCTCAAGTCAAGGCCCAT	1085	

[illegible]

ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(1110)  
US-10-027-923-3

Query Match 60.9%; Score 1110; DB 14; Length 1110;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ATGGTCCTTCTGTGATCTGTGCTGCTTCTTTGAAAGAGAGTCCGTGGAGTGA 63  
DB 1 ATGGTCCTTCTGTGATCTGTGCTGCTTCTTTGAAAGAGAGTCCGTGGAGTGA 60  
QY 64 CAGTCCAGTGAAG 123  
DB 61 CAGTCCAGTGAAG 120  
QY 124 TTTTCTGTGATCAACAGCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 183  
DB 121 TTTTCTGTGATCAACAGCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180  
QY 184 CGTGAACAGTATGAGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 243  
DB 181 CGTGAACAGTATGAGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240  
QY 244 TCAGACCCCACTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 303  
DB 241 TCAGACCCCACTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300  
QY 304 CATTGCGCTGTGCGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 363  
DB 301 CATTGCGCTGTGCGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360  
QY 364 GAAG 423  
DB 361 GAAG 420  
QY 424 AAGCCCTATGAG 483  
DB 421 AAGCCCTATGAG 480  
QY 484 TTGCTCAGCTTTTCAACATCTCAGATGCTTACTCAGAACATCATGATCTGAGT 543  
DB 481 TTGCTCAGCTTTTCAACATCTCAGATGCTTACTCAGAACATCATGATCTGAGT 540  
QY 544 GACAAAGCTCTGTTCAAAATATTTTCAAGAGAGAGAGAGAGAGAGAGAGAG 603  
DB 541 GACAAAGCTCTGTTCAAAATATTTTCAAGAGAGAGAGAGAGAGAGAGAGAG 600  
QY 604 TCCATGCTGAGCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 663  
DB 601 TCCATGCTGAGCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660  
QY 664 GGCACATGAG 723  
DB 661 GGCACATGAG 720  
QY 724 TGCATGCCCACTCTTCAAAATATTTTCAAGAGAGAGAGAGAGAGAGAGAGAG 783  
DB 721 TGCATGCCCACTCTTCAAAATATTTTCAAGAGAGAGAGAGAGAGAGAGAGAG 780  
QY 784 CTGAAG 843  
DB 781 CTGAAG 840  
QY 844 ATGACGCTGAG 903  
DB 841 ATGACGCTGAG 900  
QY 904 CTTCTGGGAG 963  
DB 901 CTTCTGGGAG 960

QY 964 GAAGACAG 1023  
DB 961 GAAGACAG 1020  
QY 1024 AGTGAAGCTGTGCTGTGCAATGCCCAAGCTCTGAATCTAGAGCTCAGTCAAGGCC 1083  
DB 1021 AGTGAAGCTGTGCTGTGCAATGCCCAAGCTCTGAATCTAGAGCTCAGTCAAGGCC 1080  
QY 1084 ATCACTGAGACTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1113  
DB 1081 ATCACTGAGACTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1110

## RESULT 4

US-10-346-241-1  
Sequence 1, Application US/10346241  
Publication No. US20030157647A1  
GENERAL INFORMATION:  
APPLICANT: STORMANN, THOMAS M.  
APPLICANT: LEVINHAL, CYNTHIA  
APPLICANT: STORJAHN, LAURA  
APPLICANT: HAMMERLAND, LANCE G.  
APPLICANT: KRAPCHO, KAREN J.  
APPLICANT: NRS PHARMACEUTICALS, INC.  
TITLE OF INVENTION: A NOVEL HUMAN METABOTROPIC GLUTAMATE RECEPTOR  
FILE REFERENCE: 1094.2.6  
CURRENT APPLICATION NUMBER: US/10/346, 241  
CURRENT FILING DATE: 2003-01-17  
PRIOR APPLICATION NUMBER: 2000-10-24  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: 60/161,481  
PRIOR FILING DATE: 1999-10-25  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 2826  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(2826)  
US-10-346-241-1

Query Match 12.2%; Score 222; DB 13; Length 2826;  
Best Local Similarity 99.1%; Pred. No. 2.4e-102; Indels 0; Gaps 0;  
Matches 422; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 464 TAGCCATTCAGTCCAGAAATTTGCTCAGCTTTCAACATCTCAGATGCTTACTCAG 523  
DB 461 TAGCCATTCAGTCCAGAAATTTGCTCAGCTTTCAACATCTCAGATGCTTACTCAG 520  
QY 524 CAACATCATGATCTGAGTGAACAAGCTCTGTTCAAAATATTTTCAAGAGAGTGTGCTT 583  
DB 521 CAACATCATGATCTGAGTGAACAAGCTCTGTTCAAAATATTTTCAAGAGAGTGTGCTT 580  
QY 584 CAGATGCTCAGCAG 643  
DB 581 CAGATGCTCAGCAG 640  
QY 644 TATCAGCCGTGACACAG 703  
DB 641 TATCAGCCGTGACACAG 700  
QY 704 TGTCAAG 763  
DB 701 TGTCAAG 760  
QY 764 AGCAGAGCTTTGATTAAGCTGTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 823  
DB 761 AGCAGAGCTTTGATTAAGCTGTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 820  
QY 824 TGCCCTACTTCTGTGAG 883



Db 821 TGGCTGCTCTCTGTGAGGGCATGCGGTGAGAGGTCTGTGATGCGCATGAGGGGCTTG 880  
QY 884 GTCTAG 889  
Db 881 GTCTAG 886

## RESULT 5

US-10-346-241-5  
; Sequence 5, Application US/10346241  
; Publication No. US20030157647A1  
; GENERAL INFORMATION:  
; APPLICANT: STORMANN, THOMAS M.  
; APPLICANT: STORMANN, LEVINTHAL, CYNTHIA  
; APPLICANT: STORJOHANN, LAURA  
; APPLICANT: HAMMERLAND, LANCE G.  
; APPLICANT: KEAPCHO, KAREN J.  
; APPLICANT: NPS PHARMACEUTICALS, INC.  
; TITLE OF INVENTION: A NOVEL HUMAN METABOTROPIC GLUTAMATE RECEPTOR  
; FILE REFERENCE: 1094.2.6  
; CURRENT APPLICATION NUMBER: US/10/346,241  
; PRIOR FILING DATE: 2003-01-17  
; PRIOR APPLICATION NUMBER: US/09/695,491  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: 60/161,481  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 3129  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Chimeric  
; OTHER INFORMATION: molecule comprising portions of human mGluR5d and  
; OTHER INFORMATION: the human calcium receptor.  
; NAME/KEY: CDS  
; LOCATION: (1)..(3129)  
US-10-346-241-5

Query Match 12.2%; Score 222; DB 13; Length 3129;

Best Local Similarity 99.1%; Pred. No. 2.4e-102; Indels 0; Gaps 0;  
Matches 422; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 464 TACCATTCAGTTCAGCAATTTGCTCCAGCTTTTCAACATACCTCAGATTGCTTACTCAG 523  
Db 461 TACCATTCAGTTCAGCAATTTGCTCCAGCTTTTCAACATACCTCAGATTGCTTACTCAG 520  
QY 524 CAACCATCATGATCTGATGACAGAACTCTGTTCAATATTTTCATGAGGTTGTGCTT 583  
Db 521 CAACCATCATGATCTGATGACAGAACTCTGTTCAATATTTTCATGAGGTTGTGCTT 580  
QY 584 CAGATGCTCAGCAGGCAAGGTCATGCTGATGACATAGTGAAGAGGTCAACTGAGCCTATG 643  
Db 581 CAGATGCTCAGCAGGCAAGGTCATGCTGATGACATAGTGAAGAGGTCAACTGAGCCTATG 640  
QY 644 TATCAGCCGTGACACAGAAAGCACTATGAGAAAGTGGATGAGAGCCTTCAAGATA 703  
Db 641 TATCAGCCGTGACACAGAAAGCACTATGAGAAAGTGGATGAGAGCCTTCAAGATA 700  
QY 704 TGTTCAGGAAAGGAGGATTTGATGCGCCCACTCTTCAAAATCTTACAGTAATGCAAGGG 763  
Db 701 TGTTCAGGAAAGGAGGATTTGATGCGCCCACTCTTCAAAATCTTACAGTAATGCAAGGG 760  
QY 764 AGCAGAGCTTGTATAGCTGCTGAAAGGTCACAGTCACTTGGCCCAAGGCCCGGGTGG 823  
Db 761 AGCAGAGCTTGTATAGCTGCTGAAAGGTCACAGTCACTTGGCCCAAGGCCCGGGTGG 820  
QY 824 TGGCCTACTTCTGTGAGGGCATGACGGTGAAGAGTCTGTGATGAGCCATGAGGCGCTTG 883  
Db 821 TGGCCTACTTCTGTGAGGGCATGACGGTGAAGAGTCTGTGATGAGCCATGAGGCGCTTG 880

QY 884 GTCTAG 889  
Db 881 GTCTAG 886

## RESULT 6

US-10-225-567A-177  
; Sequence 177, Application US/10225567A  
; Publication No. US20030113798A1  
; GENERAL INFORMATION:  
; APPLICANT: LifeSpan Biosciences  
; APPLICANT: Brown, Joseph P.  
; APPLICANT: Burner, Glenna C.  
; APPLICANT: Roush, Christine L.  
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS  
; FILE REFERENCE: 1920-4-4  
; CURRENT APPLICATION NUMBER: US/10/225,567A  
; PRIOR FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 60/257,144  
; PRIOR FILING DATE: 2000-12-19  
; NUMBER OF SEQ ID NOS: 2292  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 177  
; LENGTH: 4518  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-225-567A-177

Query Match 12.2%; Score 222; DB 15; Length 4518;

Best Local Similarity 99.1%; Pred. No. 2.4e-102; Indels 0; Gaps 0;  
Matches 422; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 464 TACCATTCAGTTCAGCAATTTGCTCCAGCTTTTCAACATACCTCAGATTGCTTACTCAG 523  
Db 611 TACCATTCAGTTCAGCAATTTGCTCCAGCTTTTCAACATACCTCAGATTGCTTACTCAG 670  
QY 524 CAACCATCATGATCTGATGACAGAACTCTGTTCAATATTTTCATGAGGTTGTGCTT 583  
Db 671 CAACCATCATGATCTGATGACAGAACTCTGTTCAATATTTTCATGAGGTTGTGCTT 720  
QY 584 CAGATGCTCAGCAGGCAAGGTCATGCTGATGACATAGTGAAGAGGTCAACTGAGCCTATG 643  
Db 731 CAGATGCTCAGCAGGCAAGGTCATGCTGATGACATAGTGAAGAGGTCAACTGAGCCTATG 720  
QY 644 TATCAGCCGTGACACAGAAAGCACTATGAGAAAGTGGATGAGAGCCTTCAAGATA 703  
Db 791 TATCAGCCGTGACACAGAAAGCACTATGAGAAAGTGGATGAGAGCCTTCAAGATA 850  
QY 704 TGTTCAGGAAAGGAGGATTTGATGCGCCCACTCTTCAAAATCTTACAGTAATGCAAGGG 763  
Db 851 TGTTCAGGAAAGGAGGATTTGATGCGCCCACTCTTCAAAATCTTACAGTAATGCAAGGG 910  
QY 764 AGCAGAGCTTGTATAGCTGCTGAAAGGTCACAGTCACTTGGCCCAAGGCCCGGGTGG 823  
Db 911 AGCAGAGCTTGTATAGCTGCTGAAAGGTCACAGTCACTTGGCCCAAGGCCCGGGTGG 970  
QY 824 TGGCCTACTTCTGTGAGGGCATGACGGTGAAGAGTCTGTGATGAGCCATGAGGCGCTTG 883  
Db 971 TGGCCTACTTCTGTGAGGGCATGACGGTGAAGAGTCTGTGATGAGCCATGAGGCGCTTG 1030  
QY 884 GTCTAG 889  
Db 1031 GTCTAG 1036

## RESULT 7

US-10-245-988-9  
; Sequence 9, Application US/10245988  
; Publication No. US20030108921A1  
; GENERAL INFORMATION:  
; APPLICANT: Jucker, Markus T.  
; APPLICANT: Brenlano, Steven T.

APPLICANT: Delgado, Francisco D.  
APPLICANT: Cleuzat, Philippe  
TITLE OF INVENTION: DETECTION OF RPOB SEQUENCES OF MYCOBACTERIUM  
TITLE OF INVENTION: TUBERCULOSIS  
FILE REFERENCE: GPI08-02.UT  
CURRENT APPLICATION NUMBER: US/10/245,988  
CURRENT FILING DATE: 2002-09-18  
PRIOR APPLICATION NUMBER: 60/323,485  
PRIOR FILING DATE: 2001-09-18  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 9  
LENGTH: 55  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: capture  
US-10-245-988-9

Query Match 1.8%; Score 33; DB 15; Length 55;  
Best Local Similarity 100.0%; Pred. No. 4.5e-06;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1791 CACAAAAA  
Db 23 CACAAAAA  
1823  
55

RESULT 8  
US-09-960-352-7296/C  
Sequence 7296, Application US/09960352  
Patent No. US20020137139A1  
GENERAL INFORMATION:  
APPLICANT: Warren, Wesley C.  
APPLICANT: Tao, Nengbing  
APPLICANT: Byatt, John C.  
APPLICANT: Mathilagan, Nagappan  
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND  
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION  
FILE REFERENCE: 16511.006/37-21(10298)C  
CURRENT APPLICATION NUMBER: US/09/960,352  
CURRENT FILING DATE: 2001-09-24  
NUMBER OF SEQ ID NOS: 15112  
SEQ ID NO 7296  
LENGTH: 111  
TYPE: DNA  
ORGANISM: Bos taurus  
OTHER INFORMATION: Clone ID: 31-LIB34-055-Q1-E1-H3  
US-09-960-352-7296

Query Match 1.8%; Score 33; DB 10; Length 111;  
Best Local Similarity 100.0%; Pred. No. 4.5e-06;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1791 CACAAAAA  
Db 103 CACAAAAA  
1823  
71

RESULT 9  
US-09-770-696-726/C  
Sequence 726, Application US/09770696  
Patent No. US2001004940A1  
GENERAL INFORMATION:  
APPLICANT: Goriach, Jorn  
APPLICANT: An, Yong-Qiang  
APPLICANT: Hamilton, Carol M.  
APPLICANT: Price, Jennifer L.  
APPLICANT: Raines, Tracy M.  
APPLICANT: Yu, Yang  
APPLICANT: Rameaka, Joshua G.  
APPLICANT: Page, Amy

APPLICANT: Matthew, Abraham V.  
APPLICANT: Ledford, Brooke L.  
APPLICANT: Woessner, Jeffrey P.  
APPLICANT: Haas, William David  
APPLICANT: Garcia, Carlos A.  
APPLICANT: Krickler, Maja  
APPLICANT: Slader, Ted  
APPLICANT: Davis, Keith R.  
APPLICANT: Allen, Keith  
APPLICANT: Hoffman, Neil  
APPLICANT: Hurban, Patrick  
TITLE OF INVENTION: Expressed Sequences of Arabidopsis  
TITLE OF INVENTION: Thaliana  
FILE REFERENCE: 2031US (PARA-020PRV)  
CURRENT APPLICATION NUMBER: US/09/770,696  
CURRENT FILING DATE: 2001-01-26  
PRIOR APPLICATION NUMBER: 60/178,278  
PRIOR FILING DATE: 2000-01-27  
NUMBER OF SEQ ID NOS: 911  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 726  
LENGTH: 116  
TYPE: DNA  
ORGANISM: Arabidopsis thaliana  
US-09-770-696-726

Query Match 1.8%; Score 33; DB 9; Length 116;  
Best Local Similarity 100.0%; Pred. No. 4.5e-06;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1791 CACAAAAA  
Db 56 CACAAAAA  
1823  
24

RESULT 10  
US-09-867-701-9576  
Sequence 9576, Application US/09867701  
Patent No. US20020132237A1  
GENERAL INFORMATION:  
APPLICANT: Aglate, Paul A.  
APPLICANT: Jones, Robert  
APPLICANT: Harlocker, Susan L.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER  
FILE REFERENCE: 210121.497  
CURRENT APPLICATION NUMBER: US/09/867,701  
CURRENT FILING DATE: 2001-05-29  
NUMBER OF SEQ ID NOS: 10912  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 9576  
LENGTH: 166  
TYPE: DNA  
ORGANISM: Homo sapien  
US-09-867-701-9576

Query Match 1.8%; Score 33; DB 10; Length 166;  
Best Local Similarity 100.0%; Pred. No. 4.6e-06;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1791 CACAAAAA  
Db 78 CACAAAAA  
1823  
110

RESULT 11  
US-09-925-299-750  
Sequence 750, Application US/09925299  
Patent No. US20020055627A1  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
FILE REFERENCE: PA102

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; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 750
; LENGTH: 174
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (155)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (159)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (164)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (165)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (173)
; OTHER INFORMATION: n equals a,t,g, or c
; US-09-925-299-750

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Query Match          1.8%; Score 33; DB 9; Length 174;
Best Local Similarity 100.0%; Pred. No. 4,6e-06;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1791 CACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1823
DB      46 CACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 78

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RESULT 12
; US-09-925-299-750
; Sequence 750, Application US/09925299
; Publication No. US2003040617A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 750
; LENGTH: 174
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (155)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (159)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (164)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (165)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature

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; LOCATION: (173)
; OTHER INFORMATION: n equals a,t,g, or c
; US-09-925-299-750

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Query Match          1.8%; Score 33; DB 11; Length 174;
Best Local Similarity 100.0%; Pred. No. 4,6e-06;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY      1791 CACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1823
DB      46 CACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 78

```

```

RESULT 13
; US-09-867-701-9295
; Sequence 9295, Application US/09867701
; Patent No. US2002013237A1
; GENERAL INFORMATION:
; APPLICANT: Agiata, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9295
; LENGTH: 190
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-867-701-9295

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Query Match          1.8%; Score 33; DB 10; Length 190;
Best Local Similarity 100.0%; Pred. No. 4,6e-06;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1791 CACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1823
DB      146 CACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 178

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RESULT 14
; US-09-960-352-4816/C
; Sequence 4816, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathiasagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 4816
; LENGTH: 200
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 21-LIB3057-015-Q1-K1-F1
; US-09-960-352-4816

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Query Match          1.8%; Score 33; DB 10; Length 200;
Best Local Similarity 100.0%; Pred. No. 4,6e-06;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY      1791 CACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1823
DB      42 CACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 10

```

RESULT 15

US-09-867-701-9190  
 ; Sequence 9190, Application US/09867701  
 ; Patent No. US20020132237A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Agiate, Paul A.  
 ; APPLICANT: Jones, Robert  
 ; APPLICANT: Harlocker, Susan L.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
 ; FILE REFERENCE: 210121.497  
 ; CURRENT APPLICATION NUMBER: US/09/867,701  
 ; CURRENT FILING DATE: 2001-05-29  
 ; NUMBER OF SEQ ID NOS: 10912  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 9190  
 ; LENGTH: 212  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapien  
 US-09-867-701-9190

Query Match 1.8%; Score 33; DB 10; Length 212;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-06;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1791 CACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1823  
 Db 166 CACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 198

Search completed: December 14, 2003, 18:32:25  
 Job time : 606.28 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 14, 2003, 06:02:02 : Search time 366.72 seconds  
(without alignments)  
10059.976 Million cell updates/sec

Title: US-10-027-923-3

Perfect score: 1110  
Sequence: 1 atgagctctctgtgtatcct.....tgaggagcagctcatctaa 1110

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 2201672 seqs, 1661799599 residues

Total number of hits satisfying chosen parameters: 4403344

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Published Applications NA:  
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2: /cgn2\_6/prodata/2/pubpna/PCF\_NEW\_PUB.seq:\*  
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8: /cgn2\_6/prodata/2/pubpna/US08\_PUBCOMB.seq:\*  
9: /cgn2\_6/prodata/2/pubpna/US09A\_PUBCOMB.seq:\*  
10: /cgn2\_6/prodata/2/pubpna/US09B\_PUBCOMB.seq:\*  
11: /cgn2\_6/prodata/2/pubpna/US09C\_PUBCOMB.seq:\*  
12: /cgn2\_6/prodata/2/pubpna/US09\_NEW\_PUB.seq:\*  
13: /cgn2\_6/prodata/2/pubpna/US09\_NEW\_PUB.seq2:\*  
14: /cgn2\_6/prodata/2/pubpna/US10A\_PUBCOMB.seq:\*  
15: /cgn2\_6/prodata/2/pubpna/US10B\_PUBCOMB.seq:\*  
16: /cgn2\_6/prodata/2/pubpna/US10\_NEW\_PUB.seq:\*  
17: /cgn2\_6/prodata/2/pubpna/US60\_NEW\_PUB.seq:\*  
18: /cgn2\_6/prodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1110	100.0	1110	14	US-10-027-923-3
2	1110	100.0	1110	14	US-10-027-923-1
3	1108	99.8	1788	10	US-09-822-830A-61
4	888.4	80.0	2826	13	US-10-346-241-1
5	888.4	80.0	3129	13	US-10-346-241-5
6	888.4	80.0	4518	13	US-10-225-567A-177
7	458.2	41.3	3295	13	US-09-826-509-346
8	458.2	41.3	3295	13	US-10-101-510-258
9	458.2	41.3	6619	15	US-10-225-567A-169
10	449.2	40.5	3384	15	US-10-300-473-3
11	449.2	40.5	3384	15	US-10-300-473-1
12	444.4	40.0	3219	15	US-10-300-473-4
13	145.8	13.1	2736	10	US-10-255-149-1
14	143.6	12.9	2736	10	US-09-817-464-1
15	143.6	12.9	2736	15	US-10-331-289-1

16	143.6	12.9	3884	10	US-09-820-809-14	Sequence 14, Appl
17	143.6	12.9	3884	15	US-10-225-567A-175	Sequence 175, App
18	138.6	12.5	6122	15	US-10-225-567A-179	Sequence 179, Appl
19	131.6	11.9	2621	13	US-10-251-661-3	Sequence 3, Appl
20	131.6	11.9	2621	15	US-10-225-567A-171	Sequence 171, Appl
21	124	11.2	2830	10	US-09-900-714A-1	Sequence 1, Appl
22	123.6	11.1	3410	15	US-10-225-567A-173	Sequence 173, App
23	118.8	10.7	2745	15	US-09-817-464-11	Sequence 11, Appl
24	118.8	10.7	2745	15	US-10-331-289-11	Sequence 11, Appl
25	118.8	10.7	2748	15	US-10-083-168-7	Sequence 7, Appl
26	118.8	10.7	2748	15	US-10-083-168-66	Sequence 66, Appl
27	118.8	10.7	2748	15	US-10-083-168-68	Sequence 68, Appl
28	118.8	10.7	2748	15	US-10-083-168-70	Sequence 70, Appl
29	118.8	10.7	2748	15	US-10-083-168-72	Sequence 72, Appl
30	118.8	10.7	2766	15	US-09-817-464-13	Sequence 13, Appl
31	118.8	10.7	2766	15	US-10-331-289-13	Sequence 13, Appl
32	118.8	10.7	3804	15	US-09-817-464-3	Sequence 3, Appl
33	118.8	10.7	3804	15	US-10-331-289-3	Sequence 3, Appl
34	118.8	10.7	4312	15	US-10-225-567A-181	Sequence 181, App
35	114.8	10.3	3321	15	US-10-353-699-85	Sequence 85, Appl
36	114.8	10.3	3321	15	US-10-225-567A-183	Sequence 183, Appl
37	92	8.3	2595	15	US-10-151-208-13	Sequence 13, Appl
38	85.8	7.7	600	13	US-10-029-386-9681	Sequence 9681, Ap
39	84	7.6	227	13	US-10-029-386-23381	Sequence 23381, A
40	83.8	7.5	3361	14	US-10-002-854-1	Sequence 1, Appl
41	82.8	7.5	2456	15	US-10-270-333-5	Sequence 5, Appl
42	82.4	7.4	2877	15	US-10-151-208-1	Sequence 1, Appl
43	82.2	7.4	2925	15	US-10-346-241-3	Sequence 3, Appl
44	82.2	7.4	3783	15	US-10-225-567A-117	Sequence 117, App
45	82.2	7.4	4000	15	US-10-300-473-2	Sequence 2, Appl

## ALIGNMENTS

RESULT 1  
US-10-027-923-3  
Sequence 3, Application US/10027923  
Publication No. US20020142330A1  
GENERAL INFORMATION:  
APPLICANT: Brian Galtner Bates  
APPLICANT: Kamalaka Gulukota  
APPLICANT: Yuhong Xie  
APPLICANT: Janet Elizabeth Paulsen  
TITLE OF INVENTION: NOVEL GLUTAMATE RECEPTOR MODULATORY PROTEINS AND  
FILE REFERENCE: NUCLEIC ACID MOLECULES AND USES THEREFOR  
CURRENT APPLICATION NUMBER: US/10/027,923  
CURRENT FILING DATE: 2001-12-21  
PRIOR APPLICATION NUMBER: 60/257,589  
PRIOR FILING DATE: 2000-12-22  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 3  
LENGTH: 1110  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(1110)  
US-10-027-923-3  
Query Match 100.0%; Score 1110; DB 14; Length 1110;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGCTCTCTGTGTATCTCTGACGCTTACTTTTAAAGAGATGTCCTGGAGATGCA 60  
DB 1 ATGAGCTCTCTGTGTATCTCTGACGCTTACTTTTAAAGAGATGTCCTGGAGATGCA 60  
QY 61 CAGTTCAGTGAAGAGAGAGGAGTGTGCTGACATGCTGGTGAATCATTTATTTGAGCTTC 120  
DB 61 CAGTTCAGTGAAGAGAGAGGAGTGTGCTGACATGCTGGTGAATCATTTATTTGAGCTTC 120

QY 121 TTTTCTGTATCAACAGCTTCTGTGAGCAAGATTTCATAGAGAAAGTGTGGGCAATC 180  
DB 121 TTTTCTGTATCAACAGCTTCTGTGAGCAAGATTTCATAGAGAAAGTGTGGGCAATC 180  
QY 181 CGTGAACAGTATGACATTCAGAGAGTGGAGGCAATGCTGATCTTACCTTGAAGATCAAT 240  
DB 181 CGTGAACAGTATGACATTCAGAGAGTGGAGGCAATGCTGATCTTACCTTGAAGATCAAT 240  
QY 241 TCAGACCCCACTCTTGGCCCAATCACTGAGGCTGTGAGATTAAGGATTCCTGCTGG 300  
DB 241 TCAGACCCCACTCTTGGCCCAATCACTGAGGCTGTGAGATTAAGGATTCCTGCTGG 300  
QY 301 CATTCGGCTGTGGCCCTAGAGCAGAGCATGATTCATTAAGATTCCTCATTTCTTGG 360  
DB 301 CATTCGGCTGTGGCCCTAGAGCAGAGCATGATTCATTAAGATTCCTCATTTCTTGG 360  
QY 361 GAAGAGGAAGAGGCTTGTATGCTGTGTGATGAGTCTTCTTCTTCCCTCCGCTCAAG 420  
DB 361 GAAGAGGAAGAGGCTTGTATGCTGTGTGATGAGTCTTCTTCTTCCCTCCGCTCAAG 420  
QY 421 AAGCCCATAGTAGGGGCTCATTTGGGCTGTGCTTCAAGTCTTGAAGCATTCAGATC 480  
DB 421 AAGCCCATAGTAGGGGCTCATTTGGGCTGTGCTTCAAGTCTTGAAGCATTCAGATC 480  
QY 481 TTGCTCAGCTTTTCAACATCACTGATGCTTCAAGTCTTCAAGCAACATTCATGAT 540  
DB 481 TTGCTCAGCTTTTCAACATCACTGATGCTTCAAGTCTTCAAGCAACATTCATGAT 540  
QY 541 GACAGAAGCTCTGTTCAAAATATTTATGAGAGGTTGCTGCTTCAAGTCTCAAGCAAG 600  
DB 541 GACAGAAGCTCTGTTCAAAATATTTATGAGAGGTTGCTGCTTCAAGTCTCAAGCAAG 600  
QY 601 TCCATGTGTGACATATGTGAGAGGTAACAATGATGATGATGATGATGATGATGAT 660  
DB 601 TCCATGTGTGACATATGTGAGAGGTAACAATGATGATGATGATGATGATGATGAT 660  
QY 661 GGCAACTATGAGAAAGTGGGATGGAAGGCTTCAAGATGATGATGATGATGATGATGAT 720  
DB 661 GGCAACTATGAGAAAGTGGGATGGAAGGCTTCAAGATGATGATGATGATGATGATGAT 720  
QY 721 TGCAATGCTTCTTCAAAATCTACAGTATGACAGGAGAGCAAGCTTGTATGATGATG 780  
DB 721 TGCAATGCTTCTTCAAAATCTACAGTATGACAGGAGAGCAAGCTTGTATGATGATG 780  
QY 781 CTGAAGAAGCTCAAGATCACTTGGCCCAAGGCTGGGCTGTGCTTCACTTGTGAGG 840  
DB 781 CTGAAGAAGCTCAAGATCACTTGGCCCAAGGCTGGGCTGTGCTTCACTTGTGAGG 840  
QY 841 ATGACGGTGAAGGCTGTGATGATGAGGAGGCTTCAAGATGATGATGATGATGATGAT 900  
DB 841 ATGACGGTGAAGGCTGTGATGATGAGGAGGCTTCAAGATGATGATGATGATGATGAT 900  
QY 901 CTTCCTGGGCAAGGAGCAAGATGATGATGATGATGATGATGATGATGATGATGATG 960  
DB 901 CTTCCTGGGCAAGGAGCAAGATGATGATGATGATGATGATGATGATGATGATGATG 960  
QY 961 GAAGACAGAAAGAAATGCAAGGCTGCTTCTTCAAGGCTTGTGAGACATATTAACA 1020  
DB 961 GAAGACAGAAAGAAATGCAAGGCTGCTTCTTCAAGGCTTGTGAGACATATTAACA 1020  
QY 1021 AGTAGAGTCCCTGCTGCTGCAATGCCCCAGGCTTGAATCTTAAGAGCTTCAAGG 1080  
DB 1021 AGTAGAGTCCCTGCTGCTGCAATGCCCCAGGCTTGAATCTTAAGAGCTTCAAGG 1080  
QY 1081 ATCACTGAGTGAAGGAGCAAGGCTCATCTTA 1110  
DB 1081 ATCACTGAGTGAAGGAGCAAGGCTCATCTTA 1110

RESULT 2  
US-10-027-923-1  
; Sequence 1, Application US/10027923

Publication No. US20020142330A1  
GENERAL INFORMATION:  
APPLICANT: Brian Galtner Bates  
APPLICANT: Kamalaka Gulikota  
APPLICANT: Yuhong Xie  
APPLICANT: Janet Elizabeth Paulsen  
TITLE OF INVENTION: NOVEL GLUTAMATE RECEPTOR MODULATORY PROTEINS AND  
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND USES THEREFOR  
FILE REFERENCE: GNN-024  
CURRENT APPLICATION NUMBER: US/10/027,923  
PRIOR FILING DATE: 2001-12-21  
PRIOR APPLICATION NUMBER: 60/257,589  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: Patent Ver. 2.0  
SEQ ID NO 1  
LENGTH: 1823  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (4)..(1110)  
US-10-027-923-1  
Query Match 100.0%; Score 1110; DB 14; Length 1823;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGCTCTTCTGTGATCTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 60  
DB 4 ATGCTCTTCTGTGATCTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 63  
QY 61 CAGTCCAGTGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120  
DB 64 CAGTCCAGTGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 123  
QY 121 TTTTCTGTATCAACAGCTTCTGTGAGCAAGATTTCATAGAGAAAGTGTGGGCAATC 180  
DB 124 TTTTCTGTATCAACAGCTTCTGTGAGCAAGATTTCATAGAGAAAGTGTGGGCAATC 183  
QY 181 CGTGAACAGTATGACATTCAGAGAGTGGAGGCAATGCTTCAAGATTCCTTGAAGATCA 240  
DB 184 CGTGAACAGTATGACATTCAGAGAGTGGAGGCAATGCTTCAAGATTCCTTGAAGATCA 243  
QY 241 TCAGACCCCACTCTTGGCCCAATCACTGAGGCTGTGAGATTAAGGATTCCTGCTGG 300  
DB 244 TCAGACCCCACTCTTGGCCCAATCACTGAGGCTGTGAGATTAAGGATTCCTGCTGG 303  
QY 301 CATTCGGCTGTGGCCCTAGAGCAGAGCATGATTCATTAAGATTCCTCATTTCTTGG 360  
DB 304 CATTCGGCTGTGGCCCTAGAGCAGAGCATGATTCATTAAGATTCCTCATTTCTTGG 363  
QY 361 GAAGAGGAAGAGGCTTGTATGCTGTGTGATGAGTCTTCTTCTTCCCTCCGCTCAAG 420  
DB 364 GAAGAGGAAGAGGCTTGTATGCTGTGTGATGAGTCTTCTTCTTCCCTCCGCTCAAG 423  
QY 421 AAGCCCATAGTAGGGGCTCATTTGGGCTGTGCTTCAAGTCTTGAAGCATTCAGATC 480  
DB 424 AAGCCCATAGTAGGGGCTCATTTGGGCTGTGCTTCAAGTCTTGAAGCATTCAGATC 483  
QY 481 TTGCTCAGCTTTTCAACATCACTGATGCTTCAAGTCTTCAAGCAACATTCATGAT 540  
DB 484 TTGCTCAGCTTTTCAACATCACTGATGCTTCAAGTCTTCAAGCAACATTCATGAT 543  
QY 541 GACAGAAGCTCTGTTCAAAATATTTATGAGAGGTTGTGCTTCAAGTCTCAAGGCAAG 600  
DB 544 GACAGAAGCTCTGTTCAAAATATTTATGAGAGGTTGTGCTTCAAGTCTCAAGGCAAG 603  
QY 601 TCCATGTGTGACATATGTGAGAGGTAACAATGATGATGATGATGATGATGATGATGAT 660  
DB 604 TCCATGTGTGACATATGTGAGAGGTAACAATGATGATGATGATGATGATGATGATGAT 663  
QY 661 GGCAACTATGAGAAAGTGGGATGGAAGGCTTCAAGATGATGATGATGATGATGATGAT 720

Db	664	GGCAACTATGAGAAAGTGGATGGAAGCTTTCAAAAGTATGTCAAGCCAGAAAGGAGATT	723
Qy	721	TGCATGCCCCACTTTACAAAATCTTACAGTAAATGCAAGGAGAGACAGCTTTGATAGCTG	780
Db	724	TGCATGCCCCACTTTACAAAATCTTACAGTAAATGCAAGGAGAGACAGCTTTGATAGCTG	783
Qy	781	CTGAAGAAAGCTTCACAAAGTCACTTGCCCAAGGCCCGGGTGTGTGGCCTTACTTGTGAAGGC	840
Db	784	CTGAAGAAAGCTTCACAAAGTCACTTGCCCAAGGCCCGGGTGTGTGGCCTTACTTGTGAAGGC	843
Qy	841	ATGACGGTGAAGAGGCTGTGCTGATGAGCCCAATGAAGGCGCTGGGTCTATGATGAGGAATTTCTG	900
Db	844	ATGACGGTGAAGAGGCTGTGCTGATGAGCCCAATGAAGGCGCTGGGTCTATGATGAGGAATTTCTG	903
Qy	901	CTTCTGGGACAGGAAACAGATGCCATCTTATATGAGATCTCAAGAAACAGCATCCTATGG	960
Db	904	CTTCTGGGACAGGAAACAGATGCCATCTTATATGAGATCTCAAGAAACAGCATCCTATGG	963
Qy	961	GAAGACAGAAAGAAAATGCCCAAGTGCCTTCTTCAGGGTTTTGGAGACATTAACAGA	1020
Db	964	GAAGACAGAAAGAAAATGCCCAAGTGCCTTCTTCAGGGTTTTGGAGACATTAACAGA	1023
Qy	1021	AGTGAAGTCCGTGCTGCTGCAATGAGCCCAAGCCTCTGAATCTAGAGCTCAGTTCAAGGCC	1080
Db	1024	AGTGAAGTCCGTGCTGCTGCAATGAGCCCAAGCCTCTGAATCTAGAGCTCAGTTCAAGGCC	1083
Qy	1081	ATCACTGGACTGAAGGACAGGCTCATCTTA	1110
Db	1084	ATCACTGGACTGAAGGACAGGCTCATCTTA	1113

### RESULT 3

```

US-09-822-830A-61
Sequence 61, Application US/09822830A
Patent No. US20020142952A1
GENERAL INFORMATION:
APPLICANT: Genetics Institute, Inc.
APPLICANT: Wong, Gordon G.
APPLICANT: Clark, Hilary
APPLICANT: Fechtel, Kim
APPLICANT: Agostino, Michael J.
APPLICANT: Howes, Steven H.
APPLICANT: Resnick, Richard J.
APPLICANT: Gulukota, Kamalakara
APPLICANT: Graham, James R.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
FILE REFERENCE: GIN 6402
CURRENT APPLICATION NUMBER: US/09/822,830A
CURRENT FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/195,604
PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 631
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 61
LENGTH: 1788
TYPE: DNA
ORGANISM: Homo sapiens
US-09-822-830A-61

```

Query Match	99.8%	Score 1108	DB 10	Length 1788
Best Local Similarity	100.0%	Pred. No. 0		
Matches 1108	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY 3 GGTCTTGTGTCATCTCTCAGTCTTACTTTGAAAGAAGATGTCGATGGAGTGCACA 62  
Db 1 GGTCTTGTGTCATCTCTCAGTCTTACTTTGAAAGAAGATGTCGATGGAGTGCACA 60  
QY 63 GTCCAGTAGAGAGGGGTGGTGCACANCGTCGGTGCACATCATATTGAGACTCTCTT 122  
Db 61 GTCCAGTAGAGAGGGGTGGTGCACANCGTCGGTGCACATCATATTGAGACTCTCTT 120  
QY 123 TTCTCTTATCCACAGCTACTGTGTGACGAAAGTTCAATGAGAGGAAGTGTGGGCACTCCG 182

Db	121	TTCTGTTTCATACCAAGCTTACTGTGTGAGCAAGTTCTATGAGAGCAAGTGTGGGGCAGTCCG	180
OY	183	TGAACAGTATGGCAATTCAGAGATGTGAGGGCCATGTCTGCATACCTGTGAAGAGATCAATTC	242
Db	181	TGAACAGTATGGCAATTCAGAGATGTGAGGGCCATGTCTGCATACCTGTGAAGAGATCAATTC	240
OY	243	AGACCCCAACACTCTTGTGCCCAATCACACGTGGGCGTGTGAGATTAAGGGGATTCCTGTGTGCA	302
Db	241	AGACCCCAACACTCTTGTGCCCAATCACACTGGGCTGTGAGATTAAGGGGATTCCTGTGTGCA	300
OY	303	TTTCGGCTGTGGCCCTTAGAGCAGAGCAATTTAGATTCAATAAGATTCCCTCATTTCTTCGGA	362
Db	301	TTTCGGCTGTGGCCCTTAGAGCAGAGCAATTTAGATTCAATAAGATTCCCTCATTTCTTCGGA	360
OY	363	AGAGGAAGAAGGGCTTTGGTATGCTGTGTGAGATGGCTCCCTCTTCTTCCGCTCCAGAA	422
Db	361	AGAGGAAGAAGGGCTTTGGTATGCTGTGTGAGATGGCTCCCTCTTCTTCCGCTCCAGAA	420
OY	423	GCCCATAGTAGGGGTTCATTTGGGCGTGGTTCCAGTTCCTTTAGCCATTCAGTCCAGAAATTT	482
Db	421	GCCCATAGTAGGGGTTCATTTGGGCGTGGTTCCAGTTCCTTTAGCCATTCAGTCCAGAAATTT	480
OY	483	GCTCCAGCTTTTCAACATACCTCAAGATTGCTTACTCAGCAACCATCATGATCTGTAGTGA	542
Db	481	GCTCCAGCTTTTCAACATACCTCAAGATTGCTTACTCAGCAACCATCATGATCTGTAGTGA	540
OY	543	CAAGACTCTGTTCAAAATATTTCAAGAGGGTGTGGCTTCAATGCTGCAGAGGCAAGGTC	602
Db	541	CAAGACTCTGTTCAAAATATTTCAAGAGGGTGTGGCTTCAATGCTGCAGAGGCAAGGTC	600
OY	603	CATGTGTGACATYAGTGAAGAGGTACAACTGAGACCTATGTATCAGCCGTACACAGAAAG	662
Db	601	CATGTGTGACATYAGTGAAGAGGTACAACTGAGACCTATGTATCAGCCGTACACAGAAAG	660
OY	663	CAACTATGGAAGAAAGTGGGATGGAAGGCTTCAAAAGATATGTCAAGGAAGGAAGGGATTTG	722
Db	661	CAACTATGGAAGAAAGTGGGATGGAAGGCTTCAAAAGATATGTCAAGGAAGGAAGGGATTTG	720
OY	723	CATGCCCACTCTTACAAATCTACAGTATATGACAGGGAGCAGAGCTTTGATTAAGTCTCT	782
Db	721	CATGCCCACTCTTACAAATCTACAGTATATGACAGGGAGCAGAGCTTTGATTAAGTCTCT	780
OY	783	GAAAGAGTCACAAGTCACTTGGCCCAAGGCCCGGGGTGTGGCTTACTTCTGTGAGGGAT	842
Db	781	GAAAGAGTCACAAGTCACTTGGCCCAAGGCCCGGGGTGTGGCTTACTTCTGTGAGGGAT	840
OY	843	GACGGTGTGAGAGTCTGTGATGATGAGCAGATGAGGCGCTGGGCTTATGTGGGAGAAATTTCTCT	902
Db	841	GACGGTGTGAGAGTCTGTGATGATGAGCAGATGAGGCGCTGGGCTTATGTGGGAGAAATTTCTCT	900
OY	903	TCTGGGCAAGGAAACCAAGTGCATCTTTTATTGAGATCTCAAAAGAACAGCATCTATAGGGA	962
Db	901	TCTGGGCAAGGAAACCAAGTGCATCTTTTATTGAGATCTCAAAAGAACAGCATCTATAGGGA	960
OY	963	AGACAGAAAGAAATATGCCAAGGTGCTTCTTCAAGGTTTGGAGACATATTACACAGAG	1022
Db	961	AGACAGAAAGAAATATGCCAAGGTGCTTCTTCAAGGTTTGGAGACATATTACACAGAG	1020
OY	1023	TGAGTCCGTGTGTGCACATGTCCCAAGCCCTTGAAATCTTAGAGCTCAAGTTCAGGGCCCAT	1082
Db	1021	TGAGTCCGTGTGTGCACATGTCCCAAGCCCTTGAAATCTTAGAGCTCAAGTTCAGGGCCCAT	1080
OY	1083	CACGTGACTGAGGAGCAGGCTCATCTTAA	1110
Db	1081	CACGTGACTGAGGAGCAGGCTCATCTTAA	1108

## RESULT 4

US-10-346-241-1  
; Sequence 1, Application US/10346241  
; Publication No. US20030157647A1  
; GENERAL INFORMATION:





Db 181 CGTGAACAGTATGACATTCAGAGAGTGAAGGCCATGCTGATCACTCGTGAAGAGATCAAT 240  
 QY 241 TCAGACCCCACTCTTGGCCCAATCACTGAGGCTGTGAGATTAAGGATTCCTGCTGG 300  
 Db 241 TCAGACCCCACTCTTGGCCCAATCACTGAGGCTGTGAGATTAAGGATTCCTGCTGG 300  
 QY 301 CATTCGGCTGTGGCCCTTAAGCAGACGATTTAGATTCAAAAGATTCCCTCATTTCTTG 360  
 Db 301 CATTCGGCTGTGGCCCTTAAGCAGACGATTTAGATTCAAAAGATTCCCTCATTTCTTG 360  
 QY 361 GAAAGAGAAAGAGGCTGTGGATCTGTGAGATGAGGCTCTCTCTTCTTCTGCTCAAG 420  
 Db 361 GAAAGAGAAAGAGGCTGTGGATCTGTGAGATGAGGCTCTCTCTTCTTCTGCTCAAG 420  
 QY 421 AAGCCCATGTAGAGGCTCATTTGGGCTGGTTCAGTTCTTTAGCAATTCAGATTCAGAAAT 480  
 Db 421 AAGCCCATGTAGAGGCTCATTTGGGCTGGTTCAGTTCTTTAGCAATTCAGATTCAGAAAT 480  
 QY 481 TTGCTTCAGCTTTTCAACATACCTCAGATTGCTTACTCAGCAACCATCATGATCTGAGT 540  
 Db 481 TTGCTTCAGCTTTTCAACATACCTCAGATTGCTTACTCAGCAACCATCATGATCTGAGT 540  
 QY 541 GACAAAGACTCTGTTCAAATATTTCAATGAGGCTTGGCTTCAATGCTCAGATCCTCAG 600  
 Db 541 GACAAAGACTCTGTTCAAATATTTCAATGAGGCTTGGCTTCAATGCTCAGATCCTCAG 600  
 QY 601 TCCATGTTGAGACATAGTGAAGAGGTACACTGAGCCTATGATACAGCCCTGACACAGAA 660  
 Db 601 TCCATGTTGAGACATAGTGAAGAGGTACACTGAGCCTATGATACAGCCCTGACACAGAA 660  
 QY 661 GGCACATATGAGAAAGTGGAGTGAAGGCTTCAAAAGATATGTCAAGCAAGAAAGGATTT 720  
 Db 661 GGCACATATGAGAAAGTGGAGTGAAGGCTTCAAAAGATATGTCAAGCAAGAAAGGATTT 720  
 QY 721 TGCATGCCCCACTCTTCAAAATCTACAGTATGACAGGAGAGACGCTTTGATTAAGCTG 780  
 Db 721 TGCATGCCCCACTCTTCAAAATCTACAGTATGACAGGAGAGACGCTTTGATTAAGCTG 780  
 QY 781 CTGAAGAAGCTCAACAGTCACTTGGCCCAAGGCCCGGGGTGGTGGCTTACTTCTGTAGGGC 840  
 Db 781 CTGAAGAAGCTCAACAGTCACTTGGCCCAAGGCCCGGGGTGGTGGCTTACTTCTGTAGGGC 840  
 QY 841 ATGACGGTGAAGAGTCTGCTGATGAGGCGCTGAGGCTGCTGAGTGAAGAAATTTCTG 900  
 Db 841 ATGACGGTGAAGAGTCTGCTGATGAGGCGCTGAGGCTGCTGAGTGAAGAAATTTCTG 900  
 QY 901 CTTCTGGGCAAGGA 914  
 Db 901 CTTCTGGGCAAGGA 914  
 RESULT 6  
 US-10-225-567A-177  
 ; Sequence 177, Application US/10225567A  
 ; Publication No.: US20030113798A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lifespan Biosciences  
 ; APPLICANT: Brown, Joseph P.  
 ; APPLICANT: Burner, Glenn C.  
 ; APPLICANT: Roush, Christine L.  
 ; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS  
 ; FILE REFERENCE: 1920-4-4  
 ; CURRENT APPLICATION NUMBER: US/10/225,567A  
 ; PRIOR FILING DATE: 2001-12-19  
 ; PRIOR APPLICATION NUMBER: 60/257,144  
 ; NUMBER OF SEQ ID NOS: 2292  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 177  
 ; LENGTH: 4518  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-225-567A-177

Query Match 80.0%; Score 888.4; DB 15; Length 4518;  
 Best Local Similarity 98.2%; Pred. No. 3.6e-286;  
 Matches 898; Conservative 0; Mismatches 16; Indels 0; Gaps 0;  
 1 ATGCTCTTCTGTGATCTGATCTGATCTTACTTCTTGAAGAAAGATTCCTGGAGTGA 60  
 Db 151 ATGCTCTTCTGTGATCTGATCTGATCTTACTTCTTGAAGAAAGATTCCTGGAGTGA 210  
 QY 61 CAGTCCAGTGAAGAGAGGCTGTGCTCAATGCTGGGTGAATCATTTATTTGAGCTCTC 120  
 Db 211 CAGTCCAGTGAAGAGAGGCTGTGCTCAATGCTGGGTGAATCATTTATTTGAGCTCTC 270  
 QY 121 TTTTCTGTTCACTACAGCTCTCTGTGAGCAAGTTTATGAGAGAAAGTGGGGGAGTC 180  
 Db 271 TTTTCTGTTCACTACAGCTCTCTGTGAGCAAGTTTATGAGAGAAAGTGGGGGAGTC 330  
 QY 181 CGTGAACAGTATGAGATTCAGAGAGTGAAGGCCATGCTGCATACCTGGAAGAGATCAAT 240  
 Db 331 CGTGAACAGTATGAGATTCAGAGAGTGAAGGCCATGCTGCATACCTGGAAGAGATCAAT 390  
 QY 241 TCAGACCCCACTCTTGGCCCAATCACTGAGGCTGTGAGATTAAGGATTCCTGCTGG 300  
 Db 391 TCAGACCCCACTCTTGGCCCAATCACTGAGGCTGTGAGATTAAGGATTCCTGCTGG 450  
 QY 301 CATTCGGCTGTGGCCCTTAAGCAGACGATTTAGATTCAAAAGATTCCCTCATTTCTTG 360  
 Db 451 CATTCGGCTGTGGCCCTTAAGCAGACGATTTAGATTCAAAAGATTCCCTCATTTCTTG 510  
 QY 361 GAAAGAGAAAGAGGCTGTGGATCTGTGAGATGAGGCTCTCTCTTCTTCTGCTCAAG 420  
 Db 511 GAAAGAGAAAGAGGCTGTGGATCTGTGAGATGAGGCTCTCTCTTCTTCTGCTCAAG 570  
 QY 421 AAGCCCATGTAGAGGCTCATTTGGGCTGGTTCAGTTCTTTAGCAATTCAGATTCAGAAAT 480  
 Db 571 AAGCCCATGTAGAGGCTCATTTGGGCTGGTTCAGTTCTTTAGCAATTCAGATTCAGAAAT 630  
 QY 481 TTGCTTCAGCTTTTCAACATACCTCAGATTGCTTACTCAGCAACCATCATGATCTGAGT 540  
 Db 631 TTGCTTCAGCTTTTCAACATACCTCAGATTGCTTACTCAGCAACCATCATGATCTGAGT 690  
 QY 541 GACAAAGACTCTGTTCAAATATTTCAATGAGGCTTCAAAAGATATGTCAAGCAAGAAAGGATTT 600  
 Db 691 GACAAAGACTCTGTTCAAATATTTCAATGAGGCTTCAAAAGATATGTCAAGCAAGAAAGGATTT 750  
 QY 601 TCCATGTTGAGACATAGTGAAGAGGTACACTGAGCCTATGATACAGCCCTGACACAGAA 660  
 Db 751 TCCATGTTGAGACATAGTGAAGAGGTACACTGAGCCTATGATACAGCCCTGACACAGAA 810  
 QY 661 GGCACATATGAGAAAGTGGAGTGAAGGCTTCAAAAGATATGTCAAGCAAGAAAGGATTT 720  
 Db 811 GGCACATATGAGAAAGTGGAGTGAAGGCTTCAAAAGATATGTCAAGCAAGAAAGGATTT 870  
 QY 721 TGCATGCCCCACTCTTCAAAATCTACAGTATGACAGGAGAGACGCTTTGATTAAGCTG 780  
 Db 871 TGCATGCCCCACTCTTCAAAATCTACAGTATGACAGGAGAGACGCTTTGATTAAGCTG 930  
 QY 781 CTGAAGAAGCTCAACAGTCACTTGGCCCAAGGCCCGGGGTGGTGGCTTACTTCTGTAGGGC 840  
 Db 931 CTGAAGAAGCTCAACAGTCACTTGGCCCAAGGCCCGGGGTGGTGGCTTACTTCTGTAGGGC 990  
 QY 841 ATGACGGTGAAGAGTCTGCTGATGAGGCGCTGAGGCTGCTGAGTGAAGAAATTTCTG 900  
 Db 991 ATGACGGTGAAGAGTCTGCTGATGAGGCGCTGAGGCTGCTGAGTGAAGAAATTTCTG 1050  
 QY 901 CTTCTGGGCAAGGA 914  
 Db 1051 CTTCTGGGCAAGGA 1064  
 RESULT 7  
 US-09-826-509-346  
 ; Sequence 346, Application US/09826509

Publication No. US20030204073A1  
 GENERAL INFORMATION:  
 APPLICANT: Lehmann-Brulinsma, Karin  
 APPLICANT: Liaw, Chen W.  
 APPLICANT: Lin, I-Hsin  
 TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G  
 FILE REFERENCE: Protein-Coupled Receptors  
 CURRENT APPLICATION NUMBER: US/09/826,509  
 CURRENT FILING DATE: 2001-04-05  
 PRIOR APPLICATION NUMBER: 60/195,747  
 PRIOR FILING DATE: 2000-04-07  
 PRIOR APPLICATION NUMBER: 09/170,496  
 PRIOR FILING DATE: 1998-10-13  
 NUMBER OF SEQ ID NOS: 589  
 SOFTWARE: PatentIn Version 2.1  
 SEQ ID NO 346  
 LENGTH: 2634  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-09-826-509-346

Query Match 41.3%; Score 458.2; DB 13; Length 2634;  
 Best Local Similarity 72.5%; Pred. No. 3.9e-142;  
 Matches 611; Conservative 0; Mismatches 223; Indels 9; Gaps 1;

81 GGTGGCTACATGCTGGGTGACATCATTTATTTGAGCTCTCTTTCTGTTTCATCACCGCC 140  
 |||||  
 111 GGTGGCCAGATGACGAGATGTCATCATTTGAGCCCTCTTCTCATCATCACCGCC 170  
 |||||  
 141 TACTGTGACGAGATTGATGAGAGAGTGTGGGCGAGTCCGTTGAACAGATGAGCATTTCA 200  
 |||||  
 171 TCCGGCCGAGAAAGTGTCCGAGAGAGTGTGGGAGATAGAGGAGAGATGTGATCCCA 230  
 |||||  
 201 GAGAGTGAGAGCCATGCTGATACCTTGAAAGATCAATTCAGACCCCACTTTGCC 260  
 |||||  
 231 GAGGGTGAGAGCCATGTTCCACAGTTGATTAAGATCAAGCCGAGCCGGTCTCTGCC 290  
 |||||  
 261 CAACATCACTGGGCTGTGAGATTAAGGATTCCTGTGCTGCTTGGCTGTGGCCCTTGA 320  
 |||||  
 291 CAACATCACCTGGGCGATGAGATCCGGGACTCTGTGCTGCACTTTCGTTGGCTTGA 350  
 |||||  
 321 GCAGAGCATTTGATTTCAATAAGATTCCTCATTTCTTCGAAAGAGAGGAGCTTGT 380  
 |||||  
 351 ACAGAGCATTTGATTTCAATAAGATTCCTCATTTCTTCGAAAGAGAGGAGCTTGT 410  
 |||||  
 381 ATGC-----TCTGTGATGAGCTCTCTCTTCTTCTTCCGCTCAAGAGCCATAGT 431  
 |||||  
 411 CAACCGGTGTCTGCTGACGCGCAGTCCCTCCCGCCAGGACGACTAAGAGCCATTTGC 470  
 |||||  
 432 AGGGGTCAATGGGCTGTGCTTCAATTTTATGCAATTCAGATCCAGAAATTTGCTCCAGT 491  
 |||||  
 471 GGGAGTATGAGTCCCGCTCCAGCTCTGTAGCCATTCAGTCAAGTCAAGTCTCCAGCT 530  
 |||||  
 492 TTTCAACATCACTCAATGCTTACTCAGCAACCATATGATCTGAGTGAACAAGCTCT 551  
 |||||  
 531 CTTGCAATCCCCCAAGTCTCTTATTCAGCCACAAGATGAGCTGAGTGAACAATTTT 590  
 |||||  
 552 GTTCAATATTTTCAATGAGGCTTGTGCTTCAATGATCTCAGAGGCAAGTCTCATGTGA 611  
 |||||  
 591 GTCAATATCTTCTGAGGCTTGTGCTTCAATGATCTCAGAGGCAAGTCTCATGTGA 650  
 |||||  
 612 CATATGTAAGAGTGAAGTGAAGTATATATGAGCCGTACACACAAGAGCAATATGG 671  
 |||||  
 651 CATATGTAAGAGTGAAGTGAAGTATATATGAGCCGTACACACAAGAGCAATATGG 710  
 |||||  
 672 AGAAGTGAAGTGAAGTGAAGTGAAGTATATATGAGCCGTACACACAAGAGCAATATGG 731  
 |||||  
 711 GAGAGGCGAATGAGAGCTTTTCAAGAGCTGTGCTCCAGAGAGCCCTCTGTATGCGCCA 770  
 |||||  
 732 CTTTCAATCAATCTTCAATGAGTGAAGGAGCAAGCTTTGATTAAGCTGTGAAGAGCT 791  
 |||||  
 771 TTTGACAAATATCTTCAATGAGTGAAGGAGCAAGCTTTGATTAAGCTGTGAAGAGCT 830  
 |||||

792 CACAAGTCACTTGGCCCAAGCCGAGTGTGCTTCTGTTGAGGAGGATGACGCTGAG 851  
 |||||  
 831 CCGAGAGAGCTTCCCAAGGCTTAGAGTGTGTGCTCTCTGTGAGAGGATGACAGTGG 890  
 |||||  
 852 AGGTCTGTGATGAGCCATGAGGCGCTGTGATGAGGAAATTTGCTTGTGGCAG 911  
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 891 AGGATCTGTGAGGCGCATGCGGCGCTTGGCGTGTGAGGAGGAGTCTCATTTTGAAG 950  
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 912 GGA 914  
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 951 TGA 953

# RESULT 8 US-10-101-510-258

Sequence 258, Application US/10101510  
 Publication No. US20030148295A1

GENERAL INFORMATION:

APPLICANT: MAN, JACKSON

APPLICANT: WANG, YIXIN

TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE

FILE REFERENCE: 15117.0012

CURRENT APPLICATION NUMBER: US/10/101,510

CURRENT FILING DATE: 2002-03-20

PRIOR APPLICATION NUMBER: 60/276,947

PRIOR FILING DATE: 2001-03-20

NUMBER OF SEQ ID NOS: 805

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 258

LENGTH: 3295

TYPE: DNA

ORGANISM: Homo sapiens

US-10-101-510-258

Query Match 41.3%; Score 458.2; DB 13; Length 3295;  
 Best Local Similarity 72.5%; Pred. No. 4.4e-142;  
 Matches 611; Conservative 0; Mismatches 223; Indels 9; Gaps 1;

81 GGTGGCTACATGCTGGGTGACATCATTTATTTGAGCTCTCTTTCTGTTTCATCACCGCC 140  
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 481 GGTGGCCAGATGACGAGATGTCATCATTTGAGCCCTCTTCTCATCATCACCGCC 540  
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 141 TACTGTGACGAGATTGATGAGAGAGTGTGGGCGAGTCCGTTGAACAGATGAGCATTTCA 200  
 |||||  
 541 TCCGGCCGAGAAAGTGTCCGAGAGAGTGTGGGAGATTAAGGAGAGATGTGATCCCA 600  
 |||||  
 201 GAGAGTGAGAGCCATGCTGATACCTTGAAAGATCAATTCAGACCCCACTTTGCC 260  
 |||||  
 601 GAGGGTGAGAGCCATGTTCCACAGTTGATTAAGATCAAGCCGAGCCGGTCTCTGCC 660  
 |||||  
 261 CAACATCACTGGGCTGTGAGATTAAGGATTCCTGTGCTGCTTCCGCTGTGGCCCTTGA 320  
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 661 CAACATCACCTGGGCGATGAGATCCGGGACTCTGTGCTGCACTTTCGTTGGCTTGA 720  
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 321 GCAGAGCATTTGATTTCAATAAGATTCCTCATTTCTTCGAAAGAGAGGAGCTTGT 380  
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 721 ACAGAGCATTTGATTTCAATAAGATTCCTCATTTCTTCGAAAGAGAGGAGCTTGT 780  
 |||||  
 381 ATGC-----TCTGTGATGAGCTCTCTCTTCTTCTTCCGCTCAAGAGCCATAGT 431  
 |||||  
 781 CAACCGGTGTCTGCTGACGCGCAGTCCCTCCCGCCAGGACGACTAAGAGCCATTTGC 840  
 |||||  
 432 AGGGGTCAATGGGCTGTGCTTCAATTTTATGCAATTCAGATCCAGAAATTTGCTCCAGT 491  
 |||||  
 841 GGGAGTATGAGTCCCGCTCCAGCTCTGTAGCCATTCAGTCAAGTCAAGTCTCCAGCT 900  
 |||||  
 492 TTTCAACATCACTCAATGCTTACTCAGCAACCATATGATCTGAGTGAACAAGCTCT 551  
 |||||  
 901 CTTGCAATCCCCCAAGTCTCTTATTCAGCCACAAGATGAGCTGAGTGAACAATTTT 960  
 |||||  
 552 GTTCAATATTTTCAATGAGGCTTGTGCTTCAATGATCTCAGAGGCAAGTCTCATGTGA 611  
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Db 961 GTACAAATCTTCCTGAGGGTGTCCCTTGTGACATTTGCAAGGCAAGGCCAATGCTTGA 1020  
Qy 612 CATAGTGAAGAGGATCAACTGACCTATGTATGACCGCTACACAGAGGCAACTATGG 671  
Db 1021 CATAGTGAAGAGGATCAACTGACCTATGTATGACCGCTACACAGAGGCAACTATGG 1080  
Qy 672 AGAAGTGGAGTGAAGACCTTCAAGATATGTACAGCAAGAAAGGATTTGACGCCA 731  
Db 1081 GGAGAGGAGATGAGACCTTTCAAGAGCTGCGTCCAGAGAAAGCCTCTGTATCGCCA 1140  
Qy 732 CTCTTCAAAATCTACAGTAATGAGGAGAGAGAGCTTTGATAGCTGTGAAAGACT 791  
Db 1141 TTCTGCAAAATCTACAGCAACGCTGAGGAGAAAGAGCTTGAACGACTTGGCAAACT 1200  
Qy 792 CACAAGTCACTTGGCCCAAGGCGCGGTGTGCTTACTTCTGTAGAGGCAATGACGCTGAG 851  
Db 1201 CCGAGAGAGGCTTCCCAAGGCTAGAGTGTGCTTCTGTGAAAGCAATGACAGTGC 1260  
Qy 852 AGGTCTGCTGATGGCCATGAGGCGCTGGGCTAGTGGAGAAATTTCTGCTTGGGCGAG 911  
Db 1261 AGGACTCTTGAAGCGCCATGCGCGCCCTTGGCGTGTGGGAGATTCTCATCTATGGAG 1320  
Qy 912 GGA 914  
Db 1321 TGA 1323

RESULT 9  
US-10-225-567A-169  
; Sequence 169, Application US/10225567A  
; Publication No. US20030113798A1  
; GENERAL INFORMATION:  
; APPLICANT: Lifespan Biosciences  
; APPLICANT: Brown, Joseph P.  
; APPLICANT: Burmer, Glennia C.  
; APPLICANT: Roush, Christine L.  
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS  
; FILE REFERENCE: 1920-4-4  
; CURRENT APPLICATION NUMBER: US/10/225,567A  
; CURRENT FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 60/257,144  
; PRIOR FILING DATE: 2000-12-19  
; NUMBER OF SEQ ID NOS: 2292  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 169  
; LENGTH: 6619  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; US-10-225-567A-169

Query Match 41.3%; Score 458.2; DB 15; Length 6619;  
Best Local Similarity 72.5%; Pred. No. 6.5e-142;  
Matches 611; Conservative 0; Mismatches 223; Indels 9; Gaps 1;

Qy 81 GGTGGCTCACATGCTGGGATGACATATTATGAGGCTCTTTTCTGTGATACACCGCC 140  
Db 346 GGTGGCTCACATGAGCAAGATGATCATATGAGCCCTCTTCTCATCTACACCGCC 405  
Qy 141 TACTGTGAGCAAGATTATGAGAGAGAGTGTGGGCGAGTCCGTGAACATATGATGCA 200  
Db 406 TCCGGCCGAAGAGTGTCCGAGAGAGAGTGTGGGAGATCATGGAGAGCATATGGCA 465  
Qy 201 GAGAGTGGAGGCGCATGCTGATACCTCTGGAAGAGATTAATTCAGACCCCACTTTGCC 260  
Db 466 GAGGGTGGAGGCGCATGCTGATACCTCTGGAAGAGATTAATTCAGACCCCGCTCTCCGCC 525  
Qy 261 CACATCACTGGGCTGTGAGATTAAGGATTCCTGTGGCAATTCGGCTGGCCCTAGA 320  
Db 526 CACATCACTGGGCTGTGAGATTAAGGATTCCTGTGGCAATTCGGCTGGCCCTAGA 585  
Qy 321 GCAAGCATTTAGTTCTAATGAAGATTCCTCATTTCTTGGAAAGAGAGAGGCTTGGT 380  
Db 586 ACAGAGCATTTAGTTCTAATGAAGATTCCTCATTTCTTGGAAAGAGAGAGGAT 645

Qy 381 ATGC-----TCTGTGAGATGCTCTTCCTTCCGCTCCAGAAAGCCATAGT 431  
Db 646 CAACCGGTGTCTCTGTGAGCGCCAGATCTCTCCCAAGGAGACTTAAGAGCCATTTGC 705  
Qy 432 AGGGTCAATTTGGGCTGTGTTCAGATTCCTTATGACATTCAGATTCAGATTTGCTCAGCT 491  
Db 706 GGAAGTATGATGATCGCGGCTCCAGCTCTGTAGCATTTCAAGTACAGAACTGTCCAGCT 765  
Qy 492 TTTCACATCACTCAATTTGCTTACTGAGCAACATCATGATGATGTGATGACAACTCT 551  
Db 766 CTTCGACATCCCAATGCTTATTCAGCCACAAACATGACCTGTGATGACAAACTTT 825  
Qy 552 GTTCAAAATTTTCATAGAGGTTGTGCTTCAGATTCCTGACAGCAAGGCTCCATTTGGA 611  
Db 826 GTACAAATATCTTCTGAGAGGTTGTCTTCTGTGACATTTGCAAGGCGCAATGCTTGA 885  
Qy 612 CATATGAAGAGGATCAACTGACCTATATGATGACCGCTACACAGAAAGCAACTATGG 671  
Db 886 CATATGAAGAGGATCAACTGACCTATATGATGACCGCTACACAGAAAGCAACTATGG 945  
Qy 672 AGAAGTGGAGTGAAGCTTCAAGATATGTCAGCGAAGAGAAAGGATTTGCAATCGCCA 731  
Db 946 GGAGAGCGAATGAGCGCTTCAAGAGCTGCGTCCAGAAAGGCGCTGTATCGCCA 1005  
Qy 732 CTCTTCAAAATCTACAGTAATGACAGGAGAGAGAGCTTTGATAGCTGTGAAGAGCT 791  
Db 1006 TTCTGCAAAATCTACAGCAACGCTGAGGAGAAAGCTTTGACCACTTGTGGCAACT 1065  
Qy 792 CACAAGTCACTTGGCCCAAGGCGCGGTGTGCTTACTTGTGAGGCGATGACGCTGAG 851  
Db 1066 CCGAGAGAGGCTTCCCAAGGCTAGAGTGTGTCTGCTTGTGAAAGGATGACAGTGC 1125  
Qy 852 AGGTCTGCTGATGGCCATGAGGCGCTGGGCTAGTGGAGAAATTTCTTGGGCGAG 911  
Db 1126 AGGACTCTGAGCGCATGCGCGCTTGGCGTGTGGGCGAGTTCTCATCTATGGAG 1185  
Qy 912 GGA 914  
Db 1186 TGA 1188

RESULT 10  
US-10-300-473-3  
; Sequence 3, Application US/10300473  
; Publication No. US20030113873A1  
; GENERAL INFORMATION:  
; APPLICANT: STORMANN, THOMAS M.  
; APPLICANT: STORMANN, THOMAS M.  
; APPLICANT: HAMMERLAND, LANCE G.  
; APPLICANT: FULLER, FORREST H.  
; APPLICANT: KAPCHO, KAREN J.  
; TITLE OF INVENTION: CHIMERIC RECEPTORS AND METHODS FOR IDENTIFYING  
; TITLE OF INVENTION: COMPOUNDS ACTIVE AT METABOTROPIC GLUTAMATE  
; TITLE OF INVENTION: RECEPTORS AND THE USE OF SUCH COMPOUNDS IN THE  
; FILE REFERENCE: TREATMENT OF NEUROLOGICAL DISORDERS AND DISEASES  
; CURRENT APPLICATION NUMBER: US/10/300,473  
; CURRENT FILING DATE: 2003-02-21  
; PRIOR APPLICATION NUMBER: 09/435,897  
; PRIOR FILING DATE: 1999-11-08  
; PRIOR APPLICATION NUMBER: 08/687,289  
; PRIOR FILING DATE: 1996-07-25  
; PRIOR APPLICATION NUMBER: 60/001,526  
; PRIOR FILING DATE: 1995-07-26  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 3219  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthesized rat









PRIOR FILING DATE: 1993-09-20  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 1  
LENGTH: 2736  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..(2736)  
US-10-331-289-1

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Best Local Similarity	55.7%	Pred. No.	1.1e-36				
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						Gaps	2

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QY 229 GAAAGGATCAATTAGACCCCACTCTTGCCCAATCAACTGAGGCTGTGAGATAGG 288

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QY 289 GATTTCCTGCTGGCATTTGGGCTGTGGCCCTTAAGACAGACATTGATTTATTAAGATTCC 348

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QY 349 CTCATTTCTTGGAGAGAGAGGCGTTGGATGTCTGTGGAATGGCTCTCTCTTCC 408

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QY 409 TTCGCTCCAAAGAGCCCAATGATAGGGAGTCATTGGGCTGTTCAGTTCTTTAGCCATT 468

Db 430 ATCAACCAAGCCTGAACGTGTGGGTGTTCATCGGTCTTCAAGAGAGCTGGTCTCATC 489

QY 469 CAGGTCCAGAAATTGCTCCAGCTTTTCAACATACCTCAAGATTGCTTACTCAGAACCATC 528

Db 490 ATGTGTGGCCAAATCTTCCTGCTCTTTCAGAAATACCCCAATCAGCTACGCTTCCACAGCG 549

QY 529 ATGATCTGAGTGACAGAAGCTCTGTTCAAAATATTTTCATGAGGGGTGTGCTTCAGATGCT 588

Db 550 CCAAGACTGAGTGACAAAGCCGCTACAGCTTCTTCCCGCGTGGTGGCCCTTGACACG 609

QY 589 CAGCAGGCAAGGTTCATGTGTGACATAGTAAGAAGGTACAATGGAACCTTAATATATCAGCC 648

Db 610 TACCAAGGCCAGGCGCATGTGTGACATCGTCCGAGCCCTCAAGTGGAACATAATGTGCACA 669

QY 649 GTACACACAGAAAGGCACTATGTGAGAAAGTGGAGTGAAGCCTTCAAGATATGTCAAGC 708

Db 670 GTGGCTCTGGAGGGCAGCTATGTGTGAGACGGGTGTGAGAGGCTTTCATCCAGAGTCCGT 729

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Db 730 GAGGACGGGGCGGTGTGATGCGCCAGTGGTGGAAT 767

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GenCore version 5.1.6  
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OW protein - nucleic search, using frame\_plus\_p2n model

Run on: December 14, 2003, 21:52:04 ; Search time 415 Seconds  
(without alignments)  
2935.200 Million cell updates/sec

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Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 2201672 seqs, 1661799599 residues

Total number of hits satisfying chosen parameters: 4403344

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

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-DB=Published Applications NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1  
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Database :

Published Applications NA:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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1	1873	100.0	1110	14	US-10-027-923-3	Sequence 3, Appl1
2	1873	100.0	1823	10	US-10-027-923-1	Sequence 1, Appl1
3	1868	99.7	1786	14	US-09-822-830A-61	Sequence 61, Appl1
4	1484.5	79.3	2826	13	US-10-346-241-1	Sequence 1, Appl1
5	1484.5	79.3	3129	13	US-10-346-241-5	Sequence 5, Appl1
6	1484.5	79.3	4518	13	US-10-225-567A-177	Sequence 177, Appl1
7	1118.5	59.7	2634	13	US-09-826-509-346	Sequence 346, App
8	1118.5	59.7	3295	13	US-10-101-510-258	Sequence 258, App
9	1118.5	59.7	6669	13	US-10-225-567A-159	Sequence 169, App
10	1117.5	59.7	3219	15	US-10-300-473-4	Sequence 4, Appl1
11	1117.5	59.7	3384	15	US-10-300-473-1	Sequence 1, Appl1
12	1117.5	59.7	3830	10	US-10-300-714A-1	Sequence 1, Appl1
13	550	29.4	2830	10	US-09-900-714A-1	Sequence 1, Appl1
14	548	29.3	3321	13	US-10-353-699-85	Sequence 85, Appl1
15	548	29.3	3321	10	US-10-225-567A-183	Sequence 183, App
16	546.5	29.2	2736	10	US-09-817-464-1	Sequence 0, Appl1
17	546.5	29.2	2736	15	US-10-331-289-1	Sequence 1, Appl1
18	546.5	29.2	3884	10	US-09-820-809-14	Sequence 14, Appl1
19	546.5	29.2	3884	15	US-10-225-567A-175	Sequence 175, App
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21	538.5	28.8	2745	10	US-09-817-464-11	Sequence 11, Appl1
22	538.5	28.8	2745	15	US-10-331-289-11	Sequence 11, Appl1
23	538.5	28.8	2748	15	US-10-083-168-7	Sequence 7, Appl1
24	538.5	28.8	2748	15	US-10-083-168-66	Sequence 66, Appl1
25	538.5	28.8	2748	15	US-10-083-168-68	Sequence 68, Appl1
26	538.5	28.8	2748	15	US-10-083-168-70	Sequence 70, Appl1
27	538.5	28.8	2748	15	US-10-083-168-72	Sequence 72, Appl1
28	538.5	28.8	2766	10	US-09-817-464-13	Sequence 13, Appl1
29	538.5	28.8	2766	10	US-10-331-289-13	Sequence 13, Appl1
30	538.5	28.8	4312	15	US-10-225-567A-181	Sequence 181, App
31	532	28.4	2621	13	US-10-251-667-3	Sequence 3, Appl1
32	532	28.4	2621	15	US-10-225-567A-171	Sequence 171, App
33	525.5	28.1	6122	15	US-10-225-567A-179	Sequence 179, App
34	522	27.9	3410	15	US-10-225-567A-173	Sequence 173, App
35	511.5	27.3	3804	15	US-09-817-464-3	Sequence 3, Appl1
36	511.5	27.3	3804	15	US-10-331-289-3	Sequence 3, Appl1
37	381.5	20.4	2295	15	US-10-346-241-3	Sequence 3, Appl1
38	381.5	20.4	3783	14	US-10-002-854-1	Sequence 1, Appl1
39	381.5	20.4	3783	15	US-10-225-567A-117	Sequence 117, App
40	381.5	20.4	4000	15	US-10-300-473-2	Sequence 2, Appl1
41	379.5	20.3	3237	9	US-09-727-205-1	Sequence 1, Appl1
42	362.5	19.4	2877	15	US-10-151-208-1	Sequence 1, Appl1
43	361	19.3	3824	15	US-10-125-776-11	Sequence 11, Appl1
44	361	19.3	3824	15	US-10-125-776-11	Sequence 11, Appl1
45	361	19.3	3824	15	US-10-125-772-11	Sequence 11, Appl1

#### ALIGNMENTS

RESULT 1  
US-10-027-923-3  
Sequence 3, Application US/10027923  
Publication No. US20020142330A1  
GENERAL INFORMATION:  
APPLICANT: Brian Galtner Bates  
APPLICANT: Kamataka Gutukota  
APPLICANT: Yuhong Xie  
TITLE OF INVENTION: NOVEL GLUTAMATE RECEPTOR MODULATORY PROTEINS AND  
FILE REFERENCE: GNM-024  
CURRENT APPLICATION NUMBER: US/10/027, 923  
CURRENT FILING DATE: 2001-12-21  
PRIOR APPLICATION NUMBER: 60/257,589  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 3  
LENGTH: 1110  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS

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: LOCATION: (1) .. (1110)
US-10-027-923-3

Alignment Scores:
Pred. No.: 4,44e-231 Length: 1110
Score: 1873.00 Matches: 369
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-027-923-2 (1-369) x US-10-027-923-3 (1-1110)

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Qy 21 GlnSerSerGluArgArgValAlaAlaMetLeuGlyAspIleIleIleGlyAlaLeu 40
Db 61 CAGTCCAGTGAGAGAGAGGTGGTGCATGCTGGGTGACATATTATGGAGCTCTC 120

Qy 41 PheSerValHisHisGlnProThrValAspGluValHisGluArgGlySerGlyAlaVal 60
Db 121 TTTTCTGTTTCATCACCGCTACTGTCGAGCAAGTTTCATGAGAGAGTGTGGGCTC 180

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Db 181 CGTGAACAGTATGGCATTCACAGAGTGGAGGCAATGCTGCACTCGAAGAGATCAAT 240

Qy 81 SerAspProThrLeuLeuProAsnIleThrLeuGlyCysGluIleArgAspSerCysTrp 100
Db 241 TCAGACCCCACTCTTGGCCCAATCACTGGGCTGTGAGATTAAGGATTCCTGCTGG 300

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Db 301 CATTCGGCTGTGGCTTACAGAGCAGAGCATTGAGTTCTAAGAGATTCCTCATTTCTTCG 360

Qy 121 GluGluGluGluGluLeuValCysSerValAspGlySerSerSerSerPheArgSerIle 140
Db 361 GAGAGAGAGAGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420

Qy 141 LysProIleValGlyValIleGlyProGlySerSerSerSerLeuAlaIleGlnValGlnAsn 160
Db 421 AAGCCCATATGATAGGGGCTCATTTGGGCTGTGCTTCAAGTTCTTATGACATTCAGTCCAGAT 480

Qy 161 LeuLeuGlnLeuPheAsnIleProGlnIleAlaTyrSerAlaThrIleMetAspLeuSer 180
Db 481 TTGCTCCAGCTTTTCAACATACCTCAGATTGCTTACTCAGCAACCATCATGATGATCTGAGT 540

Qy 181 AspLysThrLeuPheLysTyrPheMetArgValValProSerAspAlaGlnIleAlaArg 200
Db 541 GACAGAGCTTGTTCANAATTTTCATGAGAGGTGTGCTTCAGATGCTCAGGAGGAGG 600

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Qy 221 GlyAsnTyrGlyLeuSerGlyMetGluAlaPheLysPheMetSerAlaLysGlyGlyTle 240
Db 661 GGCACACTATGAGAAAGTGGAGTGGAGGCTTCAAAATATGTCAGAGGAGAGAGGAGGATTT 720

Qy 241 CysIleIleHisSerTyrLysIleTyrSerAspAlaGlyGluGlnSerPheAspValLeu 260
Db 721 TGCATGCCCACTCTTACANAATTTTCATGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780

Qy 261 LeuLysLeuLeuThrSerHisLeuProLysAlaArgValValAlaTyrPheCysGlyGly 280
Db 781 CTGAAGAGAGTCACTCACTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 840

Qy 281 MetThrValArgGlyLeuLeuMetAlaMetArgArgLeuGlyLeuValGlyGluPheLeu 300
Db 841 ATGACGAGTGAAGAGTGTGATGAGCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900

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Qy 301 LeuLeuGlyValArgGluProAspAlaIlePheIleGluIleSerTyrAsnSerIleLeuTrp 320
Db 901 CTTTGGGAGGAGAGACCATGATGCCATCTTATTGAGATCTCAAGAGACATCTATGG 960

Qy 321 GluAspArgArgGlyCysGlnGlyArgPheLeuGlnGlyPheGlyAspIleLeuHisArg 340
Db 961 GAAAGACAGAAAGAAATGCCAAAGTCCCTTCCAGGGTTTGGAGACATATTACACAGA 1020

Qy 341 SerGluSerValLeuLeuHisMetProGlnProLeuAsnLeuGluLeuSerSerGlyPro 360
Db 1021 AGTGAAGTCCGTGTGCTGACATGATGCCCCAGCCTTGAATCTAAGGCTCAGTTCAAGGCCC 1080

Qy 361 IleThrGlyLeuArgAspArgLeuIle 369
Db 1081 ATCAGTGAAGTGAAGGAGAGGCTCATC 1107

RESULT 2
US-10-027-923-1
: Sequence 1, Application US/10027923
: Publication No. US2002014230A1
: GENERAL INFORMATION:
: APPLICANT: Brian Gaither Bates
: APPLICANT: Kamalaka Gulukota
: APPLICANT: Yuhong Xie
: APPLICANT: Janet Elizabeth Paulsen
: TITLE OF INVENTION: NOVEL GLUTAMATE RECEPTOR MODULATORY PROTEINS AND
: TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND USES THEREFOR
: FILE REFERENCE: GSN-024
: CURRENT APPLICATION NUMBER: US/10/027,923
: CURRENT FILING DATE: 2001-12-21
: PRIOR APPLICATION NUMBER: 60/257,589
: PRIOR FILING DATE: 2000-12-22
: NUMBER OF SEQ ID NOS: 6
: SOFTWARE: Patentin Ver. 2.0
: SEQ ID NO 1
: LENGTH: 1823
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (4) .. (1110)
: US-10-027-923-1

Alignment Scores:
Pred. No.: 9,94e-231 Length: 1823
Score: 1873.00 Matches: 369
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-027-923-2 (1-369) x US-10-027-923-1 (1-1823)

Qy 1 MetValLeuLeuLeuLeuSerValLeuLeuLeuLeuValArgGlySerAla 20
Db 4 ATGGCTCTTGTGTTGATCTGCTGCTGCTTTTGAAGAAGATGCTCGGAGATGCA 63

Qy 21 GlnSerSerGluArgArgValAlaAlaMetLeuGlyAspIleIleIleGlyAlaLeu 40
Db 64 CAGTCCAGTGAGAGAGGTGGTGCATGCTGGGTGACATCTTATTGAGCTCTC 123

Qy 41 PheSerValHisHisGlnProThrValAspGluValHisGluArgGlySerGlyAlaVal 60
Db 124 TTTTCTGTTTCATCACCGCTACTGTCGAGCAAGATTCATGAGAGAGTGTGGGCACTC 183

Qy 61 ArgGluGlnTyrGlyIleGlnArgValGluAlaMetLeuHisThrLeuGluArgIleAsn 80
Db 184 CGTGAACAGTATGGCATTCACAGAGTGGAGGCAATGCTGATCCTGGAAGAGATCAAT 243

Qy 81 SerAspProThrLeuLeuProAsnIleThrLeuGlyCysGluIleArgAspSerCysTrp 100
Db 244 TCAGACCCCACTCTTGGCCCAATCACTGGGCTGTGAGATTAAGGATTCCTGCTGG 303

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QY 101 Hisservalalaleuuglunserileglupheilaargaspserleuileser 120
DB 304 CATTGGCTGTGGCCCTAGAGGACATTGATTCATAGAAATCCCTCATTTCTTG 363
QY 121 GIUGLUGLUGLUGLUGLUGLUGLUGLUGLUGLUGLUGLUGLUGLUGLUGL 140
DB 364 GAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 423
QY 141 LysProIleValIleValIleValIleValIleValIleValIleValIle 160
DB 424 AAGCCCATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 483
QY 161 LeuleuGlnLeuPheAsnIleProGlnIleAlaIleAlaIleAlaIleAla 180
DB 484 TTGCTCCACACTTTTCAACATACCTCAGATTGCTTACTACGACCACTCATG 543
QY 181 AaplyrThLeuPheIlePheMetArgValIleProSerAspAlaGlnIle 200
DB 544 GACAGAGACTCTGTTCAAAATATTTCAAGAGGAGGAGGAGGAGGAGGAGG 603
QY 201 SerMetValAspIleValIleValIleValIleValIleValIleValIle 220
DB 604 TCATAGTGTGACATGATGAAAGAGTACACTGAGCCTATGATCAGCCGTAACA 663
QY 221 GlyAsnIleGlyGlnSerGlyMetGluAlaPheIleAspMetSerAlaIle 240
DB 664 GGCACCTATGAGAAAGTGGAGTGAAGAGCTTCAAAAGATATGTACAGCAAG 723
QY 241 CysIleAlaHisSerIleIleIleIleIleIleIleIleIleIleIleIle 260
DB 724 TGCATGCCCACTCTTACAAATCTACATGATGAGGAGGAGGAGGAGGAGG 783
QY 261 LeuIleValLeuIleTherIlePheIlePheIlePheIlePheIlePhe 280
DB 784 CGGAAAGACCTCAAGATCACTTCCCAAGGCGCGGAGTGGCTTCTGTGAG 843
QY 281 MetThValArgIleLeuLeuMetAlaMetArgArgLeuIleValIleGlu 300
DB 844 ATGACGCTGAGAGCTGTGCTGATGCGCAGAGGCGCTGCTTATGAGGAAT 903
QY 301 LeuLeuIleArgGlnProAspAlaIlePheIleIleIleIleIleIleIle 320
DB 904 CTTCTGGGACGAGAAACCAATGCGCATTTATGAGATCTCAAGAACAGCA 963
QY 321 GluAspArgArgIleGlyGlnIleGlyGlnIleGlyGlnIleGlyGlnIle 340
DB 964 GAAGACAGAAAGAAAGCAAGGTCCTTCCAGGCTTTGGAGACATATTACA 1023
QY 341 SerGlnSerValLeuLeuHisMetProGlnProLeuAsnLeuGlnLeuSer 360
DB 1024 AGTGAATCCGCTGCTGCAATGCCCCAGCCTTGAATCTAGAGCTCAAGTT 1083
QY 361 IleThrGlyLeuArgAspArgLeuIle 369
DB 1084 ATCACTAGAGTGAAGGAGCAAGGCTCATC 1110

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RESULT 3
US-09-822-830A-61
; Sequence 61, Application US/09822830A
; Patent No. US20020142952A1
; GENERAL INFORMATION:
; APPLICANT: Genetics Institute, Inc.
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechtel, Kim
; APPLICANT: Agostino, Michael J.
; APPLICANT: Howes, Steven H.
; APPLICANT: Resnick, Richard J.
; APPLICANT: Gulukota, Kamalakari
; APPLICANT: Graham, James R.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
; FILE REFERENCE: GIN 6402
; CURRENT APPLICATION NUMBER: US/09/822,830A

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; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195,604
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 631
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 61
; LENGTH: 1788
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-830A-61

Alignment Scores:
Pred. No.: 4,25e-230 Length: 1788
Score: 1868.00 Matches: 368
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.73% Indels: 0
DB: 10 Gaps: 0

US-10-027-923-2 (1-369) x US-09-822-830A-61 (1-1788)
QY 2 ValLeuLeuLeuIleLeuSerValLeuLeuLeuIleValIleValIleValIle 21
DB 2 GTCTTCTGTGATCCTGTCAGTCTTATTTGAAAGAAAGATCCGCTGGAGTGCA 61
QY 22 SerSerGluArgArgValValAlaHisMetLeuGlyAspIleIleIleValIle 41
DB 62 TCAGTGAAGAGAGAGGAGTGGCTGCATGCTGGGAGATCATATTAATGAGCTCT 121
QY 42 SerValIleHisGlnProThrValAspGluValHisGluArgIleGlyAlaVal 61
DB 122 TCTGTTTATCACCAGCTCTGTGACAGAGTTTCAATGAGAGAGAGTGGCAGT 181
QY 62 GluGlnIleGlyIleGlnArgValGluAlaMetLeuHisThrLeuGluArgIle 81
DB 182 GAACAGTATGAGATTCAGAGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAG 241
QY 82 AspProThrLeuLeuProAsnIleThrLeuGlyCysGlnIleArgAspSerCys 101
DB 242 GACCCCACTCTTGGCCCAATCACTGAGCTGAGATTAAGAGATTCCTGCTGG 301
QY 102 SerAlaValAlaLeuGlnIleSerIleGluPheIleArgAspSerLeuIleSer 121
DB 302 TGGCTGTGGCCCTTACAGAGAGCATTTGATTCATTAAGAGATTCCTCATTT 361
QY 122 GluGlnGluGlyLeuValCysSerValAspGlySerSerSerSerPheArg 141
DB 362 GAGAAAGAGGCTTGGTATGCTCTGTGATGCTCTCTCTTCCGCTCCAGAA 421
QY 142 ProIleValIleValIleGlyProGlySerSerSerLeuAlaIleGlnVal 161
DB 422 CCCATAGTGAAGGAGTATGGGCTGCTCAATTTCTTTCAGATTCAGAGATT 481
QY 162 LeuGlnLeuPheAsnIleProGlnIleAlaIleIleAlaIleThrIleMet 181
DB 482 CTCACCTTTTCAACATACCTCAGATTGCTTACTGCAACATCAATGAGATT 541
QY 182 LysThrLeuPheIlePheMetArgValIleProSerAspAlaGlnIleArg 201
DB 542 AAGACTCTGTCAAAATATTATTCATGAGGCTGTGCTTCAGATGCTCAGCA 601
QY 202 MetValAspIleValIleValIleArgGlyAsnIlePheIleValIleHis 221
DB 602 ATGGTGAATATGATGAAAGAGTGAACAATGAGCTTGTATGAGCCGTACAC 661
QY 222 AsnIleGlyGlnSerGlyMetGluAlaPheIleAspMetSerAlaIleGly 241
DB 662 AACTATGAGAAAGTGGAGTGAAGGCTTCAAGATATTCAGCCAAAGAGAGG 721
QY 242 IleAlaHisSerIleIleIleIleIleIleIleIleIleIleIleIleIle 261
DB 722 ATGCGCCACTTTACAAATATTCAGATTCAGAGGAGGAGGAGGAGGAGGAG 781

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QY 262 LyeLyeLeuTherHisLeuProLyAlaArgValAlaIleThrPheCysGluGlyMet 281  
DB 782 AAAAGCTCAACAGTCACTTGCCCAAGGCCGGGTGGTGGCTTCTTCTTGAGGGCATG 841  
QY 282 ThrValArgGlyLeuLeuMetAlaMetArgArgLeuGlyLeuValGlyIlePheLeu 301  
DB 842 ACGGTAGAGGTCTGCTGATGGCCATGAGCGCCCTGGGTCTAGTGGAGAAATTTCTGCTT 901  
QY 302 LeuGlyArgGluProAspAlaIlePheIleGluIleSerIleAsnSerIleLeuTrpGlu 321  
DB 902 CTGGGAGGAGAACAGATGCTCATCTTATTGAGATCTCAAGAACAGCATCTTATGGGAA 961  
QY 322 AspArgArgLysCysGlnGlyArgPheLeuGlnGlyPheGlyAspIleLeuHisArgSer 341  
DB 962 GACAGAGAAAGAAATGCCAAGGTCCCTCTTCAAGGTTTGGAGACATTTATACAGAGAT 1021  
QY 342 GluSerValLeuLeuHisMetProGlnProLeuAsnLeuGluLeuSerSerGlyProIle 361  
DB 1022 GAGTCCGTCTGCTGCACATGCCCCAGCCTCTGATCTAGAGCTCAGTTCCAGGGCCATC 1081  
QY 362 ThrGlyLeuArgAspArgLeuIle 369  
DB 1082 ACTGACTGAGGAGACAGGCTCATC 1105

RESULT 4  
US-10-346-241-1  
; Sequence 1, Application US/10346241  
; Publication No. US20030157647A1  
; GENERAL INFORMATION:  
; APPLICANT: STORMANN, THOMAS M.  
; APPLICANT: LEVINTHAL, CYNTHIA  
; APPLICANT: STORJOHANN, LAURA  
; APPLICANT: HAMMERLAND, LANCE G.  
; APPLICANT: KRAPCHO, KAREN J.  
; APPLICANT: NPS PHARMACEUTICALS, INC.  
; TITLE OF INVENTION: A NOVEL HUMAN METABOTROPIC GLUTAMATE RECEPTOR  
; FILE REFERENCE: 1094.2.6  
; CURRENT APPLICATION NUMBER: US/10/346,241  
; PRIOR FILING DATE: 2003-01-17  
; PRIOR APPLICATION NUMBER: US/09/695,481  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: 60/161,481  
; PRIOR FILING DATE: 1999-10-25  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 2826  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(2826)  
US-10-346-241-1

Alignment Scores:  
Pred. No.: 2,62e-180 Length: 2826  
Score: 1484.50 Matches: 306  
Percent Similarity: 87.22% Conservative: 8  
Best Local Similarity: 85.00% Mismatches: 22  
Query Match: 79.26% Indels: 24  
Gaps: 2

US-10-027-923-2 (1-369) x US-10-346-241-1 (1-2826)

QY 1 MetValLeuLeuLeuLeuLeuSerValLeuLeuLeuLysGluAspValAlaArgGlySerAla 20  
DB 1 ATGGTCTTCTGTTGATCTCTGTCAGTCTTACTTTTGAAGAAAGATGCTCGGAGAGTCA 60  
QY 21 GlnSerSerGluArgArgValAlaAlaHisMetLeuGlyAspIleIleIleGlyAlaLeu 40  
DB 61 CAGTTCAGTGAAGAGGAGGTGTGGTCCATGCCCCGGGTACATCATTTATTTAGAGCTCTC 120  
QY 41 PheSerValHisIleGlnProThrValAspGluValHisIleGluArgLysCysGlyAlaVal 60

DB 121 TTTTCTGTTCAATCAGCAGCTACTGTGGAACAAGTTCATGAGAGAAAGTGGGGCGTTC 180  
QY 61 ArgGluGlnTrpGlyIleGlnArgValGluAlaMetLeuHisPheLeuGluArgIleAsn 80  
DB 181 CGTGAACAGTATATGGCAATTCAGAGAGAGGAGCCATCTCTCATTCCTGGAAGAAATCAAT 240  
QY 81 SerAspProThrLeuLeuProAsnIleThrLeuGlyCysGluIleArgAspSerCysTrp 100  
DB 241 TCGACCTCCACACTCTTGCCCAACATCACTAGGCTGTGAGATAGAGATCTCTCTGG 300  
QY 101 HisSerAlaValAlaLeuGluGlnSerIleGluPheIleArgAspSerLeuIleSerSer 120  
DB 301 CATTGGCTGTGGCCCTTAGAGAGAGACATTTAGATTATTAAGATTCCCTCATTTCTTCA 360  
QY 121 GluGluGluGluGlyLeuValCysSerValAspGlySerSerSerPheArgSerLys 140  
DB 361 GAGAGAGAAAGAGGCTGTGATCGCTGTGTGAGTGGCTCTCTCTTCCCTCCGCTCAAG 420  
QY 141 LysProIleValGlyValIleGlyProGlySerSerSerLeuAlaIleGlnValGlnAsn 160  
DB 421 AACCCATATGATAGGGGTCAATTGGGCTGGCTCCAGTTCTGTAGCCATTCAAGTCCAGAT 480  
QY 161 LeuLeuGlnLeuPheAsnIleProGlnIleAlaTySerAlaThrIleMetAspLeuSer 180  
DB 481 TTGCTCCAGCTTTTCAACATACCTCAGATTGCTTACTCAGAACACAGCATGATCTGAGT 540  
QY 181 AspLysThrLeuPheLysTrpPheMetArgValAlaProSerAspAlaGlnGlnAlaArg 200  
DB 541 GACAAACATCTGTTCAAATATTTCAAGAGGAGGTGTGCTTCAGATCTCAGCAGGAGAGG 600  
QY 201 SerMetValAspIleValLysArgTyraAsnTrpThrTyValSerAlaValHisTrpGlu 220  
DB 601 GCCATGTGACATATGATGAAGAGTAACTGAGCCTATATGATCAGCCGTGCACAGAA 660  
QY 221 GlyAsnTrpGlyGluSerGlyMetGluAlaPheLysAspMetSerAlaLysGluGlyIle 240  
DB 661 GGCACATATGAGAAAGTGGATGGAAGAGGCTTCAAGATATGTCAGCAAGAGAGGATTT 720  
QY 241 CysIleAlaHisSerTrpLysIleTySerAsnAlaGlyGluGlnSerPheAspLysLeu 260  
DB 721 TGCATGCCCACTCTTACAAATCTACAGTAAATGCGGAGAGAGGAGCTTTGATTAAGCTG 780  
QY 261 LeuValLeuLeuTherHisLeuProLyAlaArgValAlaIleThrPheCysGluGly 280  
DB 781 CTGAAGAGCTCAACAGTCACTTGCCCAAGGCCGGGTGGTGGCTTCTTCTGTGAGGGC 840  
QY 281 MetThrValArgGlyLeuLeuMetAlaMetArgArgLeuGlyLeuValGlyIlePheLeu 300  
DB 841 ATGACGCTGAGAGGTCTGCTGATGGCCATGAGGCGCCTGGGTCTACCGGAGAAATTTCTG 900  
QY 301 LeuLeuGlyArgGluProAspAlaIlePheIleGluIleSerIleAsnSerIleLeuTrp 320  
DB 901 CTTCGGGAGTATGGC-----TGG 921  
QY 321 GluAspArgArgLysCysGlnGlyArgPheLeuGlnGlyPheGlyAspIleLeuHisArg 340  
DB 922 GCTGACAGGTATGATGTGACAG-----ATGATAT 961  
QY 340 gSerGluSerValLeuLeuHisMetProGlnProLeuAsnLeuGluLeuSerSerGly 359  
DB 952 CAGCGAAGAGCTGTTGGTGGCATCAACATCAAGCTCCATCTCCGATGTCAAGTGGT 1009

RESULT 5  
US-10-346-241-5  
; Sequence 5, Application US/10346241  
; Publication No. US20030157647A1  
; GENERAL INFORMATION:  
; APPLICANT: STORMANN, THOMAS M.  
; APPLICANT: LEVINTHAL, CYNTHIA  
; APPLICANT: STORJOHANN, LAURA  
; APPLICANT: HAMMERLAND, LANCE G.  
; APPLICANT: KRAPCHO, KAREN J.

APPLICANT: NPS PHARMACEUTICALS, INC.  
TITLE OF INVENTION: A NOVEL HUMAN METABOTROPIC GLUTAMATE RECEPTOR  
FILE REFERENCE: 1094.2.6  
CURRENT APPLICATION NUMBER: US/10/346,241  
CURRENT FILING DATE: 2003-01-17  
PRIOR APPLICATION NUMBER: US/09/695,481  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: 60/161,481  
PRIOR FILING DATE: 1999-10-25  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 5  
LENGTH: 3129  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Chimeric  
OTHER INFORMATION: molecule comprising portions of human mGluR5d and  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1..3129)  
US-10-346-241-5

Alignment Scores:  
Pred. No.: 3,09e-180 Length: 3129  
Score: 1484.50 Matches: 306  
Percent Similarity: 87.22% Conservative: 8  
Best Local Similarity: 85.00% Mismatches: 22  
Query Match: 79.26% Indels: 24  
DB: 13 Gaps: 2

US-10-027-923-2 (1-369) x US-10-346-241-5 (1-3129)

QY 1 MetValLeuLeuLeuLeuLeuSerValLeuLeuLeuGluAspValAlaArgIysSerAla 20  
DB 1 ATGGTCCTTCTGTTGATCCTGTCAGTCTTACTTTTGAAGAAGATGTCCTGGAGAGTGA 60  
QY 21 GlnSerSerGlnArgArgValValAlaHisMetLeuGlyAspIleIleIleGlyAlaLeu 40  
DB 61 CAGTCCAGAGAGAGAGAGGAGTGGCTGCACATGCCGGTACATCATTTATGAGGCTCTC 120  
QY 41 PheSerValHisIleGlnProThrValAspGluValHisGlnArgIysGlyAlaVal 60  
DB 121 TTTTCTGTTATATCAGACCTTACTGTGACAAAGTTTATAGAGAGTGTGGGCGGTC 180  
QY 61 ArgGlnGlnIysGlyIleGlnArgValGluAlaMetLeuHisThrLeuGlnArgIleAsn 80  
DB 181 CGTGAACAGATGAGCATTCAGAGAGTGAAGCCATGCTGCATACCTGGAAAGATCAAT 240  
QY 81 SerAspProThrLeuLeuProAsnIleThrLeuGlyCysGluIleLeuArgAspSerCys 100  
DB 241 TCAGACCCCACTCTTCCCAACATCACACTGGGCTGTAGATGAAGGAGCTCTGTGG 300  
QY 101 HisSerAlaValAlaLeuGlnGlnSerIleGluPheIleArgAspSerLeuIleSerSer 120  
DB 301 CATTCGGCTGTGGCCCTTAGAGCAGAGCATTTGATTAAGAATTCCTCATTTCTTCA 360  
QY 121 GlnGlnGlnGlnGlnIleuValCysSerValAspGlySerSerSerSerPheArgSerIys 140  
DB 361 GAAGAGGAGAAAGAGTGTGATGCTGTGTGATGTGGCTCTCTCTCTCCCTCCAG 420  
QY 141 LysProIleValGlyValIleGlyIysSerSerSerSerLeuAlaIleGlnValGlnAsn 160  
DB 421 AAGCCCATGATGAGGGGCTATTTGGCCCTGCTCCAGTTCTGTATCCATTCAGGTCCAGAA 480  
QY 161 LeuLeuGlnLeuPheAsnIleProGlnIleAlaIysSerAlaThrIleMetAspLeuSer 180  
DB 481 TTCTCTCAGCTTTTCAACATCACTCAGATTGCTTACTCAGCAACAGCATGATGATGAGT 540  
QY 181 AspLysThrLeuPheIleIysIysPheMetArgValValProSerAspAlaGlnGlnAlaArg 200  
DB 541 GACAAAGCTCTGTCAAAATATTTCAATGAGGGTGTGTGCTTCAGATGCTCAGCAGGAGG 600

QY 201 SerMetValAspIleValIysArgIysAsnProThrTyrValSerAlaValHisThrGlu 220  
DB 601 GCCATGTGACATATATGAAGAGTTCACCTGACCTTATGTATCAGCCGTGCACAGAA 660  
QY 221 GlyAsnTyrGlyGluSerGlyMetGluAlaPheLysAspMetSerAlaIysGlnGlyIle 240  
DB 661 GGCAACTATGAGAAAGTGGAGTGAAGAGCTTCAAGATATGTACAGAAAGAGGATTT 720  
QY 241 CysIleAlaHisSerTyrIysIleTyrSerAsnAlaGlyGlnSerPheAspIysLeu 260  
DB 721 TGCATGCCCACTTCTTACAAATCTACAGTAATGACGAGGAGCAGACTTTGATTAAGCTG 780  
QY 261 LeuLysValLeuThrSerHisLeuProLysAlaArgValAlaIleTyrPheCysGlnGly 280  
DB 781 CTGAAGAGCTCAACAGTCACTTCCCAAGGCCGGGAGTGTGGCTGTCTGTGTAGAGGC 840  
QY 281 MetThrValArgGlyLeuLeuMetAlaMetArgArgLeuGlyLeuValGlyGluPheLeu 300  
DB 841 ATGACGCTGAGAGTCTGTGATGAGCCATGAGGCGCTGGTCTTACGGGAGAAATTTCTG 900  
QY 301 LeuLeuGlyArgGluProAspAlaIlePheIleGluIleSerLysAsnSerIleLeuTyr 320  
DB 901 CTTCTGGCAGTATGCGC-----TGG 921  
QY 321 GluAspArgArgLysCys-GlnGlyArgPheLeuGlnGlyPheGlyAspIleLeuHisAr 340  
DB 922 GCTGACAGGTATGATGTGACAG-----ATGAGATAT 951  
QY 340 GSerGlnSerValLeuLeuHisMetProGlnProLeuAsnLeuGluLeuSerSerGly 359  
DB 952 CAGCGAAGAGCTGTGTGTGTCATCACAATCAAGCTCCATCTCCAGATGCAAGTGTGT 1009

RESULT 6  
US-10-225-567A-177  
Sequence 177, Application US/10225567A  
Publication No. US20030113798A1  
GENERAL INFORMATION:  
APPLICANT: Lifespan Biosciences  
APPLICANT: Brown, Joseph P.  
APPLICANT: Burner, Glenna C.  
APPLICANT: Roush, Christine L.  
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS  
FILE REFERENCE: 1920-4-4  
CURRENT APPLICATION NUMBER: US/10/225,567A  
CURRENT FILING DATE: 2001-12-19  
PRIOR APPLICATION NUMBER: 60/257,144  
PRIOR FILING DATE: 2000-12-19  
NUMBER OF SEQ ID NOS: 2292  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 177  
LENGTH: 4518  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-225-567A-177

Alignment Scores:  
Pred. No.: 5.6e-180 Length: 4518  
Score: 1484.50 Matches: 306  
Percent Similarity: 87.22% Conservative: 8  
Best Local Similarity: 85.00% Mismatches: 22  
Query Match: 79.26% Indels: 24  
DB: 15 Gaps: 2

US-10-027-923-2 (1-369) x US-10-225-567A-177 (1-4518)

QY 1 MetValLeuLeuLeuLeuSerValLeuLeuLeuGluAspValAlaArgIysSerAla 20  
DB 151 ATGGTCCTTCTGTTGATCCTGTCAGTCTTACTTTTGAAGAAGATGTCCTGGAGAGTGA 210  
QY 21 GlnSerSerGlnArgArgValValAlaHisMetLeuGlyAspIleIleIleGlyAlaLeu 40  
DB 211 CAGTCCAGAGAGAGAGGAGTGGCTGCACATGCCGGTACATCATTTATGAGGCTCTC 270



OY	41	PheSerValHisHisGlnProThrValAspGluValHisGlnArgIleValAla	60
Db	271	TTTTCTGTTTCATCACAGCTTACTGTGACAAAGTTCAATGAAGAAGTGTGGGGCGCT	330
OY	61	ArgGluGlnIYrGlyIleGlnArgValGlnAlaMetLeuHisThrLeuGluArgIleAsn	80
Db	321	COTGAACAAGTATGGCATTCAGAGAGTGAAGGCCATGGCTCATACCTGGAAAGATCAAT	390
OY	81	SerAspProThrLeuLeuProAsnIleThrLeuGlyCysGluIleArgAspSerCysTrp	100
Db	391	TCAGACCCCAACACTCTTGGCCAAATCAACACTGGCGGTGGATTAAGGACCTCTGGCG	450
OY	101	HisSerAlaValAlaLeuGluGlnSerIleGluPheIleArgAspSerLeuIleSerSer	120
Db	451	CATTGGCGTGTGGCCCTAGACGACAGACATTGAGTTCAATAAGATATTCCTCATTTCTTCA	510
OY	121	GluGluGluGluGlyLeuValCysSerValAspGlySerSerSerPheArgSerIlys	140
Db	511	GAAGGAGAAAGCGCTGGTGAAGCGTGTGGATGGCTCTCTCTCTCTCTCCGCTCAAG	570
OY	141	LysProIleValGlyValIleGlyProGlySerSerSerLeuAlaIleGlnValGlnAsn	160
Db	571	AAGCCCAATGAGGGGTCAATGGGCGTGCCTCAGTCTTGAGCCATTCAGATCAAGTCAAGAT	630
OY	161	LeuLeuGlnLeuPheAsnIleProGlnIleAlaIYrSerAlaThrIleMetAspLeuSer	180
Db	631	TTGCTCCAGCTTTTCAACATCACTCAGATGCTTACTACGACCAACGACATGGATCTGACT	690
OY	181	AspIYrThrLeuPheIYrThrPheMetArgValIleProSerAspAlaGlnGlnAlaArg	200
Db	691	GACAAAGACTGTGTTCAAAATATTCTTCAATGAGGGTGTGGCTTCAAGATGCTCAGCAGGCAAG	750
OY	201	SerMetValAspIleValIleAspArgIYrAsnIlePThrIYrValSerAlaValHisThrGlu	220
Db	751	GCCATGAGTGAATAGTGAAGAGTACAACTGACCTAATGATACAGCCGTGCAACAGAA	810
OY	221	GlyAsnIYrGlyGluSerGlyMetGluAlaPheIYsAspMetSerAlaIYsGluGlyIle	240
Db	811	GGCAACTATGGAGAAAGTGGATGGATGAAGCTTCAAAAGATATCTCAGCGAAGGAAGGATT	870
OY	241	CysIleAlaHisSerIYrIYsIleIYrSerAsnAlaGlyGluGlnSerPheArgIYsLeu	260
Db	871	TGCATCGGCCCACTCTTACAAAATCTACAGTAATGACAGGGACAGAGCTTTGATTAAGCTG	930
OY	261	LeuIYsIYsLeuThrSerHisLeuProIYsAlaArgValValAlaIYrPheCysGluGly	280
Db	931	CTGAAGAAAGCTCAACAATCACTTGGCCAAAGGCCGGAGTGGTGGCTCTCTGTGAAGGC	990
OY	281	MetThrValArgGlyLeuLeuMetAlaMetArgArgLeuGlyLeuValGlyIlePheLeu	300
Db	991	ATGACGGTGAAGAGCTGTGCTGATGGCCATGAGCGCGCTGGGCTGACGGGAGAAATTTCTG	1050
OY	301	LeuLeuGlyIYrArgGluProAspAlaIlePheIleGluIleSerIYsAsnSerIleLeuTrp	320
Db	1051	CTTCTGGCGCAGTGAAGGC-----TGG 1071	
OY	321	GluAspArgArgIYsCys-GlnGlyArgPheLeuGlnGlyPheGlyAspIleLeuHisArg	340
Db	1072	GCTGACAGGTATGATGTGACAG-----ATGATAT 1107	
OY	340	GSerGluSerValLeuLeuHisMetProGlnProLeuAsnLeuGluLeuSerSerGly 359	
Db	1102	CAGCGAAGAAGCTGTGGTGGCATCAACAATCAAGCTCCAAATCTCCGATGTCAAGTGGT 1159	

[illegible]

Db	748	CAGAAAGGCGCTGTGATGCGCCATTCTGACAAAATCTACAGACAGCGTGGGGAGAAAGAC	807
Qy	257	PhelaprylsleuLeuLysLeuLeuThersileuProlValArgValValAlaIyR	276
Db	808	TTTATCCGACCTTTGGCGMAATCCGAGAGAGCGTTCCCAAGAGCTAGAGTGATGCTTGC	867
Qy	277	PheCysglnglymetThrValArgGlyLeuLeuMetalmetArgArgLeuGlyLeuVal	296
Db	868	TTCTGTGAAGGCATGACAGTCGCGAGAGATCTCTGAGCGGCATGCGGCGCTTGGCGTGTG	927
Qy	297	GlyGluIbheLeuLeuLeuGlyArgGluIbProAspAlaIbPheIleGluIleSerIyAsn	316
Db	928	GGCAGAGTTCTCAGCTCATTTGAAAGTATGA-----	957
Qy	317	SerIleuThrIprGluAspArgArgLys---CysglnglyArgPheLeuGlnGlyPheGly	335
Db	958	-----TGGGACAGACAGATGATGATCATTTGAGCTTATGAGGTGAAGCCAAACGGG	1008
Qy	336	AspIleLeuHISArgSerGluSer	343
Db	1009	GGATTCACGATTTAAAGCTGCACTCT	1032

```

RESULT 8
US-10-101-510-258
/ Sequence 258, Application US/10101510
/ Publication No. US20030148295A1
/ GENERAL INFORMATION:
/ APPLICANT: WAN, JACKSON
/ APPLICANT: WANG, YIXIN
/ TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
/ FILE REFERENCE: 15117.0012
/ CURRENT APPLICATION NUMBER: US/10/101,510
/ PRIOR FILING DATE: 2002-03-20
/ PRIOR APPLICATION NUMBER: 60/276,947
/ PRIOR FILING DATE: 2001-03-20
/ NUMBER OF SEQ ID NOS: 805
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 258
/ LENGTH: 3295
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-101-510-258

Alignment Scores:
Pred. No.: 5,44e-133 Length: 3295
Score: 1118.50 Matches: 226
Percent Similarity: 81.10% Conservative: 40
Best Local Similarity: 68.90% Mismatches: 45
Query Match: 59.72% Indels: 17
DB: 13 Gaps: 5

US-10-027-923-2 (1-369) x US-10-101-510-258 (1-3295)
QY 20 AAGInSerSerGluArgValAlaAlaHisMetLeuGlyAepIleIleGlyAla 39
   :::::
D58 GCAGGAGCGCTCGCTCAGCGCTCGGTGCGCCAGAAATGAGAGGAGATGATATTGGAGCC 517
QY 40 LeuPhSerValHisHisGlnProThrValAlaArgIuValHisGluArgGlyCysGlyAla 59
   CTTCTTCTCAGTCCATCACCAGCGCTCGGCGCCGAGAAAGTCCCGAGAGGAGAACTGGGGAG 577
D58 ValArgGluGlnIleGlyIleGlnIleArgValGluAlaMetLeuHisIleThrLeuGluArgIle 79
   :::::
D58 ATCAGGAGAGCATATGAGCATCCAGAGGAGTGGAGGCCATGTTCCACACCTTGATTAAGATC 637
QY 80 AAnSerAAspProThrLeuLeuProAlaHisIleThrLeuGlyCysGluIleArgAAspSerCys 99
   :::::
D58 AACGCGGAGCCCGGTCTCTCGCCCAACATCACTCGGGGAGAGAGATCCGGGACTCTGCG 697
QY 100 TrpHisSerAlaValAlaLeuGluGlnSerIleGluIleHisArgAAspSerLeuIleSer 119
   :::::
D58 TGGCATCTTCCGTGCTCTGGAAACAGACATTGAGTCAATTAGGACTCTCTGATTTC 757

```

QY	120	----	Ser	Gln	Glu	Glu	Glu	Glu	Leu	----	Val	Cys	Ser	Val	Asp	Gly	Ser	Ser	----	Ser	Ser	136					
DB	758	ATTG	AG	ATG	AG	AG	AG	AG	ATG	GG	AT	AC	CG	G	T	T	CG	CT	TA	CG	CG	CA	CT	CCCC	CA	817	
QY	137	Phe	Arg	Ser	Leu	Val	Pro	Ile	Val	Gly	Val	Ile	Gly	Pro	Gly	Ser	Ser	Ser	Leu	Ala	Ile	156					
DB	818	GGC	AG	CA	G	CT	TA	GA	AG	CC	CA	T	T	G	CG	GA	G	T	AT	CG	CG	CT	CG	AG	CT	877	
QY	157	Gln	Val	Gln	Asn	Leu	Gln	Leu	Phe	Asn	Ile	Pro	Gln	Ile	Ala	Tyr	Ser	Ala	Thr	Ile	176						
DB	878	CA	AT	G	CA	GA	CC	CA	CT	TC	CA	G	CT	TC	TC	CA	AT	CC	CA	GA	AT	CC	CA	AT	CC	937	
QY	177	Met	Asp	Leu	Ser	Asp	Leu	Ser	Thr	Leu	Phe	Ile	Tyr	Phe	Met	Arg	Val	Val	Pro	Ser	Asp	Ala	196				
DB	938	AT	CA	CA	CT	GA	GT	CA	CA	AA	CT	T	T	TA	CA	AA	A	A	A	A	A	A	A	A	A	997	
QY	197	Gln	Gln	Ala	Ile	Arg	Ser	Met	Val	Asp	Ile	Val	Ile	Arg	Tyr	Asn	Thr	Tyr	Val	Ser	Ala	216					
DB	998	TT	GC	AG	CA	GA	GG	CA	AG	CC	CA	AT	G	CA	T	TA	CA	AT	TA	CA	AT	TA	CA	AT	TA	1057	
QY	217	Val	Ile	Asn	Thr	Glu	Glu	Val	Asn	Tyr	Gln	Ser	Gly	Met	Gln	Ala	Phe	Val	Asn	Met	Ser	Ala	236				
DB	1058	GT	CA	CA	CA	CG	GA	GG	AA	AT	T	AT	GG	GA	AG	CG	CA	AT	TA	CA	AA	AG	CT	GG	CT	1117	
QY	237	Lys	Gln	Glu	Gly	Ile	Cys	Val	Ile	Ala	His	Ser	Tyr	Lys	Ile	Tyr	Ser	Asn	Ala	Gly	Glu	Asn	256				
DB	1118	C	A	G	A	A	G	G	C	C	T	T	A	T	A	T	A	T	A	T	A	T	A	T	A	T	1177
QY	257	Phe	Asp	Leu	Val	Leu	Leu	Val	Ser	Thr	Ser	Ile	Leu	Pro	Gly	Val	Ala	Arg	Val	Val	Ala	Tyr	276				
DB	1178	TT	T	A	C	C	G	A	C	A	C	T	T	G	C	C	A	A	A	C	T	T	G	C	C	A	1237
QY	277	Phe	Cys	Gln	Glu	Gly	Met	Thr	Val	Arg	Gly	Leu	Leu	Met	Ala	Met	Arg	Arg	Leu	Gly	Leu	Val	296				
DB	1238	TT	C	T	C	T	A	A	G	G	C	A	T	G	A	G	A	C	T	T	G	A	C	C	G	C	1297
QY	297	Gly	Leu	Phe	Leu	Leu	Leu	Gly	Arg	Glu	Pro	Asp	Ala	Ile	Phe	Ile	Gly	Ile	Ser	Lys	Val	Asn	316				
DB	1298	G	G	C	A	G	A	T	T	C	A	C	A	T	T	G	A	G	A	G	A	T	G	A	-----	1327	
QY	317	Ser	Ile	Leu	Tyr	Gln	Asp	Arg	Arg	Lys	----	Cys	Gln	Gly	Arg	Phe	Leu	Gln	Gly	Phe	Gly	335					
DB	1328	----	T	G	G	C	A	G	A	C	A	G	A	T	A	G	A	T	A	G	A	T	A	G	A	-----	1378

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RESULT 9
US-10-225-567A-169
; Sequence 169, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 169
; LENGTH: 6619
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-225-567A-169

Alignment Scores:      1.69e-132      Length:      6619
Pred. No.:

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Db      472 GGCAGAGCTAAGAGGCTATTGCTGAGATGATGCGCCCTGCTCCAGCTCTGTGGCCATT 531
Qy      157 GlnValGlnAsnLeuLeuGlnLeuPheAsnIleProGlnIleAlaTyrSerAlaThrIle 176
Db      532 CAAGTCCAGAAATTTTTCAGCTGTTTCGACATCCACAGATCCGCTTAATTCCTGACAGAGC 591
Qy      177 MetAspLeuSerAspIleThrLeuPheLeuTyrPheMetArgValAlaProSerAspAla 196
Db      592 ATAGACTGATGATGACAAATCTTTGTAACAATACTTCTGAGGGTGGTCCCTTGTGACACT 651
Qy      197 GlnGlnAlaArgSerMetValAspIleValLeuArgTyrAsnThrThrTyrValSerAla 216
Db      652 TTGCAGGCAAGGCGGCTGCTCGACATATGCAACGTTACAACTGACCTATGTCTGACGCA 711
Qy      217 ValHisThrGlnGluYasnTyrGlnGlnSerGlnMetGlnAlaPheLeuAspMetSerAla 236
Db      712 GTCCACACGAGAGGAAATTTACGGCGAGATGAGATGATCTTTCAAGAACTGGGCTGCC 771
Qy      237 LysGlnGluYlleCysIleAlaHisSerTyrLysIleTyrSerAsnAlaGlnGlnGlnSer 256
Db      772 CAGGAAGGCTCTGTCATCGCACCTCGACAAATCTACAGCAATCTGCGCGAGAAAGC 831
Qy      257 PheAspLysLeuLeuLysLysLeuThrSerHisLeuProLysAlaArgValAlaAlaTyr 276
Db      832 TTGACCGGCTCTGCGTAAACTCCGGAGCGGCTTCCCAAGGCCAGGGTTGTGTGCTGC 891
Qy      277 PheCysGlnGluMetThrValArgGlyLeuLeuMetAlaMetArgArgLeuGlnGlyLeuVal 296
Db      892 TTCTGGAGGCGCATGACAGCGCGGCTTACTAGTGCATGCGCGGCTGCGGCGTGG 951
Qy      297 GlyGluPheLeuLeuGlnGlyArgGlnProAspAlaIlePheIleGlnIleSerLysAsn 316
Db      952 GGGGAGTTCTCACTCATCTGGAAGTATGCA----- 991
Qy      317 SerIleLeuTyrGlnAspArgArgLys--CysGlnGlyArgPheLeuGlnGlnGly 335
Db      982 -----TGCGCACAACAGAGATGAAGTCATGCAAGGCTATGAGTGGAAACCAAGCA 1032
Qy      336 AspIleLeuHisArgSerGlnSer 343
Db      1033 GGGATCACAATMAAGCTTCAGTCT 1056

RESULT 11
US-10-300-473-4
; Sequence 4, Application US/10300473
; Publication No. US20030113873A1
; GENERAL INFORMATION:
; APPLICANT: STORMANN, THOMAS M.
; APPLICANT: STORJOHANN, LAURA L.
; APPLICANT: HAMMERLAND, LANCE G.
; APPLICANT: RULIER, FORREST H.
; APPLICANT: KAPCHO, KAREN J.
; TITLE OF INVENTION: CHIMERIC RECEPTORS AND METHODS FOR IDENTIFYING
; TITLE OF INVENTION: COMPOUNDS ACTIVE AT METABOTROPIC GLUTAMATE
; TITLE OF INVENTION: RECEPTORS AND THE USE OF SUCH COMPOUNDS IN THE
; TITLE OF INVENTION: TREATMENT OF NEUROLOGICAL DISORDERS AND DISEASES
; FILE REFERENCE: 072827/0909
; CURRENT APPLICATION NUMBER: US/10/300,473
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 09/435,897
; PRIOR FILING DATE: 1999-11-08
; PRIOR APPLICATION NUMBER: 08/687,289
; PRIOR FILING DATE: 1996-07-25
; PRIOR APPLICATION NUMBER: 60/001,526
; PRIOR FILING DATE: 1995-07-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 3219
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthesized human

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; OTHER INFORMATION: mGluR and human calcium receptor
US-10-300-473-4
Alignment Scores:
Pred. No.: 7,05e-133
Score: 1117.50
Percent Similarity: 81.10%
Best Local Similarity: 68.10%
Query Match: 59,664
DB: 15
Gaps: 5
US-10-027-923-2 (1-369) x US-10-300-473-4 (1-3219)
Qy      20 AlaGlnSerSerGlnLysArgValValAlaHisMetLeuGlyAspIleIleIleGlyAla 39
Db      112 GCGAGTGCCTCTGCTCCAGCGCTCTCGTGGCAGAAATGACGAGATGTCATCTGAGGCC 171
Qy      40 LeuPheSerValHisHisGlnProThrValAspGluValHisGluArgLysCysGlyAla 59
Db      172 CTCTTCTGATGTCATCACAGGCTCCAGCCGAGAGAGTACCCGAAAGAAAGTGTGGGAG 231
Qy      60 ValArgGlnGlnTyrGlyIleGlnArgValGlnAlaMetLeuHisThrLeuGlnArgIle 79
Db      232 ATCAGGGAACAGATGATGATCCAGAGGCTGGAAGCCATGTCCACACGTTGATTAAGATT 291
Qy      80 AsnSerAspProThrLeuLeuProAsnIleThrLeuGlyCysGlnIleArgAspSerCys 99
Db      292 AACGGGAGCCCGGTGCTCTGCGCAACATCACTCGGAGTGAAGTCCGGAGCTCTGC 351
Qy      100 TrpHisSerAlaValAlaLeuGlnGlnSerIleGluPheIleArgAspSerLeuIleSer 119
Db      352 TGGCACTTTCATGAGCTCTCGAAGACAGCATGAAATTCATGAGAACCTCCGATTTC 411
Qy      120 ---SerGlnGlnGlnGlnGlyLeu---ValCysSerValAspGlySerSer---SerSer 136
Db      412 ATCCGAGATGAAGAAGATGGCTGAAACCGATGCTGCGTGAATGCGCAGACCTGCCCT 471
Qy      137 PheArgSerLeuLysProIleValGlnValIleGlyProGlnIleSerSerSerLeuAlaIle 156
Db      472 GGCAGAGCTAAGAGGCTTAATGCTGAGATGAGCGCCCTGCGCTCCAGCTCTGGGCCATT 531
Qy      157 GlnValGlnAsnLeuLeuGlnLeuPheAsnIleProGlnIleAlaTyrSerAlaThrIle 176
Db      532 CAAGTCCAGAAATTTTTCAGCTGTTTCGACATCCACAGATCCGCTTAATTCCTGACAGAGC 591
Qy      177 MetAspLeuSerAspIleThrLeuPheLeuTyrPheMetArgValAlaProSerAspAla 196
Db      592 ATAGACTGATGATGACAAATCTTTGTAACAATACTTCTGAGGGTGGTCCCTTGTGACACT 651
Qy      197 GlnGlnAlaArgSerMetValAspIleValLeuArgTyrAsnThrThrTyrValSerAla 216
Db      652 TTGCAGGCAAGGCGGCTGCTCGACATATGCAACGTTACAACTGACCTATGTCTGACGCA 711
Qy      217 ValHisThrGlnGluYasnTyrGlnGlnSerGlnMetGlnAlaPheLeuAspMetSerAla 236
Db      712 GTCCACACGAGAGGAAATTTACGGCGAGATGAGATGAGCGCTTCAAGAGCTGGGCTGCC 771
Qy      237 LysGlnGluYlleCysIleAlaHisSerTyrLysIleTyrSerAsnAlaGlnGlnGlnSer 256
Db      772 CAGGAAGGCTCTGTCATCGCACCTCGACAAATCTACAGCAATCTGCGCGAGAAAGC 831
Qy      257 PheAspLysLeuLeuLysLysLeuThrSerHisLeuProLysAlaArgValAlaAlaTyr 276
Db      832 TTGACCGGCTCTGCGTAAACTCCGGAGCGGCTTCCCAAGGCCAGGGTTGTGTGCTGC 891
Qy      277 PheCysGlnGluMetThrValArgGlyLeuLeuMetAlaMetArgArgLeuGlnGlyLeuVal 296
Db      892 TTCTGGAGGCGCATGACAGCGCGGCTTACTAGTGCATGCGCGGCTGCGGCGTGG 951
Qy      297 GlyGluPheLeuLeuGlnGlyArgGlnProAspAlaIlePheIleGlnIleSerLysAsn 316
Db      952 GGGGAGTTCTCACTCATCTGGAAGTATGCA----- 991

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QY 317 SerLeuTrpGluAspArgValys---CysGlnGlyArgPheLeuGlnGlyPheGly 335
DB 982 -----TGGGACAGACAGATGAAGTATGTAAGTATGAGGTGAGAACCAAGGG 1032
QY 336 AspLeuHisArgSerGlySer 343
DB 1033 GAATCAGATCAATGAAGTCGAGTCT 1056

RESULT 12
US-10-300-473-1
; Sequence 1, Application US/10300473
; Publication No. US20030113873A1
; GENERAL INFORMATION:
; APPLICANT: STORMANN, THOMAS M.
; APPLICANT: STORJOHANN, LAURA L.
; APPLICANT: HAMMERLAND, LANCE G.
; APPLICANT: FULLER, FORREST H.
; APPLICANT: KAPACHO, KAREN J.
; TITLE OF INVENTION: CHIMERIC RECEPTORS AND METHODS FOR IDENTIFYING
; TITLE OF INVENTION: COMPOUNDS ACTIVE AT METABOTROPIC GLUTAMATE
; TITLE OF INVENTION: RECEPTORS AND THE USE OF SUCH COMPOUNDS IN THE
; TITLE OF INVENTION: TREATMENT OF NEUROLOGICAL DISORDERS AND DISEASES
; FILE REFERENCE: 072827/0909
; CURRENT APPLICATION NUMBER: US/10/300,473
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 09/435,897
; PRIOR FILING DATE: 1999-11-08
; PRIOR APPLICATION NUMBER: 08/687,289
; PRIOR FILING DATE: 1996-07-25
; PRIOR APPLICATION NUMBER: 60/001,526
; PRIOR FILING DATE: 1995-07-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3384
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthesized rat
; US-10-300-473-1

Alignment Scores:
Pred. No.: 7.65e-133 Length: 3384
Score: 1117.50 Matches: 226
Best Similarity: 81.10% Conservative: 40
Best Local Similarity: 68.90% Mismatches: 45
Query Match: 59.66% Indels: 17
Gaps: 5

US-10-027-923-2 (1-369) x US-10-300-473-1 (1-3384)
QY 20 AlaglnSerSerGluArgValAlaHisMetLeuGlyAspIleIleGlyAla 39
DB 95 GCAGGTCCCTCCGCCAGCCCTCGTGGCGAGATGAGATGATCATCATCGAGACC 154
QY 40 LeuPheSerValHisGlnProThrValAspGluValHisGluArgValysGlyAla 59
DB 155 CTCTTCTCAGTCAATCCAGACCTCCAGCCGAGAGAGGTACCCGAAAGAGAGTGTGGGAG 214
QY 60 ValArgGlnGlnTrpGlyIleGlnArgValGluAlaMetLeuHisThrLeuGluArgIle 79
DB 215 ATCAGGACACAGATGTATGTCAGAGGTTGAGGCGCATGTTCCACACGTTGAGTAAGATT 274
QY 80 AsnSerAspProThrLeuLeuProAsnIleThrLeuGlyCysGluIleArgAspSerCys 99
DB 275 AACGGGACCCGGGTCTCCGCCACACATCATCTTGGGCGAGTGAAGATCCGGGACTCTCGC 334
QY 100 TrpHisSerAlaValAlaLeuGlnSerIleGluPheIleArgAspSerLeuIleSer 119
DB 335 TGGCACTCTTCAGTGGCTCTCGAACAGACATTCATTCAGAGACTCCCTGATTTCC 394
QY 120 ---SerGlnGlnGlnGlnGlyLeu---ValCysSerValAspGlySerSer---SerSer 136

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DB 395 ATCCGAGATGAGAGATGGGCTGAACCCAGATGCTCTGATGATGCCAGCCCTGCCCT 454
QY 137 PheArgSerIleValSerProIleValGlyAlaIleGlyProGlySerSerSerLeuAlaIle 156
DB 455 GGCAGGACTTAAGAGGCTATGTCTGAGATGATGGCCCTGGCTCGAGCTCTGTGGCCATT 514
QY 157 GlnValGlnAsnLeuLeuGlnLeuPheAsnIleProGlnIleLeuAlaIleSerAlaThrIle 176
DB 515 CAAGTCCAGATTTCTCCAGCTGTTGCATCCACAGATGCCATTTCTGCACAGC 574
QY 177 MetAspLeuSerAspIleValThrLeuPheValIleValIleValIleValIleValIle 196
DB 575 ATAGACCTGAGTGAACAACTTTGTACAAATCTTCTGAGGAGTGTCTCTTGTGACACT 634
QY 197 GlnGlnAlaArgSerMetValAspIleValIleValIleValIleValIleValIleVal 216
DB 635 TTGCAGGCAAGGCGATGCTGCACATGATCAAGCTTACAACTGACCTATGTCTAGCA 694
QY 217 ValHisThrGlnGlnValAsnTrpGlyGlnSerGlyMetGluAlaPheValAspMetSerAla 236
DB 695 GTCCACACAGAGAGGAAATTCAGGCGAGATGATGATGCTTTCAAAGACTGGCTGCC 754
QY 237 LysGlnGlyIleCysIleAlaHisSerTrpIleValIleValIleValIleValIleVal 256
DB 755 CAGGAAGGCTCTGCATCGACACCTCGACAAATCTACAGCAATCTGCGCGAGAGAGC 814
QY 257 PheAspGlyLeuLeuLeuValIleValIleValIleValIleValIleValIleValIle 276
DB 815 TTGACCGGCTCTGTGGTAAATCCCGGAGCGGCTTCCAAAGGCGAGGTTGTGTCTGC 874
QY 277 PheCysGlnGlyMetThrValArgGlyLeuLeuMetAlaMetArgArgLeuGlyLeuVal 296
DB 875 TTCTGGAGGAGGATGACAGTGGGGCTTACTGAGTGCATGGCCGCTGGCGCTG 954
QY 297 GlyGlnPheLeuLeuLeuGlnArgGlnProAspAlaIlePheIleGluIleSerIleVal 316
DB 935 GCGAGTTCCTCACTCATGGAAGTATGGA----- 964
QY 317 SerLeuTrpGlnAspArgValys---CysGlnGlyArgPheLeuGlnGlyPheGly 335
DB 965 -----TGGGACAGACAGATGAAGTCAATGCAAGCTTGAAGGTGAGAACCAAGGA 1015
QY 336 AspLeuHisArgSerGlySer 343
DB 1016 GCGATCAATTAAGCTTCAGTCT 1039

RESULT 13
US-09-900-714A-1
; Sequence 1, Application US/09900714A
; Patent No. US20020162133A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Keith D.
; TITLE OF INVENTION: TRANSGENIC MICE CONTAINING MG1URB
; TITLE OF INVENTION: METABOTROPIC GLUTAMATE RECEPTOR GENE DISRUPTIONS
; FILE REFERENCE: R-657
; CURRENT APPLICATION NUMBER: US/09/900,714A
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US 60/216,252
; PRIOR FILING DATE: 2000-07-06
; PRIOR APPLICATION NUMBER: US 60/221,490
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: US 60/262,138
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,928
; PRIOR FILING DATE: 2000-07-26
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2830
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-900-714A-1

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Db      244 CTTGTGGGAGCTGAAGAAAGGAGGATTCACAGACTGAGCCATGCTTTATGCA 303
Qy      76 LeuGluArgIleAsnSerAppProThrLeuLeuProAsnIleThrLeuGlyCysGluIle 95
Db      304 ATTGACCAAGATTAAAGAGAGCCGATGATCTCTTCCAAACATCATCTGGGGTCCGATC 363
Qy      96 ArgAspSerCysTrpHisSerAlaValAlaLeuGluGlnSerIleGluPheIleArgAsp 115
Db      364 CTCGACAGCTGCTACGAGACACCTATGCTTTGGAGCAGCTCTTAACATTCGTGCAG--- 420
Qy      116 SerLeuIleSerSerGluGluGluGluGluValCysSerValAspGlySerSerSer 135
Db      421 GCATTAATA-----GAGAAAGATGCTTCGATGTGAAGTGTGAATGAGATCCACC 474
Qy      136 SerPheArgSerIleValIleValIleGlyValIleGlyProGlySerSerSerLeuAla 155
Db      475 ATTTTCCCAAGCCCGACAGATTTCTGGGCTCATAGGTCTGACGACAGCTCCGCTGCC 534
Qy      156 IleGlnValGlnAsnLeuGlnLeuPheAsnIleProGlnIleAlaIleAlaIleAlaThr 175
Db      535 ATCATGTTGCTAATTAAGATTTTAAGATCTTAACATCACTGACATGATGATCCACA 594
Qy      176 IleMetAspLeuSerAspIleThrLeuPheIleValIleValIleValIleValIle 195
Db      595 GCCCCAGAGCTAAGTGAATACACAGGATGATGATTTCTCTCGAGGTGCTCCGCTGAC 654
Qy      196 AlaGlnGlnAlaArgSerMetValAspIleValIleValIleValIleValIleValIle 215
Db      655 TCCACCAAGCCCAAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 714
Qy      216 AlaValIleThrGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 235
Db      715 ACATGCTCTTGAAGGAGATTAAGTGAAGAGCGGTGATGAGCGCTTACCCAGATTCG 774
Qy      236 AlaIleValIleGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 254
Db      775 AGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 834
Qy      255 GlnSerPheAspIleValIleValIleValIleValIleValIleValIleValIleVal 274
Db      835 GAGGATTTTGAAGAAATTAATCAAGCGCTGCTA---GAAACACTTAATGCTCGAGCTG 891
Qy      275 AlaIleValIleGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 294
Db      892 ATTATGTTGCCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 951
Qy      295 LeuValIleGluPheLeuLeuLeuGlyArgGlu 305
Db      952 CAAAGTGGCATTTTCTCTGATGCTCAGAT 984

RESULT 15
US-10-225-567A-183
; Sequence 183, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Rounier, Glenna C.
; APPLICANT: Rounier, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 183
; LENGTH: 3321
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-225-567A-183

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## Alignment Scores:

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Pred. No.: 2,13e-59 Length: 3321
Score: 548.00 Matches: 125
Percent Similarity: 60.82% Conservative: 52
Best Local Similarity: 42.96% Mismatches: 98
Query Match: 29,26% Indels: 16
DB: 15 Gaps: 7

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US-10-027-923-2 (1-369) x US-10-225-567A-183 (1-3321)

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Qy      21 GlnSerSerGluArgArgValValAlaIleMetLeu-----GlyAspIleIleIle 37
Db      142 CAAAGATCAACACCAAGAGTATGCTTCATTCATGCGGTGATGGAGCATTAATTTTG 201
Qy      38 GlyAlaLeuPheSerValIleHisGlnProThrValIleAspIleValIleGluArg----- 55
Db      202 GGGGGTCTCTCTCTCTCCATCCGCAAG-----GAGAGAGAGGGGTG 243
Qy      56 LysCysGlyAlaValArgGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 75
Db      244 CTTGTGGGAGCTGAAGAAAGGAGATTCACAGACTGAGCCATGCTTTATGCA 303
Qy      76 LeuGluArgIleAsnSerAppProThrLeuLeuProAsnIleThrLeuGlyCysGluIle 95
Db      304 ATTGACCAAGATTAAAGAGAGCCGATGATCTCTTCCAAACATCATCTGGGGTCCGATC 363
Qy      96 ArgAspSerCysTrpHisSerAlaValAlaLeuGluGlnSerIleGluPheIleArgAsp 115
Db      364 CTCGACAGCTGCTACGAGACACCTATGCTTTGAGACAGCTCTTAACATTCGTGCAG--- 420
Qy      116 SerLeuIleSerSerGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 135
Db      421 GCATTAATA-----GAGAAAGATGCTTCGATGTGAAGTGTGAATGAGATCCACC 474
Qy      136 SerPheArgSerIleValIleValIleValIleValIleValIleValIleValIleVal 155
Db      475 ATTTTCCCAAGCCCAAGATTTCTGGGCTCATAGGTCTGACGACAGCTCCGCTGCC 534
Qy      156 IleGlnValGlnAsnLeuGlnLeuPheAsnIleProGlnIleAlaIleAlaIleAlaThr 175
Db      535 ATCATGTTGCTAATTAAGATTTTAAGATCTTAACATCACTGACATGATGATCCACA 594
Qy      176 IleMetAspLeuSerAspIleThrLeuPheIleValIleValIleValIleValIleVal 195
Db      595 GCCCCAGAGCTAAGTGAATACACAGGATGATGATTTCTCTCGAGGTGCTCCGCTGAC 654
Qy      196 AlaGlnGlnAlaArgSerMetValAspIleValIleValIleValIleValIleValIle 215
Db      655 TCCACCAAGCCCAAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 714
Qy      216 AlaValIleThrGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 235
Db      715 ACATGCTCTTGAAGGAGATTAAGTGAAGAGCGGTGATGAGCGCTTACCCAGATTCG 774
Qy      236 AlaIleValIleGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 254
Db      775 AGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 834
Qy      255 GlnSerPheAspIleValIleValIleValIleValIleValIleValIleValIleVal 274
Db      835 GAGGATTTTGAAGAAATTAATCAAGCGCTGCTA---GAAACACTTAATGCTCGAGCTG 891
Qy      275 AlaIleValIleGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 294
Db      892 ATTATGTTGCCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 951
Qy      295 LeuValIleGluPheLeuLeuLeuGlyArgGlu 305
Db      952 CAAAGTGGCATTTTCTCTGATGCTCAGAT 984

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Search completed: December 15, 2003, 01:01:26

Job time : 444 secs





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Result No.	Query			Description	
	Score	Match Length	ID		
1	1110	100.0	1110 14	US-10-027-993-3	Sequence 3, Appl
2	1110	100.0	1893 14	US-10-027-993-1	Sequence 1, Appl
3	1108	99.8	1788 10	US-09-822-830A-61	Sequence 6, Appl
4	222	20.0	2826 13	US-10-346-241-1	Sequence 1, Appl
5	222	20.0	3139 13	US-10-346-241-5	Sequence 5, Appl
6	222	20.0	4518 15	US-10-225-567A-177	Sequence 17, Appl
7	24	2.2	611 13	US-10-027-632-221104	Sequence 221104, Appl
8	24	2.2	611 13	US-10-027-632-221105	Sequence 221105, Appl
9	24	2.2	611 14	US-10-027-632-221104	Sequence 221104, Appl
10	24	2.2	611 14	US-10-027-632-221105	Sequence 221105, Appl
11	22	2.0	126512 10	US-09-824-474A-3	Sequence 3, Appl
12	21	1.9	3874 15	US-10-125-792-11	Sequence 11, Appl
13	21	1.9	3874 15	US-10-125-778-11	Sequence 11, Appl
14	21	1.9	3874 15	US-10-125-772-11	Sequence 11, Appl
15	21	1.9	3941 15	US-10-125-792-11	Sequence 11, Appl

16	21	1.9	3341	15	US-10-125-778-7	Sequence 7, App11
17	21	1.9	3341	15	US-10-125-772-7	Sequence 7, App11
18	21	1.9	4031	15	US-10-125-792-9	Sequence 9, App11
19	21	1.9	4031	15	US-10-125-778-9	Sequence 9, App11
20	21	1.9	4031	15	US-10-125-772-9	Sequence 9, App11
21	20	1.8	858	9	US-09-822-849A-150	Sequence 150, App
22	20	1.8	15002	11	US-09-770-107-3	Sequence 3, App11
23	19	1.7	510	13	US-10-027-632-86312	Sequence 86312, A
24	19	1.7	510	13	US-10-027-632-86312	Sequence 86313, A
25	19	1.7	510	14	US-10-027-632-86312	Sequence 86312, A
26	19	1.7	510	14	US-10-027-632-86313	Sequence 86313, A
27	19	1.7	791	13	US-10-027-632-168178	Sequence 168178
28	19	1.7	791	14	US-10-027-632-168178	Sequence 168178
29	19	1.7	800	13	US-10-027-632-8323	Sequence 8323, App
30	19	1.7	800	14	US-10-027-632-8323	Sequence 8323, App
31	19	1.7	3348	10	US-09-982-610-34	Sequence 34, App1
32	19	1.7	23433	10	US-09-927-091-7	Sequence 7, App11
33	19	1.7	32038	9	US-09-764-878-292	Sequence 292, App
34	19	1.7	32038	15	US-10-079-854-292	Sequence 292, App
35	19	1.7	93483	13	US-10-034-650-49	Sequence 49, App1
36	19	1.7	126512	10	US-09-804-474A-3	Sequence 3, App11
37	18	1.6	20	13	US-10-084-833-3407	Sequence 3407, App1
38	18	1.6	136	13	US-10-029-186-17332	Sequence 17332, A
39	18	1.6	235	13	US-10-287-274-474	Sequence 108, App
40	18	1.6	298	10	US-09-834-975-474	Sequence 474, App
41	18	1.6	355	10	US-09-783-590-9874	Sequence 9874, App
42	18	1.6	381	10	US-09-867-701-5269	Sequence 5269, App
43	18	1.6	415	13	US-10-027-632-268503	Sequence 268503
44	18	1.6	415	13	US-10-027-632-268504	Sequence 268504
45	18	1.6	415	14	US-10-027-632-268503	Sequence 268503

## ALIGNMENTS

RESULT 1  
 US-10-027-923-3  
 Sequence 3, Application US/10027923  
 Publication No. US20020142330A1  
 GENERAL INFORMATION:  
 APPLICANT: Brian Galtner Bates  
 APPLICANT: Kamalaka Gulukota  
 APPLICANT: Yuhong Xie  
 APPLICANT: Janet Elizabeth Paulsen  
 TITLE OF INVENTION: NOVEL GLUTAMATE RECEPTOR MODULATORY PROTEINS AND  
 TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND USES THEREFOR  
 FILE REFERENCE: GNN-024  
 CURRENT APPLICATION NUMBER: US/10/027,923  
 CURRENT FILING DATE: 2001-12-21  
 PRIOR APPLICATION NUMBER: 60/257,569  
 PRIOR FILING DATE: 2000-12-22  
 NUMBER OF SEQ ID NOS: 6  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 3  
 LENGTH: 1110  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURES:  
 NAME/KEY: CDS  
 LOCATION: (1)..(1110)  
 US-10-027-923-3

Query Match 100.0%; Score 1110; DB 14; Length 1110;  
 Best Local Similarity 100.0%; Prcd. No. 0;  
 Matches 1110; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 121 TTTTCTGTCATACCGACGCTACTGTGGAAGAGTTGATGAGGAAGTGTGGGGCAGTC 180  
DB 121 TTTTCTGTCATACCGACGCTACTGTGGAAGAGTTGATGAGGAAGTGTGGGGCAGTC 180  
QY 181 CGTGAACAGTATGGCATTCAGAGAGTGGAGGCCATGCTGCAATACCTTGAAAGAGTCAAT 240  
DB 181 CGTGAACAGTATGGCATTCAGAGAGTGGAGGCCATGCTGCAATACCTTGAAAGAGTCAAT 240  
QY 241 TCAGACCCCACTCTTGGCCCAATCACTGGGCTGTGAGATTAAGGATTCCTGCTGG 300  
DB 241 TCAGACCCCACTCTTGGCCCAATCACTGGGCTGTGAGATTAAGGATTCCTGCTGG 300  
QY 301 CATTGGCTGTGGCCCTAGAGCAGAGCATTGAGTTGATTAAGAGTTCCCTCATTTCTTCG 360  
DB 301 CATTGGCTGTGGCCCTAGAGCAGAGCATTGAGTTGATTAAGAGTTCCCTCATTTCTTCG 360  
QY 361 GAAGAGAGAGAGGCTTGTATGCTGTGAGATGGCTCTCTCTTCCCTCCGCTCCAG 420  
DB 361 GAAGAGAGAGAGGCTTGTATGCTGTGAGATGGCTCTCTCTTCCCTCCGCTCCAG 420  
QY 421 AAGCCCATAGTGGGCTCATTTGGGCTGTGCTTCCAGTTCTTTAGCCATTCAAGTCCAGAT 480  
DB 421 AAGCCCATAGTGGGCTCATTTGGGCTGTGCTTCCAGTTCTTTAGCCATTCAAGTCCAGAT 480  
QY 481 TTGCTCAGCTTTTCAACATACCTCAGATGGCTTACCTCAGCAACCATCATGATGTGAGT 540  
DB 481 TTGCTCAGCTTTTCAACATACCTCAGATGGCTTACCTCAGCAACCATCATGATGTGAGT 540  
QY 541 GACAGAAGCTGTTCATTAATTTTCATGAGGCTGTGCTTCCAGTTCTTTAGCCATTCAAGTCCAGAT 600  
DB 541 GACAGAAGCTGTTCATTAATTTTCATGAGGCTGTGCTTCCAGTTCTTTAGCCATTCAAGTCCAGAT 600  
QY 601 TCCATGTGAGCATATGTAAGAGGTACATCTGACCTATGATACAGCCGATACACAGAA 660  
DB 601 TCCATGTGAGCATATGTAAGAGGTACATCTGACCTATGATACAGCCGATACACAGAA 660  
QY 661 GGCAACTATGAGAAAGTGGAGTGAAGGCTTCAAAAGATATGTCAGGAAAGAAAGGAT 720  
DB 661 GGCAACTATGAGAAAGTGGAGTGAAGGCTTCAAAAGATATGTCAGGAAAGAAAGGAT 720  
QY 721 TGCATGCGCCACTCTTACAAATCTACAGTAAATGACAGGAGGAGCAAGCTTGTAAAGCTG 780  
DB 721 TGCATGCGCCACTCTTACAAATCTACAGTAAATGACAGGAGGAGCAAGCTTGTAAAGCTG 780  
QY 781 CTGAAGAAGCTCAAGTCACTTGGCCCAAGGCTGGGCTGTGCTTCTGTGAGGAGC 840  
DB 781 CTGAAGAAGCTCAAGTCACTTGGCCCAAGGCTGGGCTGTGCTTCTGTGAGGAGC 840  
QY 841 ATGACGCTGAGAGTGTGCTGATGAGGAGGCTTCAAAAGATATGTCAGGAAAGAAAGGAT 900  
DB 841 ATGACGCTGAGAGTGTGCTGATGAGGAGGCTTCAAAAGATATGTCAGGAAAGAAAGGAT 900  
QY 901 CTTCTGGGAGGAGAACAGATGTCATCTTATGAGATCTCAAAAGAACAGATCTATGG 960  
DB 901 CTTCTGGGAGGAGAACAGATGTCATCTTATGAGATCTCAAAAGAACAGATCTATGG 960  
QY 961 GAAGACAGAAAGAAATGCAAGTCTGCTTCTTCAAGGCTTTTGAGACATATTAACAGA 1020  
DB 961 GAAGACAGAAAGAAATGCAAGTCTGCTTCTTCAAGGCTTTTGAGACATATTAACAGA 1020  
QY 1021 AGGAGGCTGAGTGTGCTGATGAGGAGGCTTCAAAAGATATGTCAGGAAAGAAAGGAT 1080  
DB 1021 AGGAGGCTGAGTGTGCTGATGAGGAGGCTTCAAAAGATATGTCAGGAAAGAAAGGAT 1080  
QY 1081 ATCACTGAGTGAAGGAGCAGGCTCATCTAA 1110  
DB 1081 ATCACTGAGTGAAGGAGCAGGCTCATCTAA 1110

RESULT 2  
US-10-027-923-1  
; Sequence 1, Application US/10027923

Publication No. US20020142330A1  
GENERAL INFORMATION:  
APPLICANT: Briam Galtner Bates  
APPLICANT: Kamalaka Gulukota  
APPLICANT: Yuhong Xie  
APPLICANT: Janet Elizabeth Paulsen  
TITLE OF INVENTION: NOVEL GLUTAMATE RECEPTOR MODULATORY PROTEINS AND  
NUCLEIC ACID MOLECULES AND USES THEREFOR  
FILE REFERENCE: GNM-024  
CURRENT APPLICATION NUMBER: US/10/027,923  
CURRENT FILING DATE: 2001-12-21  
PRIOR APPLICATION NUMBER: 60/257,589  
PRIOR FILING DATE: 2000-12-22  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1  
LENGTH: 1823  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (4)..(1110)  
US-10-027-923-1  
Query Match 100.0%; Score 1110; DB 14; Length 1823;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 4 ATGTCCTTCTGTGATTCCTGTCAGTCTTACCTTTGAAAGAAAGATGTCGGTGGAGTCA 63  
QY 61 CAGTCCAGAGAGAGAGGAGTGTGCTCAAGCTGGGAGTCACTATTATGAGCTTC 120  
DB 64 CAGTCCAGAGAGAGAGGAGTGTGCTCAAGCTGGGAGTCACTATTATGAGCTTC 123  
QY 121 TTTTCTGTCATACCGACGCTACTGTGGAAGAGTTGATGAGGAAGTGTGGGGCAGTC 180  
DB 124 TTTTCTGTCATACCGACGCTACTGTGGAAGAGTTGATGAGGAAGTGTGGGGCAGTC 183  
QY 181 CGTGAACAGTATGGCATTCAGAGAGTGGAGGCCATGCTGCAATACCTTGAAAGAGTCAAT 240  
DB 184 CGTGAACAGTATGGCATTCAGAGAGTGGAGGCCATGCTGCAATACCTTGAAAGAGTCAAT 243  
QY 241 TCAGACCCCACTCTTGGCCCAATCACTGGGCTGTGAGATTAAGGATTCCTGCTGG 300  
DB 244 TCAGACCCCACTCTTGGCCCAATCACTGGGCTGTGAGATTAAGGATTCCTGCTGG 303  
QY 301 CATTGGCTGTGGCCCTAGAGCAGAGCATTGAGTTGATTAAGAGTTCCCTCATTTCTTCG 360  
DB 304 CATTGGCTGTGGCCCTAGAGCAGAGCATTGAGTTGATTAAGAGTTCCCTCATTTCTTCG 363  
QY 361 GAAGAGAGAGAGGCTTGTATGCTGTGAGATGGCTCTCTCTTCCCTCCGCTCCAG 420  
DB 364 GAAGAGAGAGAGGCTTGTATGCTGTGAGATGGCTCTCTCTTCCCTCCGCTCCAG 423  
QY 421 AAGCCCATAGTGGGCTCATTTGGGCTGTGCTTCCAGTTCTTTAGCCATTCAAGTCCAGAT 480  
DB 424 AAGCCCATAGTGGGCTCATTTGGGCTGTGCTTCCAGTTCTTTAGCCATTCAAGTCCAGAT 483  
QY 481 TTGCTCAGCTTTTCAACATACCTCAGATGGCTTACCTCAGCAACCATCATGATGTGAGT 540  
DB 484 TTGCTCAGCTTTTCAACATACCTCAGATGGCTTACCTCAGCAACCATCATGATGTGAGT 543  
QY 541 GACAGAAGCTGTTCATTAATTTTCATGAGGCTTGTGCTTCCAGATGCTGAGAGG 600  
DB 544 GACAGAAGCTGTTCATTAATTTTCATGAGGCTTGTGCTTCCAGATGCTGAGAGG 603  
QY 601 TCCATGTGAGCATATGTAAGAGGTACATCTGACCTATGATACAGCCGATACACAGAA 660  
DB 604 TCCATGTGAGCATATGTAAGAGGTACATCTGACCTATGATACAGCCGATACACAGAA 663  
QY 661 GGCAACTATGAGAAAGTGGAGTGAAGGCTTCAAAAGATATGTCAGGAAAGAAAGGAT 720

Db	664	GGCAACTATGAGAAAGTGGAGTGAGACCTTTCAAAAGATATGTACGCAGAAAGGAGATT	723
Qy	721	TGCATCGCCCACTCTTACAAAATCTACAGTATATGCAGGGGAGCAGAGCTTTGATAGCTG	780
Db	724	TGCATCGCCCACTCTTACAAAATCTACAGTATATGCAGGGGAGCAGAGCTTTGATAGCTG	783
Qy	781	CTGAAGAAGCTCACAGTCACTCTTGCCCAAGGCCCGGGGTGTGTGCTACTTCTGTGAGGGC	840
Db	784	CTGAAGAAGCTCACAGTCACTCTTGCCCAAGGCCCGGGGTGTGTGCTACTTCTGTGAGGGC	843
Qy	841	ATGACGGTGAAGAGGTCTGTCATGAGCCCATGAGCGCCTGGGCTTATGTTGAGGAATTTCTG	900
Db	844	ATGACGGTGAAGAGGTCTGTCATGAGCCCATGAGCGCCTGGGCTTATGTTGAGGAATTTCTG	903
Qy	901	CTTCTGGGCAAGGAAACAGATGCGATCTTTATTTAGATCTCAAGAGACAGATCCTATGG	960
Db	904	CTTCTGGGCAAGGAAACAGATGCGATCTTTATTTAGATCTCAAGAGACAGATCCTATGG	963
Qy	961	GAAACAGAGAGAAAATGCCAAGTGCCTTCTTGAGGGTTTTGAGACATTTACACAGA	1020
Db	964	GAAACAGAGAGAAAATGCCAAGTGCCTTCTTGAGGGTTTTGAGACATTTACACAGA	1023
Qy	1021	AGTAGTCCCGTCTGTGTCACATGCGCCCAAGGCTCTGAATCTTAGAGCTCAGTTTCAGGGCCC	1080
Db	1024	AGTAGTCCCGTCTGTGTCACATGCGCCCAAGGCTCTGAATCTTAGAGCTCAGTTTCAGGGCCC	1083
Qy	1081	ATCACTGGACTGAGGGACAGGCTCATCTTAA	1110
Db	1084	ATCACTGGACTGAGGGACAGGCTCATCTTAA	1113

### RESULT 3

US-09-822-830A-61  
; Sequence 61, Application US/09822830A

Patent NO. US20020142952A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Genetics Institute, Inc.  
 : APPLICANT: Mong, Gordon G.  
 : APPLICANT: Clark, Hilary  
 : APPLICANT: Fechtel, Kim  
 : APPLICANT: Agostino, Michael J.  
 : APPLICANT: Howes, Steven H.  
 : APPLICANT: Resnick, Richard J.  
 : APPLICANT: Gulikota, Kamalkar  
 : APPLICANT: Graham, James R.  
 : TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS  
 : FILE REFERENCE: GIN 6402  
 : CURRENT APPLICATION NUMBER: US/09/822,830A  
 : CURRENT FILING DATE: 2001-03-29  
 : PRIOR APPLICATION NUMBER: 60/135,604  
 : PRIOR FILING DATE: 2000-04-06  
 : NUMBER OF SEQ ID NOS: 631  
 : SOFTWARE: PatentIn Ver. 2.0  
 : SEQ ID NO 61  
 : LENGTH: 1788  
 : TYPE: DNA  
 : ORGANISM: Homo sapiens  
 : US-09-822-830A-61

Query Match	99.8%	Score 1108;	DB 10;	Length 1768;
Best Local Similarity	100.0%	Pred. NO. 0;		
Matches 1108; Conservative	0;	Mismatches	0;	Gaps 0;

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Db 1 GGCCTCTTCGTTGATCTCTCAGTCTTAACTTTTGGAAAGAAATGTCGCGTGGAGATGCACA 60

QY 63 GTCACAGNAGAGAGGGATGGTGGCTCAATGCTGGGTACATCATTAATTTGAGAGCTCTCTT 122

Db 61 GTCACATGAGAGAGGGATGGTGGCTCAATGCTGGGTACATCATTAATTTGAGAGCTCTCTT 120

QY 123 TTCCTGTTCAATCACACGCTTACTGTGGACGAAATTCAATGAGAGGAATGTGTGGGAGCATGTCG 182

Db	121	TTCTGTTCAATCCAGGCTACTGTGAGGAAAGTTCAATGAGGAAAGTGTGGGCAAGTCCG	180
Qy	183	TGAACAGTATGGCATTTAGAGATGGAGGCGCATCTGTGATACCTTGGAAAGATCAATTC	242
Db	181	TGAACAGTATGGCATTTAGAGATGGAGGCGCATCTGTGATACCTTGGAAAGATCAATTC	240
Qy	243	AGACCCCAACCTCTGGCCCAACATCACACTGGGGGTGAGATTAAGGGATTCCTGTGCA	302
Db	241	AGACCCCAACCTCTGGCCCAACATCACACTGGGGGTGAGATTAAGGGATTCCTGTGCA	300
Qy	303	TTGGCTGTGGCCCTTAGAGACAGACATTTAGATTCTAAGAGATTCCTCATTTCTTCCGA	362
Db	301	TTGGCTGTGGCCCTTAGAGACAGACATTTAGATTCTAAGAGATTCCTCATTTCTTCCGA	360
Qy	363	AGAGGAAGAGGGCTTGGTATGCTTGTGGATGGCTCTCTCTTCTTCTTCCGCTCCAGAA	422
Db	361	AGAGGAAGAGGGCTTGGTATGCTTGTGGATGGCTCTCTCTTCTTCTTCCGCTCCAGAA	420
Qy	423	GCCCATAGTAGGGGTCAATGGGCGCTGGTCCAGTTCTTTAGCCAAATTCAGTCCAGAAATTT	482
Db	421	GCCCATAGTAGGGGTCAATGGGCGCTGGTCCAGTTCTTTAGCCAAATTCAGTCCAGAAATTT	480
Qy	483	GCTTCAGCTTTTCAACATACCTCAGATTGCTTACTCAGCAACCATCATGATCTGATGA	542
Db	481	GCTTCAGCTTTTCAACATACCTCAGATTGCTTACTCAGCAACCATCATGATCTGATGA	540
Qy	543	CAAGACTCTGTCCAAATATTTCATGAGGGTGTGCTTCAGATGCTCAGAGGCAAGGTC	602
Db	541	CAAGACTCTGTCCAAATATTTCATGAGGGTGTGCTTCAGATGCTCAGAGGCAAGGTC	600
Qy	603	CATGTGGACATGTAAGTAAGTAACTGAGCCTATGATCAGCCGTACACAGAAAG	662
Db	601	CATGTGGACATGTAAGTAAGTAACTGAGCCTATGATCAGCCGTACACAGAAAG	660
Qy	663	CAACTATGGAGAAAGTGGAGTGAAGGCTTCAAGATATGTCAAGCAAGAAAGGAATTTG	722
Db	661	CAACTATGGAGAAAGTGGAGTGAAGGCTTCAAGATATGTCAAGCAAGAAAGGAATTTG	720
Qy	723	CATGCGCCACTTTCACAAAATCTACAGTAAATGCAGGGAGCAGAGCTTGTATTAAGTGTCT	782
Db	721	CATGCGCCACTTTCACAAAATCTACAGTAAATGCAGGGAGCAGAGCTTGTATTAAGTGTCT	780
Qy	783	GAAAGAGCTACAAAGTACATTTGCCCAAGGCGCGGGTGTGCTTACTTCTGTGAGGCGAT	842
Db	781	GAAAGAGCTACAAAGTACATTTGCCCAAGGCGCGGGTGTGCTTACTTCTGTGAGGCGAT	840
Qy	843	GACGCTAGAGGCTCTGTGATGAGCATGAGGCGGCTGGGCTCTAGTGGAGAAATTTCTGCT	902
Db	841	GACGCTAGAGGCTCTGTGATGAGCATGAGGCGGCTGGGCTCTAGTGGAGAAATTTCTGCT	900
Qy	903	TTGGGAGGAGAAACAGATGCCATCTTATTTAGATCTCAAGAAACAGATCTATGGGA	962
Db	901	TTGGGAGGAGAAACAGATGCCATCTTATTTAGATCTCAAGAAACAGATCTATGGGA	960
Qy	963	AGACAGAAAGAAATGCCAAGTGGCTCTTCAAGGGTTTGGAGACATTAATTAACAAGAG	1022
Db	961	AGACAGAAAGAAATGCCAAGTGGCTCTTCAAGGGTTTGGAGACATTAATTAACAAGAG	1020
Qy	1023	TGAGTCCGTCTCTGTGACATGGCCCAAGCCTTGAATCTAGAGCTCAGTTCAAGGCCCAT	1082
Db	1021	TGAGTCCGTCTCTGTGACATGGCCCAAGCCTTGAATCTAGAGCTCAGTTCAAGGCCCAT	1080
Qy	1083	CACCTGACTGAGGAGACAGGCTCAATCTAA	1110
Db	1081	CACCTGACTGAGGAGACAGGCTCAATCTAA	1108

**9**

US-10-346-241-1

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; Sequence 1, Application US/10346241
; Publication No. US20030157647A1
; GENERAL INFORMATION:

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APPLICANT: STORMANN, THOMAS M.  
APPLICANT: LEVINTHAL, CYNTHIA  
APPLICANT: STORJOHANN, LAURA  
APPLICANT: HAMMERLAND, LANCE G.  
APPLICANT: KRAPCHO, KAREN J.  
APPLICANT: NPS PHARMACEUTICALS, INC.  
TITLE OF INVENTION: A NOVEL HUMAN METABOTROPIC GLUTAMATE RECEPTOR  
FILE REFERENCE: 1094.2.6  
CURRENT APPLICATION NUMBER: US/10/346,241  
CURRENT FILING DATE: 2003-01-17  
PRIOR APPLICATION NUMBER: US/09/695,481  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: 60/161,481  
PRIOR FILING DATE: 1999-10-25  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 2826  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(2826)  
US-10-346-241-1

Query Match 20.0%; Score 222; DB 13; Length 2826;  
Best Local Similarity 99.1%; Pred. No. 7.3e-108;  
Matches 422; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 461 TAGCCATTGAGTTCAGAAATTTGCTCCAGCTTTTCAACATACCTCAGATTGTTACTCAG 520  
DB 461 TAGCCATTGAGTTCAGAAATTTGCTCCAGCTTTTCAACATACCTCAGATTGTTACTCAG 520  
QY 521 CAACCATCATGATCTGATGAGCAAGACTCTGTTCAAAATTTTCATGAGGGTTGTGCTT 580  
DB 521 CAACCATCATGATCTGATGAGCAAGACTCTGTTCAAAATTTTCATGAGGGTTGTGCTT 580  
QY 581 CAGATCTCAGCAGGCAAGGTCATGATGAGCAATGAGAGAGTGAAGAGTGAAGAGTGAAG 640  
DB 581 CAGATCTCAGCAGGCAAGGTCATGATGAGCAATGAGAGAGTGAAGAGTGAAGAGTGAAG 640  
QY 641 TATCAGCCGTGACACAGAAAGCACTATGAGAAAGTGGAGTGAAGAGTGAAGAGTGAAG 700  
DB 641 TATCAGCCGTGACACAGAAAGCACTATGAGAAAGTGGAGTGAAGAGTGAAGAGTGAAG 700  
QY 701 TGTCAAGCAAGAAAGGATTTGATGCGCCCACTTTCAAAATCTACAGTAATGCAAGGG 760  
DB 701 TGTCAAGCAAGAAAGGATTTGATGCGCCCACTTTCAAAATCTACAGTAATGCAAGGG 760  
QY 761 AGCAGAGCTTTGATAGCTGCTGAAGAGTCAAGTCACTTCCCAAGGCCCGGGTGG 820  
DB 761 AGCAGAGCTTTGATAGCTGCTGAAGAGTCAAGTCACTTCCCAAGGCCCGGGTGG 820  
QY 821 TGGCCTACTTCTGTGAGGCGATGACGGTGAAGAGTCTGCTGATGAGCCATGAGGCGCTGG 880  
DB 821 TGGCCTACTTCTGTGAGGCGATGACGGTGAAGAGTCTGCTGATGAGCCATGAGGCGCTGG 880  
QY 881 GTCTAG 886  
DB 881 GTCTAG 886

RESULT 5  
US-10-346-241-5  
Sequence 5, Application US/10346241  
Publication No. US20030157647A1  
GENERAL INFORMATION:  
APPLICANT: STORMANN, THOMAS M.  
APPLICANT: LEVINTHAL, CYNTHIA  
APPLICANT: STORJOHANN, LAURA  
APPLICANT: HAMMERLAND, LANCE G.  
APPLICANT: KRAPCHO, KAREN J.  
APPLICANT: NPS PHARMACEUTICALS, INC.

TITLE OF INVENTION: A NOVEL HUMAN METABOTROPIC GLUTAMATE RECEPTOR  
FILE REFERENCE: 1094.2.6  
CURRENT APPLICATION NUMBER: US/10/346,241  
CURRENT FILING DATE: 2003-01-17  
PRIOR APPLICATION NUMBER: US/09/695,481  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: 60/161,481  
PRIOR FILING DATE: 1999-10-25  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 5  
LENGTH: 3129  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Chimeric  
OTHER INFORMATION: molecule comprising portions of human mGluR5 and  
OTHER INFORMATION: the human calcium receptor.  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(3129)  
US-10-346-241-5

Query Match 20.0%; Score 222; DB 13; Length 3129;  
Best Local Similarity 99.1%; Pred. No. 7.3e-108;  
Matches 422; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 461 TAGCCATTGAGTTCAGAAATTTGCTCCAGCTTTTCAACATACCTCAGATTGTTACTCAG 520  
DB 461 TAGCCATTGAGTTCAGAAATTTGCTCCAGCTTTTCAACATACCTCAGATTGTTACTCAG 520  
QY 521 CAACCATCATGATCTGATGAGCAAGACTCTGTTCAAAATTTTCATGAGGGTTGTGCTT 580  
DB 521 CAACCATCATGATCTGATGAGCAAGACTCTGTTCAAAATTTTCATGAGGGTTGTGCTT 580  
QY 581 CAGATCTCAGCAGGCAAGGTCATGATGAGCAATGAGAGTGAAGAGTGAAGAGTGAAG 640  
DB 581 CAGATCTCAGCAGGCAAGGTCATGATGAGCAATGAGAGTGAAGAGTGAAGAGTGAAG 640  
QY 641 TATCAGCCGTGACACAGAAAGCACTATGAGAAAGTGGAGTGAAGAGTGAAGAGTGAAG 700  
DB 641 TATCAGCCGTGACACAGAAAGCACTATGAGAAAGTGGAGTGAAGAGTGAAGAGTGAAG 700  
QY 701 TGTCAAGCAAGAAAGGATTTGATGCGCCCACTTTCAAAATCTACAGTAATGCAAGGG 760  
DB 701 TGTCAAGCAAGAAAGGATTTGATGCGCCCACTTTCAAAATCTACAGTAATGCAAGGG 760  
QY 761 AGCAGAGCTTTGATAGCTGCTGAAGAGTCAAGTCACTTCCCAAGGCCCGGGTGG 820  
DB 761 AGCAGAGCTTTGATAGCTGCTGAAGAGTCAAGTCACTTCCCAAGGCCCGGGTGG 820  
QY 821 TGGCCTACTTCTGTGAGGCGATGACGGTGAAGAGTCTGCTGATGAGCCATGAGGCGCTGG 880  
DB 821 TGGCCTACTTCTGTGAGGCGATGACGGTGAAGAGTCTGCTGATGAGCCATGAGGCGCTGG 880  
QY 881 GTCTAG 886  
DB 881 GTCTAG 886

RESULT 6  
US-10-225-567A-177  
Sequence 177, Application US/10225567A  
Publication No. US20030113798A1  
GENERAL INFORMATION:  
APPLICANT: Lifespan Biosciences  
APPLICANT: Brown, Joseph P.  
APPLICANT: Burner, Glenn C.  
APPLICANT: Roush, Christine L.  
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS  
FILE REFERENCE: 1920-4-4  
CURRENT APPLICATION NUMBER: US/10/225,567A  
CURRENT FILING DATE: 2001-12-19

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; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 177
; LENGTH: 4518
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-225-567A-177

Query Match
Best Local Similarity 99.1%; Score 222; DB 15; Length 4518;
Pred. No. 7,3e-108; Mismatches 4; Indels 0; Gaps 0;
Matches 422; Conservative 0;

461 TAGCCATTGAGTCCGAATTTGCTCCAGCTTTTCAACATCTGATGCTTACTG 520
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611 TAGCCATTGAGTCCGAATTTGCTCCAGCTTTTCAACATCTGATGCTTACTG 670
|||||
521 CAACCATCATGATCTGATGACAGACTCTGTTCAAAATTTTCAAGGGTTGCTT 580
|||||
671 CAACCATCATGATCTGATGACAGACTCTGTTCAAAATTTTCAAGGGTTGCTT 730
|||||
581 CAGATCTTCAAGCAGCAAGGCTTCATGTCATGTAAGTAAGTAACAATGACCTATG 640
|||||
731 CAGATCTTCAAGCAGCAAGGCTTCATGTCATGTAAGTAAGTAACAATGACCTATG 790
|||||
641 TATCAGCCGTACACAGAAAGGCACTATGAGAAAGTGGATGAAAGCTTCAAGATA 700
|||||
791 TATCAGCCGTACACAGAAAGGCACTATGAGAAAGTGGATGAAAGCTTCAAGATA 850
|||||
701 TGTCAAGCAAGAAAGGATTTGATGCGCCACTCTTACAAATCTACATGATGACGGG 760
|||||
851 TGTCAAGCAAGAAAGGATTTGATGCGCCACTCTTACAAATCTACATGATGACGGG 910
|||||
911 AGCAGAGCTTTGATGAGCTGCTGTAAGAGCTCAAGTCACTTGCACCAAGGCGG 970
|||||
821 TGGCTACTTCTGTGAGGGCATACGGTGAAGAGTCTGCTGATGCGCATGAGCGCTTG 880
|||||
971 TGGCTACTTCTGTGAGGGCATACGGTGAAGAGTCTGCTGATGCGCATGAGCGCTTG 1030
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881 GCTTAG 886
|||||
1031 GCTTAG 1036

RESULT 7
US-10-027-632-221104
; Sequence 221104, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827,129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 221104
; LENGTH: 611
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-221104

Query Match
Best Local Similarity 100.0%; Score 24; DB 13; Length 611;
Pred. No. 0.05; Mismatches 0; Indels 0; Gaps 0;
Matches 24; Conservative 0;

885 AGTGGAGAAATTTCTGCTTCTGGG 908
|||||
49 AGTGGAGAAATTTCTGCTTCTGGG 72
|||||

RESULT 8
US-10-027-632-221105
; Sequence 221105, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827,129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 221105
; LENGTH: 611
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-221105

Query Match
Best Local Similarity 100.0%; Score 24; DB 13; Length 611;
Pred. No. 0.05; Mismatches 0; Indels 0; Gaps 0;
Matches 24; Conservative 0;

885 AGTGGAGAAATTTCTGCTTCTGGG 908
|||||
49 AGTGGAGAAATTTCTGCTTCTGGG 72
|||||

RESULT 9
US-10-027-632-221104
; Sequence 221104, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827,129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
```

```
/ PRIOR FILING DATE: 2000-03-29
/ PRIOR APPLICATION NUMBER: US 60/185,218
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: US 60/167,363
/ PRIOR FILING DATE: 1999-11-23
/ PRIOR APPLICATION NUMBER: US 60/156,358
/ PRIOR FILING DATE: 1999-09-28
/ PRIOR APPLICATION NUMBER: US 60/146,002
/ PRIOR FILING DATE: 1999-08-09
/ NUMBER OF SEQ ID NOS: 325720
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 221104
/ LENGTH: 611
/ TYPE: DNA
/ ORGANISM: Human
US-10-027-632-221104
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Query Match      2.2%; Score 24; DB 14; Length 611;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      885 AGTGGAGAAATTTCTGCTCGGG 908
DB      49 AGTGGAGAAATTTCTGCTCGGG 72
```

## RESULT 10

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US-10-027-632-221105
/ Sequence 221105, Application US/10027632
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
/ FILE REFERENCE: 108827.129
/ CURRENT APPLICATION NUMBER: US/10/027,632
/ CURRENT FILING DATE: 2002-04-30
/ PRIOR APPLICATION NUMBER: US 60/218,006
/ PRIOR FILING DATE: 2000-07-12
/ PRIOR APPLICATION NUMBER: US 60/198,676
/ PRIOR FILING DATE: 2000-04-20
/ PRIOR APPLICATION NUMBER: US 60/193,483
/ PRIOR FILING DATE: 2000-03-29
/ PRIOR APPLICATION NUMBER: US 60/185,218
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: US 60/167,363
/ PRIOR FILING DATE: 1999-11-23
/ PRIOR APPLICATION NUMBER: US 60/156,358
/ PRIOR FILING DATE: 1999-09-28
/ PRIOR APPLICATION NUMBER: US 60/146,002
/ PRIOR FILING DATE: 1999-08-09
/ NUMBER OF SEQ ID NOS: 325720
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 221105
/ LENGTH: 611
/ TYPE: DNA
/ ORGANISM: Human
US-10-027-632-221105
```

```
Query Match      2.2%; Score 24; DB 14; Length 611;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      885 AGTGGAGAAATTTCTGCTCGGG 908
DB      49 AGTGGAGAAATTTCTGCTCGGG 72
```

```
RESULT 11
US-09-804-474A-3
/ Sequence 3, Application US/09804474A
/ Patent No. US20020119518A1
/ GENERAL INFORMATION:
/ APPLICANT: KODET, Stefan et al
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/ TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
/ TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
/ FILE REFERENCE: C1000891
/ CURRENT APPLICATION NUMBER: US/09/804,474A
/ CURRENT FILING DATE: 2001-03-13
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 3
/ LENGTH: 126512
/ TYPE: DNA
/ ORGANISM: Human
/ FEATURE:
/ NAME/KEY: misc.feature
/ LOCATION: (1)...(126512)
/ OTHER INFORMATION: n = A,T,C or G
US-09-804-474A-3
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Query Match      2.0%; Score 22; DB 10; Length 126512;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      357 TTGGAAGAGAGAGAGGCTTG 378
DB      87864 TTGGAAGAGAGAGAGGCTTG 87885
```

## RESULT 12

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US-10-125-792-11
/ Sequence 11, Application US/10125792
/ Publication No. US20030051269A1
/ GENERAL INFORMATION:
/ APPLICANT: Marical
/ APPLICANT: Harris, H. William
/ APPLICANT: Nearing, Jacqueline A.
/ TITLE OF INVENTION: Polyvalent Cation-Sensing Receptor in Atlantic Salmon
/ FILE REFERENCE: 2213.1006-007
/ CURRENT APPLICATION NUMBER: US/10/125,792
/ CURRENT FILING DATE: 2002-08-16
/ PRIOR APPLICATION NUMBER: 10/121,441
/ PRIOR FILING DATE: 2002-04-11
/ PRIOR APPLICATION NUMBER: PCT/US01/31704
/ PRIOR FILING DATE: 2001-10-11
/ PRIOR APPLICATION NUMBER: 60/240,392
/ PRIOR FILING DATE: 2000-10-12
/ PRIOR APPLICATION NUMBER: 60/240,003
/ PRIOR FILING DATE: 2000-10-12
/ NUMBER OF SEQ ID NOS: 28
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 11
/ LENGTH: 3824
/ TYPE: DNA
/ ORGANISM: Salmo salar
US-10-125-792-11
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Query Match      1.9%; Score 21; DB 15; Length 3824;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      257 TGCCCAACATCACACTGGGCT 277
DB      443 TGCCCAACATCACACTGGGCT 463
```

```
RESULT 13
US-10-125-778-11
/ Sequence 11, Application US/10125778
/ Publication No. US20030082574A1
/ GENERAL INFORMATION:
/ APPLICANT: Marical
/ APPLICANT: Harris, H. William
/ APPLICANT: Nearing, Jacqueline A.
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; APPLICANT: Betka, Marlies  
; TITLE OF INVENTION: Polyvalent Cation-Sensing Receptor in Atlantic Salmon  
; FILE REFERENCE: 2213.1006-005  
; CURRENT APPLICATION NUMBER: US/10/125,778  
; CURRENT FILING DATE: 2002-08-16  
; PRIOR APPLICATION NUMBER: 10/121,441  
; PRIOR FILING DATE: 2002-04-11  
; PRIOR APPLICATION NUMBER: PCT/US01/31704  
; PRIOR FILING DATE: 2001-10-11  
; PRIOR APPLICATION NUMBER: 60/240,392  
; PRIOR FILING DATE: 2000-10-12  
; PRIOR APPLICATION NUMBER: 60/240,003  
; PRIOR FILING DATE: 2000-10-12  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 11  
; LENGTH: 3824  
; TYPE: DNA  
; ORGANISM: Salmo salar  
US-10-125-778-11

Query Match 1.9%; Score 21; DB 15; Length 3824;  
Best Local Similarity 100.0%; Pred. No. 2;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 257 TGCCCAACATCACACTGGGCT 277  
DB 443 TGCCCAACATCACACTGGGCT 463

RESULT 14  
US-10-125-772-11  
; Sequence 11, Application US/10125772  
; Publication No. US20030124657A1  
; GENERAL INFORMATION:  
; APPLICANT: Marical  
; APPLICANT: Harris, H. William  
; APPLICANT: Nearing, Jacqueline A.  
; APPLICANT: Betka, Marlies  
; TITLE OF INVENTION: Polyvalent Cation-Sensing Receptor in Atlantic Salmon  
; FILE REFERENCE: 2213.1006-006  
; CURRENT APPLICATION NUMBER: US/10/125,772  
; CURRENT FILING DATE: 2002-08-16  
; PRIOR APPLICATION NUMBER: 10/121,441  
; PRIOR FILING DATE: 2002-04-11  
; PRIOR APPLICATION NUMBER: PCT/US01/31704  
; PRIOR FILING DATE: 2001-10-11  
; PRIOR APPLICATION NUMBER: 60/240,392  
; PRIOR FILING DATE: 2000-10-12  
; PRIOR APPLICATION NUMBER: 60/240,003  
; PRIOR FILING DATE: 2000-10-12  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 11  
; LENGTH: 3824  
; TYPE: DNA  
; ORGANISM: Salmo salar  
US-10-125-772-11

Query Match 1.9%; Score 21; DB 15; Length 3824;  
Best Local Similarity 100.0%; Pred. No. 2;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 257 TGCCCAACATCACACTGGGCT 277  
DB 443 TGCCCAACATCACACTGGGCT 463

RESULT 15  
US-10-125-792-7  
; Sequence 7, Application US/10125792  
; Publication No. US20030051269A1  
; GENERAL INFORMATION:

; APPLICANT: Marical  
; APPLICANT: Harris, H. William  
; APPLICANT: Nearing, Jacqueline A.  
; APPLICANT: Betka, Marlies  
; TITLE OF INVENTION: Polyvalent Cation-Sensing Receptor in Atlantic Salmon  
; FILE REFERENCE: 2213.1006-007  
; CURRENT APPLICATION NUMBER: US/10/125,792  
; CURRENT FILING DATE: 2002-08-16  
; PRIOR APPLICATION NUMBER: 10/121,441  
; PRIOR FILING DATE: 2002-04-11  
; PRIOR APPLICATION NUMBER: PCT/US01/31704  
; PRIOR FILING DATE: 2001-10-11  
; PRIOR APPLICATION NUMBER: 60/240,392  
; PRIOR FILING DATE: 2000-10-12  
; PRIOR APPLICATION NUMBER: 60/240,003  
; PRIOR FILING DATE: 2000-10-12  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7  
; LENGTH: 3941  
; TYPE: DNA  
; ORGANISM: Salmo salar  
US-10-125-792-7

Query Match 1.9%; Score 21; DB 15; Length 3941;  
Best Local Similarity 100.0%; Pred. No. 2;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 257 TGCCCAACATCACACTGGGCT 277  
DB 442 TGCCCAACATCACACTGGGCT 462

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GenCore version 5.1.6  
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Run on: December 14, 2003, 23:43:52 ; Search time 355 Seconds  
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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2552756 seqs, 1349719017 residues  
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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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13: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:\*  
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15: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:\*  
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19: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:\*  
20: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:\*  
21: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:\*  
22: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:\*  
23: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:\*  
24: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:\*  
25: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:\*  
26: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1873	100.0	1823	ABV73899	Human glutamate re
2	1870	99.8	2172	AAF29993	Human GRXK-1e DNA.
3	1868	99.7	1788	AA562274	CDNA sequence #61
4	1830.5	97.7	2349	AAF29990	Human GRXK-1b DNA.
5	1794	95.8	2149	AAF29994	Human GRXK-1f DNA.
6	1780	95.0	2551	AAF29989	Human GRXK-1c DNA.
7	1754.5	93.7	2326	AAF29991	Human GRXK-1g DNA.
8	1648	88.0	2064	AAF29995	Human GRXK-1d DNA.
9	1608.5	85.9	2241	AAF29992	Human GRXK-1e DNA.
10	1484.5	79.3	2826	AA085785	CDNA encoding meta
11	1484.5	79.3	3129	AA085787	CDNA encoding chim
12	1484.5	79.3	4078	AA085789	Human signaling p
13	1484.5	79.3	4207	AA085790	Human metabotropic
14	1484.5	79.3	4207	AA085791	Human metabotropic
15	1484.5	79.3	4207	AA085792	Human metabotropic
16	1484.5	79.3	4207	AA085793	Human metabotropic
17	1484.5	79.3	4303	AA085794	Human metabotropic
18	1484.5	79.3	4303	AA085795	Human metabotropic
19	1484.5	79.3	4303	AA085796	Human metabotropic
20	1484.5	79.3	4303	AA085797	Human metabotropic
21	1470.5	78.5	3282	AA080421	Human metabotropic
22	1470.5	78.5	4085	AA080422	Human metabotropic
23	1470.5	78.5	4181	AA080423	Human metabotropic
24	1460	77.9	3591	AA210801	Mouse metabotropic
25	1460	77.9	3591	AA210802	Rat metabotropic
26	1118.5	59.7	3235	AA235146	Non-endogenous hum
27	1118.5	59.7	3321	AA235147	Human gene express
28	1118.5	59.7	3321	AA235148	Human metabotropic
29	1118.5	59.7	3321	AA235149	Human metabotropic
30	1118.5	59.7	3321	AA235150	Human metabotropic
31	1118.5	59.7	3321	AA235151	Human metabotropic
32	1118.5	59.7	3321	AA235152	Human metabotropic
33	1117.5	59.7	3384	AA235153	Human metabotropic
34	1117.5	59.7	3384	AA235154	Human metabotropic
35	1117.5	59.7	3384	AA235155	Human metabotropic
36	1111.5	59.3	3319	AA235156	Human metabotropic
37	1111.5	59.3	3319	AA235157	Human metabotropic
38	550	29.4	2830	AA172375	Human metabotropic
39	550	29.4	2830	AA172376	Human metabotropic
40	548	29.3	2727	AA072799	Human GRM8 gene co
41	548	29.3	3177	AA231061	Chimeric hmglur8/h
42	548	29.3	3177	AA231062	Chimeric hmglur8/h
43	548	29.3	3380	AA593639	DNA encoding novel
44	548	29.3	3321	AAV04206	Human metabotropic
45	548	29.3	3321	AAV04207	Human metabotropic

## ALIGNMENTS

RESULT 1  
ABV73899 standard; CDNA; 1823 BP.  
XX ABV73899;  
XX 08-JUN-2003 (first entry)  
XX Human glutamate receptor modulatory protein mglur5m cdna.  
XX Metabotropic glutamate receptor subtype 5 modulatory protein;  
XX metabotropic glutamate receptor coupled receptor; receptor; schizophrenia;  
XX schizophrenia; human; G-protein coupled receptor; receptor; schizophrenia;  
XX unipolar affective disorder; bipolar affective disorder;  
XX unipolar affective disorder; adolescent conduct disorder;  
XX neurotropic; neuroprotective; neuroleptic; chromosome 11;  
XX gene therapy; gene; ss.

OS Homo sapiens.  
 XX Key Location/Qualifiers  
 XX CDS 4...113  
 FT /\*tag= a  
 FT /product= "mglur5m"  
 FT /note= "the CDS is specifically claimed in Claim 1"  
 FT sig\_peptide 4...63  
 FT /\*tag= b  
 FT mat\_peptide 64...110  
 FT /\*tag= c  
 XX WO200270708-A2.  
 XX 12-SEP-2002.  
 XX 21-DEC-2001; 2001WO-US49817.  
 XX 22-DEC-2000; 2000US-257589P.  
 XX (AMHP ) WYETH.  
 XX Bates BG, Xie Y, Gulukoca K, Paulsen JB;  
 PI WPI; 2002-750462/81.  
 DR P-PSDB; ABP54921.  
 XX  
 XX New mglur5m nucleic acid molecules and proteins, useful for treating  
 PT neurological or psychiatric disorders such as schizophrenia,  
 PT schizoaffective disorder, bipolar or unipolar affective disorder, or  
 PT adolescent conduct disorder -  
 XX  
 PS Claim 11, Fig 1A; 999P; English.  
 XX  
 XX The present sequence is that of cDNA clone Y1176 (deposited as  
 CC ATCC PTA-2775) encoding a novel human metabotropic glutamate  
 CC receptor subtype modulatory protein (mglur5m). The cDNA was  
 CC isolated from a human brain cDNA library. Expression of mglur5m  
 CC is predominant in cells and tissues of the central nervous system.  
 CC The gene maps to a region of chromosome 11 associated with  
 CC schizophrenia and related psychiatric disorders. The invention  
 CC provides mglur5m polypeptides and nucleic acids, and methods for  
 CC their detection, as well as methods for using them to identify  
 CC compounds that modulate metabotropic receptor (mglur) activity.  
 CC Such modulators include a mglur5m nucleic acid, a mglur5m antibody,  
 CC a ribozyme, an antisense oligonucleotide, a small molecule  
 CC modulator, a peptide and a peptidomimetic. They can be used in a  
 CC claimed method for treating a subject having a neurological  
 CC disorder, especially a psychiatric disorder selected from  
 CC schizophrenia, schizoaffective disorder, bipolar affective disorder,  
 CC unipolar affective disorder or adolescent conduct disorder (all  
 CC claimed). mglur5m polypeptides, nucleic acids and antibodies are  
 CC also useful for screening assays, and in predictive medicine, e.g.  
 CC diagnostic assays (e.g. chromosome mapping and tissue typing),  
 CC prognostic assays, monitoring clinical trials, and pharmacogenomics.  
 XX  
 XX Sequence 1823 BP; 488 A; 397 C; 444 G; 493 T; 1 other;  
 XX  
 Alignment Scores:  
 Pred. No.: 1,71e-203 Length: 1823  
 Score: 1873.00 Matches: 369  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 24 Gaps: 0  
 US-10-027-923-2 (1-369) X ABV73899 (1-1823)  
 QY 1 MetValLeuLeuLeuLeuSerValLeuLeuLeuLysGluAspValArgGlySerAla 20  
 DB 4 ATGGTCCTTCTGTGATCTGTCTGATCTCTTTGAAAGAGATGTCCTGGAGAGCA 63  
 QY 21 GluSerGluArgValAlaValAlaHisMetLeuLysAspLeuLeuLeuGlyAlaLeu 40

DB 64 CAGTCCAGTCAGAGAGGGGTGGCTCAGATCTGGGTACATCTATTATGAGCTCTC 123  
 QY 41 PheSerValHisHisGlnProthrValAspGluValHisGluArgLysCysGlyAlaVal 60  
 DB 124 TTTTCTGTTTCATCAGCAGCTTACTGTGAGCAAGATTTCATATGAGGAAGTGTGGGAGTC 183  
 QY 61 ArgGluGlnThrCylLysLeuArgValGluAlaMetLeuHisGlnLeuGluAlaGln 80  
 DB 184 CGTGAACAGATGACATTCAGAGAGTGAAGCCATCTGCATACCTCGAAGAGATCAT 243  
 QY 81 SerAspProThrLeuLeuProAsnHisLeuGluCysGluLysLeuArgAspSerCysTrp 100  
 DB 244 TCAGACCCACACATCTTGGCCACATCAGCTGGGCTGTGAGATTAAGGATTCCTGCTGG 303  
 QY 101 HisSerAlaValAlaLeuGluGlnSerLysLeuPheLeuArgAspSerLeuLysSer 120  
 DB 304 CATTCGGCTGTGGCCCTAGAGCAGACATTTGAGTTCAATAGACATTCCTCATTTCTTCG 363  
 QY 121 GluGluGluGluGluLeuValCysSerValAspGlySerSerSerPheArgSerLys 140  
 DB 364 GAAGAGAGAGAGGGCTTGTGATCTCTGTGATGAGCTCTCTCTTCTTCCCTCCAG 423  
 QY 141 LysProLysValGlyValLysGlyProGlySerSerSerLeuAlaLysGlnValGlnAsn 160  
 DB 424 AAGCCCATGATGAGGGGTCAATGGGCTGTGTCAGATTCCTTACCATTCAGCTCCAGAT 483  
 QY 161 LeuLeuGlnLeuPheAsnHisLeuGlnLysLeuAlaLysSerAlaThrLysMetAspLeuSer 180  
 DB 484 TTGCTCAGCTTTTCAACATCTCAGATTCGATTCAGCAACCATTCATGAGTCTGAGT 543  
 QY 181 AspLysThrLeuPheLysTrpPheMetArgValValProSerAspLysGlnGlnAlaArg 200  
 DB 544 GACAGAGCTCTGTCAAAATTTTCATGAGGGTGTGCTTCAGATCTCAGCAGGAGAG 603  
 QY 201 SerMetValAspLysLeuValLysArgTrpAsnTrpThrLysValSerAlaValHisThrGlu 220  
 DB 604 TCATGATGACATCATGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 663  
 QY 221 GlyAsnTrpGlyGluSerGlyMetGluAlaPheLysAspMetSerAlaLysGluGlyLys 240  
 DB 664 GGCACATCATGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 723  
 QY 241 CysAlaHisSerLysTrpLysLysLysLysLysLysLysLysLysLysLysLysLys 260  
 DB 724 TGCATGCCCATCTTACAAATCTACAGATGACAGGGAGGAGCTTTGATTAAGCTG 783  
 QY 261 LeuLysLysLeuThrSerHisLeuProLysAlaArgValAlaLysLysPheCysGluGly 280  
 DB 784 CTGAAGAGCTCAAGATGATCTTGGCCAGAGCCGGGTGGCTTACTTCTGTAGAGGC 843  
 QY 281 MetThrValArgGlyLeuLeuMetAlaMetArgArgLeuGlyLeuValGlyLeuPheLeu 300  
 DB 844 ATACCGGTGAGAGTGTGCTGAGAGGCAATGAGGCTGTGCTGTGAGAGATTTCTG 903  
 QY 301 LeuLeuGluValArgLysProAspAlaLysPheLeuGlnLysSerLysAsnSerLysLeuTrp 320  
 DB 904 CTTCGGGAGGGAGACAGATGCTTATTTGAAATCTCAAGAACAGATCTCTATGG 963  
 QY 321 GluAspArgArgLysCysGlnGlyArgPheLeuGlnGlyPheGlyAspLysLysArg 340  
 DB 964 GAAGACAG 1023  
 QY 341 SerGluSerValLeuLeuHisMetProGlnProLeuAsnLeuGluLysSerSerGlyPro 360  
 DB 1024 AGTGAATCGGTGTGCTGCAATGAGCCAGCTGTGAATCTAGAGCTCAGTTGAGGGCCC 1083  
 QY 361 IleThrGlyLeuArgAspArgLeuLys 369  
 DB 1084 ATCACTGAGATGAGGAGAGAGCTCATC 1110  
 RESULT 2  
 AAF29993

ID AAF29993 standard; DNA; 2172 BP.  
 XX AAF29993;  
 AC  
 XX  
 DT 06-APR-2001 (first entry)  
 XX  
 DE Human GRM-X-1e DNA.  
 XX  
 KW Human; metabotropic glutamate receptor; schizophrenia; GRM-X;  
 XX Alzheimer's; Parkinson's; stroke; depression; anxiety; pain; ds.  
 OS Homo sapiens.  
 XX  
 PN MO200102566-A1.  
 XX  
 PD 11-JUN-2001.  
 XX  
 PF 27-JUN-2000; 2000MO-US17798.  
 XX  
 PR 02-JUL-1999; 99US-0346326.  
 XX  
 PA (NEUR-) NEUROCKINE BIOSCIENCES INC.  
 XX  
 PI Schwarz DA, Maki RA;  
 XX  
 DR MPI; 2001-123112/13.  
 XX  
 PT Novel metabotropic glutamate receptor for prevention, treatment of  
 PT conditions associated with undesirable glutamate levels, e.g.  
 PT Alzheimer's, Parkinson's disease, stroke, depression, anxiety, pain and  
 PT schizophrenia -  
 XX  
 PS Claim 2; Fig 7; 59pp; English.  
 XX  
 CC The present invention relates to human metabotropic glutamate  
 CC receptor. An agent that decreases expression or activity of the  
 CC metabotropic glutamate receptor is useful for treating schizophrenia.  
 CC Metabotropic glutamate receptor polynucleotides, polypeptides  
 CC are useful for treating diseases associated with undesirable  
 CC levels of glutamate, such as Alzheimer's disease, Parkinson's  
 CC disease, stroke, depression, anxiety, pain and schizophrenia.  
 CC  
 SQ Sequence 2172 BP; 554 A; 488 C; 544 G; 586 T; 0 other;  
 Alignment Scores:  
 Pred. No.: 4,92e-203 Length: 2172  
 Score: 1870.00 Matches: 368  
 Percent Similarity: 100.00% Conservative: 1  
 Best Local Similarity: 99.73% Mismatches: 0  
 Query Match: 22 Gaps: 0  
 DB: 22  
 US-10-027-923-2 (1-369) x AAF29993 (1-2172)  
 QY 1 MetValLeuLeuLeuLeuLeuSerValLeuLeuLeuValArgLysSerAla 20  
 DB 365 ATGCTCTCTGTTGATCTCTGCTGCTCTTCTTTGAAGAAGTCTCGGAGTGA 424  
 QY 21 GlnSerSerGluArgValValAlaMetLeuGlyAspIleIleIleGlyAlaLeu 40  
 DB 425 CAGTCAGTCAGAGAGGGGTGGTGCATGCTGGTGACATCTATTGAGGCTTC 484  
 QY 41 PheSerValIleHisGlnProThrValAspGluValIleGluArgLysCysGlyAlaVal 60  
 DB 485 TTTTCTGTTCTATCAGACGCTCTGTCGAGGAAGTTCATAGAGAGTGTGGGCGAGTC 544  
 QY 61 ArgGluGlnTyrGlyIleGlnArgValGluAlaMetLeuHisThrLeuGluArgLys 80  
 DB 545 CGGAAACGATGACATTCAGAGAGTGGAGCCATGCTGATCCCTGGAAAGATCAT 604  
 QY 81 SerAspProThrLeuLeuProAsnIleThrLeuGlyCysGluIleArgAspSerCysTyr 100  
 DB 605 TCAGACCCCACTCTTGGCCCAATCATCAGCTGGGCTGTAGATAGGAGATTCTGCTGG 664

QY 101 HisSerAlaValAlaLeuGluGlnSerIleGluPheIleArgAspSerLeuIleSerSer 120  
 DB 665 CATTCGGCTGTGGCCCTTAGACAGACATTGAGTTCATTAAGATTCCTCATTTCTTGG 724  
 QY 121 GluGluGluGluGlyLeuValCysSerValAspGlySerSerSerSerPheArgSerLys 140  
 DB 725 GAAGAGAGAGAGGGCTTGGTGTCTCTGTGAGTGGCTCTCTCTCTCTCTCTCTCTCAAG 784  
 QY 141 LysProIleValGlyValIleGlyProGlySerSerSerLeuAlaIleGlnValGlnAsn 160  
 DB 785 AAGCCCATGATGAGGGGTCACTGGGCTGGTTCAGATTCCTAGCCCATTCAGGTCAGAAAT 844  
 QY 161 LeuLeuGlnLeuPheAsnIleProGlnIleAlaTyrSerAlaThrIleMetAspLeuSer 180  
 DB 845 TTGCTCAAGCTTTTCAACATACCTCAGATTGCTTACTCAGACACCATCATGATTCGAGT 904  
 QY 181 AspLysThrLeuPheLysTyrPheMetArgValAlaProSerAspAlaGlnGlnAlaArg 200  
 DB 905 GACAAAGCTCTGTTCAAAATATTTTCAAGAGGGTTGTGCTTCAATCTCAGAGGCAAGG 964  
 QY 201 SerMetValAspIleValIleValArgTyrAsnTyrThrTyrValSerAlaValHisThrGlu 220  
 DB 965 TCCATGCTGACATAGTGAAGAGTCAACCTGACCTATGATACACCCGTACACACAGAA 1024  
 QY 221 GlyAsnTyrGlyGlnSerGlyMetGluAlaPheLysAspMetSerAlaLysGluGlyIle 240  
 DB 1025 GGCNACTATGAGAAAGTGGAGTGAAGGCTTAAAGATATGTCACAGAAAGAGGATTT 1084  
 QY 241 CysIleAlaHisSerTyrIleTyrSerAsnAlaGlyGluGlnSerPheAspLysLeu 260  
 DB 1085 TGCATGCCCACTCTACAAANCTACATTAAGCAGGGAGCAGAGCTTGTATTAAGCTG 1144  
 QY 261 LeuLysLysLeuThrSerHisLeuProLysAlaArgValAlaTyrPheCysGluGly 280  
 DB 1145 CTGAAAGACCTCAAGATCACTTGGCCCAAGGCGGGGTGTGCTTACTTCTGTAGGGGC 1204  
 QY 281 MetThrValArgGlyLeuLeuMetAlaMetArgArgLeuGlyLeuValGlyGluPheLeu 300  
 DB 1205 ATGACCGTGAAGGTGTGCTGATGGCCATGAGGCGCTGGGTATGAGGAGAAATTTCTG 1264  
 QY 301 LeuLeuGlyArgGluProAspAlaIlePheIleGluIleSerLysAsnSerIleLeuTyr 320  
 DB 1265 CTTCTGGGAGGGAACAGATGCTATTATTTAGATCTCAAGAACAGCATCTATGG 1324  
 QY 321 GluAspArgArgLysCysGlnGlyArgPheLeuGlnGlyPheGlyAspIleLeuHisArg 340  
 DB 1325 GAAGACAGAAAGAAATGCAAGGTCGCTTCTTCAAGGTTTGGAGACATATTACACAGA 1384  
 QY 341 SerGlnSerValLeuLeuHisMetProGlnProLeuAsnLeuGluLeuSerSerGlyPro 360  
 DB 1385 AGTGAATCCGTGCTGTGACATGCCCCAGCCCTGAATCTTAGAGCTCAGTTAGGGGCC 1444  
 QY 361 IleThrGlyLeuArgAspArgLeuIle 369  
 DB 1445 ATCACTGAGCTAGGAGCAGGCTCATC 1471  
 RESULT 3  
 ID AAS62274 standard; cDNA; 1788 BP.  
 XX AAS62274;  
 AC  
 XX  
 DT 14-FEB-2002 (first entry)  
 XX  
 DE cDNA sequence #61 encoding novel human secreted protein.  
 XX  
 KW Human secreted protein; hyperproliferative disorder; autoimmune disorder;  
 KW immune deficiency disorder; blood disorder; inflammatory disorder;  
 KW infectious disorder; gene therapy; antimicrobial; hepatotropic;  
 KW immunosuppressive; antineoplastic; ss.  
 XX  
 OS Homo sapiens.



XX	02-JUL-1999;	99US-0346326.
PR		
XX		

PA (NEUR-) NEUROCRINE BIOSCIENCES INC.

PI Schwarz DA, Maki RA;  
XX

DR WPI; 2001-123112/13.

*Spinnaker*

DR WPI; 2001-123112/13.

PT Novel metabotropic glutamate receptor for prevention, treatment of conditions associated with undesirable glutamate levels, e.g. Alzheimer's, Parkinson's disease, stroke, depression, anxiety, pain and

PS Claim 2; Fig 3; 59pp; English

CC The present invention relates to human metabotropic glutamate  
CC receptor. An agent that decreases expression or activity of the  
CC metabotropic glutamate receptor is useful for treating schizophrenia  
CC Metabotropic glutamate receptor polymorphisms, polypeptides  
CC are useful for treating diseases associated with undesirable  
CC levels of glutamate, such as Alzheimer's disease, Parkinson's  
CC disease, stroke, depression, anxiety, pain and schizophrenia.

**SQ** Sequence 2349 BP; 588 A; 538 C; 586 G; 637 T; 0 other;

**Alignment Scores:**

Pred. No.:	1,81e-198	Length:	2349
Score:	1030.50	Matches:	368
Percent Similarity:	86.21%	Conservative:	1
Best Local Similarity:	85.98%	Mismatches:	0
Query Match:	97.73%	Indels:	59
DB:	22	Gaps:	1

US-10-027-923-2 (1-369) X AAF29990 (1-2349)

QY	1	MeValLeuLeuLeuLeuLeuSerValLeuLeuLeuValGluAspValArgLysSerAla	20
Db	365	ATGGTCCTCTGTATCTCTGACGCTTACTTTTGAAAGAAAGATGCCGTGGAGATGCA	42
QY	21	GlnSerSerGluArgArgValAlaAlaHisMetLeuGluAspLysIleIleGluValLeu	40
Db	425	CAGTCCAGTAGAGAGAGGGGTGGGTGCATGCTGGGTGACATCATATTATGGAGCTTC	48
QY	41	PhsSerValHisHisGlnProThrValAlaArgGluValHisGluArgLysCysGluValAla	60
Db	485	TTTTCCTGTCATCACCACGACTCTGTGGACGAAGTTCATGACAGAAAGATGTGGGGCAGTC	54
QY	61	ArgGluGlnThrGlyIleGluArgValGluHisMetLeuHisThrLeuGluArgLysAsn	80
Db	545	CGGAAACAAGATGGCAATTCAGAGAGTGGAGGGCCAGTGCATACCTGTGAAAGAGATCAAT	604
QY	81	SerAspProThrLeuLeuProAsnIleThrLeuGluCysGluIleArgAspSerCysTrp	100
Db	605	TCAGACCCACCACTCTTGGCCAAACATCACTGGGCTGTGAGATTAAGGATTTCTGCTGG	66
QY	101	HisSerAlaValAlaLeuGluGlnSerIleGluPheIleArgAspSerLeuIleSerSer	120
Db	665	CATTCGGCTGTGGCCCTTAGAGCAGACATGTGAGTTCATTAAGAGATTCCTCATATTTCTTGG	724
QY	121	GluGluGluGluGluLeuValCysSerValAlaArgLysSerSerSerPheArgSerLys	140
Db	725	GAAAGAGAAAGAGGGCTTGGATGTGCTCTTGAGATGGCTCTCTCTTCTTCCCTTCGCTCAAG	784
QY	141	LysProGluValGluValIleGlyProGlySerSerSerSerLeuAlaIleGluValGluAsn	160
Db	785	AAAGCCCATAGTAGGGGCTATTGGGCTGGATTCAGTTCTGTATGCCATTCAAGGTCCAGAAAT	844
QY	161	LeuLeuGluLeuPheAsnIleProGluIleAlaIleArgSerAlaThrIleMetAspLeuSer	180
Db	845	TTGCTCCAGCTTTTCAACATCACTCAGATGTGCTTACTCAGCAACCATATGAGATCTAGT	904
QY	181	AspLysThrLeuPheLysTrpPheMetArgValValProSerAspAlaGlnGlnAlaArg	200

Db	905	GACAGAGCTGTTCCAAATTTTCATATGAGGTTTGCTTCAGATGCTCAGACAGGCAAG	964
Qy	201	SerMetValAspIleValIyAsArgYzAsnTThrTYrValSerAlaValHisThrGlu	220
Db	965	TCCATGGTGGACATAGTGAAGAGGTGACACTGGACTATGATCAGCCGTACACAGAA	1024
Qy	220	-----	220
Db	1025	GGTTCAAGCTATTCTCATGCTCAGCCTCAGAGAGCTAGGCTGTCTTCAACTTTGG	1084
Qy	220	-----	220
Db	1085	CCTCAAGTATCTGCGCTGCTTTGGCCTTCCAAATTTGCTGGATTATGCGCATGACCA	1144
Qy	221	-----Gly	221
Db	1145	ACAGACACCCGGCCAGTCCCGATCTTAGAACACTCTTGAGGTGCTTCTGATTTTAA	1204
Qy	222	AsnTYrGlyIyGlySerGlyMetGluAlaPheIyAsPheSerAlaIyGlyGlyIleCy	241
Db	1205	AACATATGAGAAAGTGGATGGAGAGCCTTCAAGATATGTCAAGGAAAGGAGATTTC	1264
Qy	242	IleAlaHisSerTYrIyIleTYrSerAsnAlaGlyGlyGlyIyGlyIyGlyIyGlyIyGly	261
Db	1265	ATCCGCCACTCTTACAAATATCTACAGTATGACAGGGAGGACAGACCTTGTATAGCT	1324
Qy	262	IyAlIySerThrSerHisIleuProIyAlaArgValAlaIATyrPheCyGlyIyMet	281
Db	1325	AAGAAGCTCACAAGTCACTTGCCCAAGCCCGGTGGTGGCTATCTCTGAGAGGCATG	1384
Qy	282	ThrValIArgGlyIyLeuIeMetAlaMetArgArgIyGlyIyLeuValGlyIyPheIyLeu	301
Db	1385	ACGGTGAAGGCTCTGATGAGCCATGAGCGCGCTGGGTCTAGTGGAGAAATTCCTCT	1444
Qy	302	IeuGlyIyArgIyPProAspAlaIlePheIleGlyIySerIyAsnSerIleuTTrGly	321
Db	1445	CTGGGCGAGGAAACGATGCCATCTTTATGAGATCTCAAGAACACACATCTTAGGGAA	1504
Qy	322	AspArgArgIySvCyGlyGlyIyArgPheIyGlyIyPheGlyAspIleIyLeuHisArgSer	341
Db	1505	GACGAAAGAAATGCCAAGGTCGCTTCCTCAGGGTTTGGAGACATTTACACAGAACT	1564
Qy	342	GlySerValIyLeuHisIyMetProGlyIyProIyAsnIyGlyIyLeuSerSerGlyProIle	361
Db	1565	GAGTCCGTGCTGTCGACATAGCCCAAGCTCTGAATCTAGAGCTCAGTTCAAGGCCCATC	1624
Qy	362	ThrGlyIyLeuArgAspArgIyIle 369	
Db	1625	ACTGGACTGAGGACAGGCTCATC 1648	
RESULT 5			
ID	AAE29994	standard; DNA, 2149 BP.	
XX	AAE29994;		
AC	06-APR-2001	(first entry)	
DT			
XX	Human GRMX-1f DNA.		
DE			
XX			
XX	Human; metabotropic glutamate receptor; schizophrenia; GRMX;		
KW	Alzheimer's; Parkinson's; stroke; depression; anxiety; pain; de.		
XX			
OS	Homo sapiens.		
XX			
FN	WO200102566-A1.		
XX			
PD	11-JAN-2001.		
XX			
PF	27-JUN-2000; 2000MO-US17798.		
XX			
PR	02-JUL-1999; 99US-0346326.		

XX (NEUR-) NEUROCRINE BIOSCIENCES INC.  
 PA Schwarz DA, Maki RA;  
 PI WPI; 2001-123112/13.  
 XX Novel metabotropic glutamate receptor for prevention, treatment of  
 XX PT conditions associated with undesirable glutamate levels, e.g.  
 PT Alzheimer's, Parkinson's disease, stroke, depression, anxiety, pain and  
 PT schizophrenia -  
 XX  
 PS Claim 2; Fig 9; 59pp; English.  
 XX  
 CC The present invention relates to human metabotropic glutamate  
 CC receptor. An agent that decreases expression or activity of the  
 CC metabotropic glutamate receptor is useful for treating schizophrenia.  
 CC Metabotropic glutamate receptor polynucleotides, polypeptides  
 CC are useful for treating diseases associated with undesirable  
 CC levels of glutamate, such as Alzheimer's disease, Parkinson's  
 CC disease, stroke, depression, anxiety, pain and schizophrenia.  
 XX  
 SQ Sequence 2149 BP; 547 A; 485 C; 538 G; 579 T; 0 other;  
 Alignment Scores:  
 Pred. No.: 2,34e-194 Length: 2149  
 Score: 1794.00 Matches: 359  
 Percent Similarity: 97.30% Conservative: 1  
 Best Local Similarity: 97.03% Mismatches: 1  
 Query Match: 95.78% Indels: 9  
 Gaps: 1  
 US-10-027-923-2 (1-369) x AAF29994 (1-2149)

QY 201 SerMetValAspIleValIysArgIYrAsnTrpThrTyValSerAlaValHisThrGlu 220  
 DB 965 TCATGGTGGACATATGTAAGAGGTACACTGGAACCTTATATACAGCCGACACAGAA 1024  
 QY 221 GlysAsnTrpIYgluSerGlyMetGluAlaPheLysAspMetSerAlaIysGluIYle 240  
 DB 1025 GGCACCTATGAAAGGTGGATGGAAGCCTTCAAGATATGTACAGCAAGAAAGGATT 1084  
 QY 241 CysIleAlaHisSerTrpIYrIYrSerAsnAlaGlyGluIYnSerPheAspIYleu 260  
 DB 1085 TGCATGCCACCTTACAAATCTACATTAATGACGGGAGCAAGAGCTTGTATAGCTG 1144  
 QY 261 LeuIYleuLysLeuThrSerHisLeuProLysAlaArgValAlaIYrPheCysGluIY 280  
 DB 1145 CTGAAGAGCTCAACAGTCACTTGCCCAAGCCCGGTGTGCTGACTTGTAGAGGC 1204  
 QY 281 MetThrValArgGlyLeuLeuMetAlaMetArgArgLeuGlyLeuValGlyIYnLeu 300  
 DB 1205 ATGACGGTGAAGGTCTGCTGATGACATGAGCGCCTGGGTCTAAGTGGAGAAATTCTG 1264  
 QY 301 LeuLeuGlyYArgGluProAspAlaIlePheIleGluIYleSerIYnAsnSerIleLeuTrp 320  
 DB 1265 CTCTGGGACGGGAGACAGATGCACTTATTTGAGATCTCAAAAGAACAGCATCTATGG 1324  
 QY 321 GluAspArgArgLysCysGluIYrArgPhe-LeuGluIYnIYpHeGlyAspIleLeuHisAr 340  
 DB 1325 GAGGACAGAGAAATGCCAAAGGTCCGCTTCCTC-----AG 1360  
 QY 340 gSerGluSerValLeuLeuHisMetProGluProLeuAsnLeuGluLeuSerGlyPr 360  
 DB 1361 AAGTGAATCCGTCTGCTGACATGCCCCAGCCTTGAATCTAGACTCAGTTCAGGGCC 1420  
 QY 360 oIleThrGlyLeuArgAspArgLeuIle 369  
 DB 1421 CATCACTGACGTGAGGACAGGCTCATC 1448  
 RESULT 6  
 AAF29989  
 ID AAF29989 standard; DNA; 2551 BP.  
 AC AAF29989;  
 XX  
 XX 06-APR-2001 (first entry)  
 DT  
 XX  
 DE Human GRMX-1a DNA.  
 XX  
 XX Human; metabotropic glutamate receptor; schizophrenia; GRMX;  
 KW Alzheimer's; Parkinson's; stroke; depression; anxiety; pain; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200102566-A1.  
 PN  
 XX  
 PD 11-JAN-2001.  
 XX  
 XX 27-JUN-2000; 2000MO-US17798.  
 PR  
 XX 02-JUL-1999; 99US-0346326.  
 XX  
 PA (NEUR-) NEUROCRINE BIOSCIENCES INC.  
 PI Schwarz DA, Maki RA;  
 DR WPI; 2001-123112/13.  
 XX  
 XX Novel metabotropic glutamate receptor for prevention, treatment of  
 XX PT conditions associated with undesirable glutamate levels, e.g.  
 PT Alzheimer's, Parkinson's disease, stroke, depression, anxiety, pain and  
 PT schizophrenia -  
 XX  
 PS Claim 2; Fig 1; 59pp; English.  
 XX



CC The present invention relates to human metabotropic glutamate  
 CC receptor. An agent that decreases expression or activity of the  
 CC metabotropic glutamate receptor is useful for treating schizophrenia.  
 CC Metabotropic glutamate receptor polypeptides, polypeptides  
 CC are useful for treating diseases associated with undesirable  
 CC levels of glutamate, such as Alzheimer's disease, Parkinson's  
 CC disease, stroke, depression, anxiety, pain and schizophrenia.

XX Sequence 2551 BP, 666 A; 566 C; 630 G; 689 T; 0 other;

# Alignment Scores:

Pred. No.:	1,21e-192	Length:	2551
Score:	1780.00	Matches:	368
Percent Similarity:	74.40%	Conservative:	1
Best Local Similarity:	74.19%	Mismatches:	0
Query Match:	95.03%	Indels:	127
DB:	22	Gaps:	1

US-10-027-923-2 (1-369) x AAF29989 (1-2551)

QY 1 MetValLeuLeuLeuLeuSerValLeuLeuLeuLeuValArgIysSerAla 20  
 DB 365 ATGGTCCTTCTGTGATCCTGTCAGTCTTACTTTGAAAGAGATGCTCCGTGGAGTGA 424  
 QY 21 GlnSerSerGluArgArgValAlaAlaMetLeuGluAspIleIleIleGluAlaLeu 40  
 DB 425 CAGTCAGAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 484  
 QY 41 pheSerValHisIleGlnProThrValAspGluValHisGluArgIysCysGluAlaVal 60  
 DB 485 TTTTCTGTCATCAGCAGGCTACTGTGAGAGAGATTTCATAGAGAGAGAGAGAGAGT 544  
 QY 61 ArgGluGlnIleIleIleGlnIleGlnIleGlnIleGlnIleGlnIleGlnIleGlnIle 80  
 DB 545 CCGGAAACAGATGAGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 604  
 QY 81 SerAspProThrLeuLeuProAsnIleThrLeuGluCysGluIleArgAspSerCysTrp 100  
 DB 605 TCGAGCCCACTCTTGGCCCACTCACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 664  
 QY 101 HisSerAlaValAlaLeuGlnIleGlnIleGlnIleGlnIleGlnIleGlnIleGlnIle 120  
 DB 665 CATTGGCTGTGGCCCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 724  
 QY 121 GluGluGlnGluGluGluValCysSerValAspGluSerSerSerSerPheArgSerIys 140  
 DB 725 GAAGAGAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 784  
 QY 141 LysProIleValAlaGlyValIleGlyProGlySerSerSerSerLeuAlaIleGlnValGln 160  
 DB 785 AAGCCCAATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 844  
 QY 161 LeuLeuGlnLeuPheAsnIleProGlnIleAlaIleSerAlaThrIleMetAspLeuSer 180  
 DB 845 TTGCTCAGGCTTTCAACACTCACTGATGCTTACTCAGCAACCACTCAAGATCTGAGT 904  
 QY 181 AspIleThrLeuPheLeuIleIleIleIleIleIleIleIleIleIleIleIleIleIle 200  
 DB 905 GACAAAGACTCTGTTCAAAATTTTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 964  
 QY 201 SerMetValAspIleValIleValArgIleAsnTrpThrValSerAlaValHisIleGln 220  
 DB 965 TCCATGATGAGATGATGAGAGAGATCACTGAGACCTATATATACCGCTACACAGAA 1024  
 QY 220 ----- 220  
 DB 1025 GAGCAGGCTAATTGTGAGAAAGATTGGCTACAAGTGAGAGAGAAAGCTGATCTACTA 1084  
 QY 220 ----- 220  
 DB 1085 TGAATAATGCGCAGTTTCTATATGATPACCAATAAAGTAGATATATCTTAAGATATA 1144  
 QY 220 ----- 220

DB 1145 TAAGCAAAATGCTGAATGAAAAGGCAATTGATGCCAAATPACATTCATGTCATTTG 1204  
 QY 220 ----- 220  
 DB 1205 CATTAAGCAGACAGAAATTTTGAAGTTTCAAGTATTTCTCATGCTCAGCTCCAGAGAGC 1264  
 QY 220 ----- 220  
 DB 1265 TAGGCTGTTCAACTCTTGCCCTCAAGTATCTGCTGCTTTGGCTTCCAAATTTGCT 1324  
 QY 220 ----- 220  
 DB 1325 GGGATTATGGCATGATGACCAACAGCAGCCCGGCGATGCCGATTTAGAACACTTTG 1384  
 QY 221 ----- GlyAsnTrpIleGluSerGluMetGluAlaPheIleAspPhe 234  
 DB 1385 AGGTGCTTCTGATTTTGTAGCAACTATGAGAAAGTGGATGAGAGCTTCAAAAGATAT 1444  
 QY 234 tSerAlaIleGluGluIleCysIleAlaHisSerTrpIleIleTrpSerAsnAlaGlyG 254  
 DB 1445 GTCAAGCAAGAGAGGAGATTTGATGCGCCACTTTACAAATCTACATGATGACAGGGA 1504  
 QY 254 uGlnSerPheAspIleLeuLeuIleIleIleIleIleIleIleIleIleIleIleIleIle 274  
 DB 1505 GCAAGCTTTGATTAAGCTCTGAAGAGCTCAAGATCACTTCCCAAGGCCGGGTGCT 1564  
 QY 274 lAlaTrpPheCysGluIleMetThrValArgIleLeuLeuMetAlaMetArgArgLeuG 294  
 DB 1565 GGCCTACTCTGTGAGAGGAGATGACGGGTGAGAGGTCTGTGATGAGGAGGAGGCTGGG 1624  
 QY 294 yLeuValGlyIlePheLeuLeuLeuGluArgIlePheAsnAlaIlePheIleGluIle 314  
 DB 1625 TCTAGGAGAGAAATTTCTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1684  
 QY 314 rIlyAsnSerIleLeuTrpGluAspArgArgIysCysGlnIleArgPheLeuGlnIlePh 334  
 DB 1685 AAGAAACACATCTCTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1744  
 QY 334 eGlyAspIleLeuHisArgSerGluSerValLeuLeuHisMetProGlnProLeuAsn 354  
 DB 1745 TGGAGACATATTACAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 1804  
 QY 354 uGluLeuSerSerGlyProIleThrGlyLeuArgAspArgLeuIle 369  
 DB 1805 AGAGCTCAGTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGATC 1850  
 DB 1850 ----- 1850  
 RESULT 7  
 AAF29991 standard; DNA; 2326 BP.  
 AC AAF29991;  
 DT 06-APR-2001 (first entry)  
 XX Human GRMX-1c DNA.  
 DE Human GRMX-1c DNA.  
 XX Human; metabotropic glutamate receptor; schizophrenia; GRMX;  
 KW Alzheimer's; Parkinson's; stroke; depression; anxiety; pain; ds.  
 OS Homo sapiens.  
 XX Homo sapiens.  
 PN WO200102566-A1.  
 PD 11-JAN-2001.  
 PF 27-JUN-2000; 2000WO-US17798.  
 PR 02-JUL-1999; 99US-0346326.  
 PA (NEUR-) NEUROCRINE BIOSCIENCES INC.  
 XX Schwarz DA, Maki RA;  
 PI



QY 464 TAGCCATTGAGGTCGAGAAATTTGCTCAGCTTTTCAACATCTAGATTGCTTACTCAG 523  
 DB 611 TAGCCATTGAGGTCGAGAAATTTGCTCAGCTTTTCAACATCTAGATTGCTTACTCAG 670  
 QY 524 CAACCATCATGATCTGATGAGACAGACTCTGTTCAAAATTTTCATGAGGGTTGTGCTT 583  
 DB 671 CAACCATCATGATCTGATGAGACAGACTCTGTTCAAAATTTTCATGAGGGTTGTGCTT 730  
 QY 584 CAGATGCTCAGCAGGCAAGGTCATGATGAGACATGATGAAAGAGTACACTGACCTATG 643  
 DB 731 CAGATGCTCAGCAGGCAAGGTCATGATGAGACATGATGAAAGAGTACACTGACCTATG 790  
 QY 644 TATCAGCCGTCACACAGAAAGGCACTATGAGAAAGTGGATGGAAGCTTTCAAAAGATA 703  
 DB 791 TATCAGCCGTCACACAGAAAGGCACTATGAGAAAGTGGATGGAAGCTTTCAAAAGATA 850  
 QY 704 TGTCAAGCAAGAAAGGATTTGATGCGCCCACTCTTACAAATCTACATGATGCAAGGG 763  
 DB 851 TGTCAAGCAAGAAAGGATTTGATGCGCCCACTCTTACAAATCTACATGATGCAAGGG 910  
 QY 764 AGCAGAGCTTTGATTAAGCTGCTGAAGAGCTCACTCAAGTCACTTGCCCAAGGCCGGGTG 823  
 DB 911 AGCAGAGCTTTGATTAAGCTGCTGAAGAGCTCACTCAAGTCACTTGCCCAAGGCCGGGTG 970  
 QY 824 TGGCTTAATCTCTGTGAGGGGATGACCGGTGAGAGGTCTGTGATGAGCCATGAGCGCTTG 883  
 DB 971 TGGCTTAATCTCTGTGAGGGGATGACCGGTGAGAGGTCTGTGATGAGCCATGAGCGCTTG 1030  
 QY 884 GTCTAG 889  
 DB 1031 GTCTAG 1036

## RESULT 13

AAD04990 standard; cDNA; 4207 BP.

AAD04990;

17-JUL-2001 (first entry)

Human metabotropic glutamate receptor, mGluR5A cDNA mutant.

Human, metabotropic glutamate receptor; mGluR5A; excitatory amino acid;  
 EAA; central nervous system; CNS; presynaptic release; neurotransmitter;  
 postsynaptic sensitivity; glutamate excitation; mutant; ss.

Homo sapiens.

Synthetic.

Key Location/Qualifiers  
 mutation replace (416, T)  
 mutation /\*tag= a  
 mutation replace (425, A)  
 mutation /\*tag= b

US6211353-B1.

03-APR-2001.

07-JUN-1996; 96US-0660148.

29-JUL-1994; 94US-0282853.

(ELIL) LILLY & CO ELI.

Burnett JP, Mayne NG, Sharp RL, Snyder YM;

WPI; 2001-289639/30.

New isolated nucleic acids for producing human metabotropic glutamate  
 receptors, which are useful for modulating the presynaptic release of

PT glutamate or the postsynaptic sensitivity of the neuronal cell to  
 PT glutamate excitation -  
 PS Disclosure; Column -; 53pp; English.

CC The present sequence is a cDNA mutant encoding human metabotropic  
 CC glutamate receptor, mGluR5A. L-glutamate, the most abundant  
 CC neurotransmitter in the central nervous system (CNS), mediates excitatory  
 CC pathway in mammals. L-glutamate is referred to as excitatory amino acid  
 CC (EAA) and the receptors that respond to glutamate are EAA receptors. The  
 CC receptors are useful for modulating the presynaptic release of glutamate  
 CC and the postsynaptic sensitivity of the neuronal cell to glutamate  
 CC excitation.  
 CC Note: The present sequence is not shown in the specification, but is  
 CC derived from the sequence referred to as SEQ ID NO.1, shown in column  
 CC 59-68 (AAD05029) of the specification.

CC Sequence 4207 BP; 1010 A; 1121 C; 1112 G; 964 T; 0 other;

Query Match 12.2%; Score 222; DB 22; Length 4207;  
 Best Local Similarity 99.1%; Pred. No. 7, 1e-77;  
 Matches 422; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 464 TAGCCATTGAGGTCGAGAAATTTGCTCAGCTTTTCAACATCTAGATTGCTTACTCAG 523  
 DB 920 TAGCCATTGAGGTCGAGAAATTTGCTCAGCTTTTCAACATCTAGATTGCTTACTCAG 979  
 QY 524 CAACCATCATGATCTGATGAGACAGACTCTGTTCAAAATTTTCATGAGGGTTGTGCTT 583  
 DB 980 CAACCATCATGATCTGATGAGACAGACTCTGTTCAAAATTTTCATGAGGGTTGTGCTT 1039  
 QY 584 CAGATGCTCAGCAGGCAAGGTCATGATGAGACATGATGAAAGAGTACACTGACCTATG 643  
 DB 1040 CAGATGCTCAGCAGGCAAGGTCATGATGAGACATGATGAAAGAGTACACTGACCTATG 1099  
 QY 644 TATCAGCCGTCACACAGAAAGGCACTATGAGAAAGTGGATGGAAGCTTTCAAAAGATA 703  
 DB 1100 TATCAGCCGTCACACAGAAAGGCACTATGAGAAAGTGGATGGAAGCTTTCAAAAGATA 1159  
 QY 704 TGTCAAGCAAGAAAGGATTTGATGCGCCCACTCTTACAAATCTACATGATGCAAGGG 763  
 DB 1160 TGTCAAGCAAGAAAGGATTTGATGCGCCCACTCTTACAAATCTACATGATGCAAGGG 1219  
 QY 764 AGCAGAGCTTTGATTAAGCTGCTGAAGAGCTCACTCAAGTCACTTGCCCAAGGCCGGGTG 823  
 DB 1220 AGCAGAGCTTTGATTAAGCTGCTGAAGAGCTCACTCAAGTCACTTGCCCAAGGCCGGGTG 1279  
 QY 824 TGGCTTAATCTCTGTGAGGGGATGACCGGTGAGAGGTCTGTGATGAGCCATGAGCGCTTG 883  
 DB 1280 TGGCTTAATCTCTGTGAGGGGATGACCGGTGAGAGGTCTGTGATGAGCCATGAGCGCTTG 1339  
 QY 884 GTCTAG 889  
 DB 1340 GTCTAG 1345

## RESULT 14

AAD05029 standard; cDNA; 4207 BP.

AAD05029;

17-JUL-2001 (first entry)

Human metabotropic glutamate receptor, mGluR5A cDNA.

Human, metabotropic glutamate receptor; mGluR5A; excitatory amino acid;  
 EAA; central nervous system; CNS; presynaptic release; neurotransmitter;  
 postsynaptic sensitivity; glutamate excitation; ss.

Homo sapiens.

Key Location/Qualifiers

DE cDNA encoding chimeric receptor containing hmglur5d portion.  
 XX Human: metabotropic glutamate receptor; mglur; splice variant;  
 XX mglur5; G-protein-coupled receptor; glutamate; neurological disorder;  
 KM anticonvulsant; neuroprotectant; analgesic; cognitive enhancer;  
 KM muscle relaxant; calcium receptor; Ca<sub>v</sub>; mglur5d; ss.  
 XX Chimeric - Homo sapiens.  
 OS  
 PN MO200130829-A1.  
 XX  
 PD 03-MAY-2001.  
 XX  
 PF 25-OCT-2000; 2000MO-US29356.  
 XX  
 PR 25-OCT-1999; 99US-0161481.  
 XX 24-OCT-2000; 2000US-0695481.  
 PA (NPSB-) NPS PHARM INC.  
 PI Krapcho K, Stormann T, Levinthal C, Hammerland L, Scorfjohann L;  
 XX WPI, 2001-308615/32.  
 DR P-PSDB; AAB47219.  
 XX  
 PT New nucleic acid encoding an isoform of human metabotropic glutamate  
 PT receptor, for identifying potential therapeutic agents for neurological  
 PT disease  
 CC  
 CC Claim 18; Page 70-75; 86pp; English.  
 XX  
 XX This sequence encodes a chimeric receptor comprising the intracellular  
 CC cytoplasmic tail of the human calcium receptor (Ca<sub>v</sub>) and the extra-  
 CC cellular and seven transmembrane domains of the human metabotropic  
 CC glutamate receptor (mglur) splice variant of the human metabotropic  
 CC glutamate receptor 5 (mglur5), mglur5d. mglur5 are G-protein-coupled  
 CC receptors capable of activating a variety of intracellular second  
 CC messenger systems following the binding of glutamate. Recombinant  
 CC mglur5d DNA and compounds that bind to, or modulate activity of it  
 CC are useful for diagnosing or treating neurological disorders, e.g.  
 CC as anticonvulsants, neuroprotectants, analgesics, cognitive enhancers  
 CC and muscle relaxants.  
 CC  
 XX Sequence 3129 BP; 806 A; 782 C; 804 G; 737 T; 0 other;  
 XX  
 Query Match 12.2%; Score 222; DB 22; Length 3129;  
 Best Local Similarity 99.1%; Pred. No. 7, 4e-77;  
 Matches 422; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 464 TAGCCATTGAGTCCAGAAATTTGCTCCAGCTTTCAACATACCTCAGATTGTTACTCAG 523  
 DB 461 TAGCCATTGAGTCCAGAAATTTGCTCCAGCTTTCAACATACCTCAGATTGTTACTCAG 520  
 QY 524 CAACCATCATGATCTGAGTACAGACTCTGTTCAAAATATTTTCATGAGGGTTGTCCTT 583  
 DB 521 CAACCATCATGATCTGAGTACAGACTCTGTTCAAAATATTTTCATGAGGGTTGTCCTT 580  
 QY 584 CAGATCTCAGCAGGCAAGTCTCATGTGACATAGTGAAGAGTCAACTGAGCTTATG 643  
 DB 581 CAGATCTCAGCAGGCAAGTCTCATGTGACATAGTGAAGAGTCAACTGAGCTTATG 640  
 QY 644 TATCAGCCGTCACACAGAAAGCACTATGGAAGAAAGTGGAGTGAAGGCTTCAAGATA 703  
 DB 641 TATCAGCCGTCACACAGAAAGCACTATGGAAGAAAGTGGAGTGAAGGCTTCAAGATA 700  
 QY 704 TGTCAAGCAAGAAAGGATTTGATGCGCCACTCTTACAAATCTACAGTAAATGACAGGG 763  
 DB 701 TGTCAAGCAAGAAAGGATTTGATGCGCCACTCTTACAAATCTACAGTAAATGACAGGG 760  
 QY 764 AGCAGAGCTTTGATTAAGTGTGTAAGAGTCAAGATCACTTGGCCAAAGGCCGGGTGG 823  
 DB 761 AGCAGAGCTTTGATTAAGTGTGTAAGAGTCAAGATCACTTGGCCAAAGGCCGGGTGG 820

QY 824 TGGCTACTTCTGTGAGGAGCATGAGTGTGCTGATGACCATGAGCGCCTGG 883  
 DB 821 TGGCTACTTCTGTGAGGAGCATGAGTGTGCTGATGACCATGAGCGCCTGG 880  
 QY 884 GTCTAG 889  
 DB 881 GTCTAG 886

RESULT 12  
 ACAS6535  
 ID ACAS6535 standard; cDNA; 4078 BP.  
 XX  
 AC ACAS6535;  
 XX  
 DT 06-JUN-2003 (first entry)  
 XX  
 DE Human signalling pathway polynucleotide probe SEQ ID NO 1133.  
 XX  
 KM Human; probe; ss; array element; Parkinson's disease;  
 KM signalling pathway population; cancer; adenocarcinoma; leukaemia;  
 KM immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6500938-B1.  
 XX  
 PD 31-DEC-2002.  
 XX  
 PF 30-JAN-1998; 98US-0016434.  
 XX  
 PR 30-JAN-1998; 98US-0016434.  
 XX  
 PA (INCY-) INCYTE GENOMICS INC.  
 PI Au-Young J, Seilhamer JU;  
 XX WPI; 2003-352189/33.  
 DR  
 XX  
 PT Combination of polynucleotide probes, useful as array elements in a  
 PT microarray for monitoring the expression of a number of target  
 PT polynucleotides  
 CC  
 PS Claim 1; SEQ ID NO 1133; 65pp; English.  
 XX  
 XX The invention relates to a combination which, comprises a number of  
 CC polynucleotide probes comprising a sequence selected from one of the 1490  
 CC sequences mentioned in the specification. The combination is useful as an  
 CC array element in a microarray for monitoring the expression of a number  
 CC of target polynucleotides. The microarray is particularly useful in the  
 CC diagnosis and treatment of cancer and immunopathology and neuropathology.  
 CC The microarray is useful in diagnostics and treatment regimens, drug  
 CC discovery and development, toxicological and carcinogenicity studies,  
 CC forensics and pharmacogenomics. The microarray is also useful for  
 CC monitoring progression of diseases and for developing sophisticated  
 CC profiles for the effects of currently available therapeutic drugs. The  
 CC combination is also useful for purifying a subpopulation of mRNAs, cDNAs  
 CC and genomic fragments and in research and diagnostic applications. The  
 CC array can detect changes in expression in a large number of genes coding  
 CC for different signalling pathway populations which can be used to diagnose  
 CC various diseases including cancer e.g. adenocarcinoma and leukaemia,  
 CC immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease  
 CC and Parkinson's disease. The present sequence represents a polynucleotide  
 CC probe of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification but was obtained in electronic format directly from USPTO  
 CC at seqdata.uspto.gov/sequence.html?DocID=06500938B1.  
 XX  
 XX Sequence 4078 BP; 994 A; 1074 C; 1076 G; 934 T; 0 other;  
 XX  
 Query Match 12.2%; Score 222; DB 25; Length 4078;  
 Best Local Similarity 99.1%; Pred. No. 7, 1e-77;  
 Matches 422; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 1535 CAGAAAGTGAATGCTGCTGCTGCAATGCCACCTCTGATCTAGAGCTAGTTCAGG 1594  
 Qy 1080 GCCCATCACTGCACTGAGGAGGAGGCTCATCTAATCTGAGTGGATTTACTTGCATTA 1139  
 Db 1595 GCCCATCACTGCACTGAGGAGGAGGCTCATCTAATCTGAGTGGATTTACTTGCATTA 1654  
 Qy 1140 TATGAAAGCAACAGTCATATCTTCTGAGTGGAGATTTGAGAAAGCATTTGATGGAAG 1199  
 Db 1655 TATGAAAGCAACAGTCATATCTTCTGAGTGGAGATTTGAGAAAGCATTTGATGGAAG 1714  
 Qy 1200 TGAACCTCAAAATGCGCCCATATCACTGCAACACCTACAAAGTTTCTTGATGAGGATG 1259  
 Db 1715 TGAACCTCAAAATGCGCCCATATCACTGCAACACCTACAAAGTTTCTTGATGAGGATG 1774  
 Qy 1260 TCAAGCTTTCACCTCTGCGCAAGTATTAAGTGGAGTTCATGAGGAGCTCTTGGAATTG 1319  
 Db 1775 TCAAGCTTTCACCTCTGCGCAAGTATTAAGTGGAGTTCATGAGGAGCTCTTGGAATTG 1834  
 Qy 1320 GGGCTTCGGGTGTTGTAATAGTACAGGAAAGGAAAGAAATCAGAAATGGCAATATATATG 1379  
 Db 1835 GGGCTTCGGGTGTTGTAATAGTACAGGAAAGGAAAGAAATCAGAAATGGCAATATATATG 1894  
 Qy 1380 AGAGAGAGGAGCTCTTATAGTCTGAGATTTGTAAGAGACATTCAGTGCAGTCTCTTAC 1439  
 Db 1895 AGAGAGAGGAGCTCTTATAGTCTGAGATTTGTAAGAGACATTCAGTGCAGTCTCTTAC 1954  
 Qy 1440 CACCTCCCAAGTTACACTGCAATATGTCCTCAAGACCTACCAACCATGATGATTAATTCCT 1499  
 Db 1955 CACCTCCCAAGTTACACTGCAATATGTCCTCAAGACCTACCAACCATGATGATTAATTCCT 2014  
 Qy 1500 GGAATGGAAGCTAGAACTGCTGAGCTGCTGATGTTAATCAAAAGCTCCCTTATATAC 1559  
 Db 2015 GGAATGGAAGCTAGAACTGCTGAGCTGCTGATGTTAATCAAAAGCTCCCTTATATAC 2074  
 Qy 1560 CATCCCTAATGCTCTCTCTCACTCCTCTCAGGCCCTATCTTGTGATTCATCTCTG 1619  
 Db 2075 CATCCCTAATGCTCTCTCTCACTCCTCTCAGGCCCTATCTTGTGATTCATCTCTG 2134  
 Qy 1620 ACAGAGACAAATCAGAAATGTTATCTGCTGTGGAAACCCCTTATCCCATTAAGCC 1679  
 Db 2135 ACAGAGACAAATCAGAAATGTTATCTGCTGTGGAAACCCCTTATCCCATTAAGCC 2194  
 Qy 1680 CTCTCCCTGCTGCTTATCAAAAGAGCAAAATGCTCTGTTTATGCTTGAATTCAT 1739  
 Db 2195 CTCTCCCTGCTGCTTATCAAAAGAGCAAAATGCTCTGTTTATGCTTGAATTCAT 2254  
 Qy 1740 TCTAATGTTATTAATCAATTTATGTTACTATTAATGTTGTTAAAA 1789  
 Db 2255 TCTAATGTTATTAATCAATTTATGTTACTATTAATGTTGTTAAAA 2304  
 RESULT 10  
 AAC85785  
 ID AAC85785 standard; cDNA; 2826 BP.  
 XX  
 AC AAC85785;  
 XX  
 DT 18-JUL-2001 (first entry)  
 XX  
 DE cDNA encoding metabotropic glutamate receptor.  
 XX  
 KW Human; metabotropic glutamate receptor; mglur; splice variant;  
 KW mglur5; G-protein-coupled receptor; glutamate; neurological disorder;  
 KW anticonvulsant; neuroprotectant; analgesic; cognitive enhancer;  
 KW muscle relaxant; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W0200130829-A1.  
 XX  
 PD 03-MAY-2001.  
 XX  
 PF 25-OCT-2000; 2000WO-US29356.

XX 25-OCT-1999; 99US-0161481.  
 PR 24-OCT-2000; 2000US-0695481.  
 PA (NPSP-) NPS PHARM INC.  
 PI Krapcho K, Stormann T, Levinthal C, Hammerland L, Storchmann L;  
 XX WPI, 2001-308615/32.  
 DR P-PSDB; AAB47217.  
 XX  
 PT New nucleic acid encoding an isoform of human metabotropic glutamate  
 PT receptor, for identifying potential therapeutic agents for neurological  
 PT disease.  
 XX  
 PS Claim 2; Page 51-56; 86pp; English.  
 XX  
 CC This sequence encodes a human metabotropic glutamate receptor (mglur).  
 CC mglur is a splice variant of human metabotropic glutamate receptor 5  
 CC (mglur5). mglur's are G-protein-coupled receptors capable of activating  
 CC a variety of intracellular second messenger systems following the  
 CC binding of glutamate. Recombinant mglur DNA and compounds that bind to,  
 CC or modulate activity of mglur are useful for diagnosing or treating  
 CC neurological disorders, e.g. as anticonvulsants, neuroprotectants,  
 CC analgesics, cognitive enhancers and muscle relaxants.  
 XX  
 SQ Sequence 2826 BP; 729 A; 679 C; 712 G; 706 T; 0 other;  
 Query Match 12.2%; Score 222; DB 22; Length 2826;  
 Best Local Similarity 99.1%; Pred. No. 7.5e-77;  
 Matches 422; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 Qy 464 TAGCATTGAGTTCAGATTTGCTCCAGCTTTTCAACATCTGATGATCTTACTCG 523  
 Db 461 TAGCATTGAGTTCAGATTTGCTCCAGCTTTTCAACATCTGATGATCTTACTCG 520  
 Qy 524 CAACCATCATGATCTGATGACAAAGACTCTGTTCAATATTTTATGAGGTTGCTT 583  
 Db 521 CAACCATCATGATCTGATGACAAAGACTCTGTTCAATATTTTATGAGGTTGCTT 580  
 Qy 584 CAGATCTCAGCAGGAGGATTCATGATGATGATGATGATGATGATGATGATGATGATG 643  
 Db 581 CAGATCTCAGCAGGAGGATTCATGATGATGATGATGATGATGATGATGATGATGATG 640  
 Qy 644 TATCAGCCGTGACACAGAAAGGCACTATGAGAAAGTGGAGTGAAGCTTAAAGATA 703  
 Db 641 TATCAGCCGTGACACAGAAAGGCACTATGAGAAAGTGGAGTGAAGCTTAAAGATA 700  
 Qy 704 TGTCAAGGAAGAAAGGATTTGATGATGATGATGATGATGATGATGATGATGATGATG 763  
 Db 701 TGTCAAGGAAGAAAGGATTTGATGATGATGATGATGATGATGATGATGATGATGATG 760  
 Qy 764 AGCAGAGCTTTGATTAAGCTGCTGAGAAAGCTCAAGTCACTTGCCCAAGGCCGAGTGG 823  
 Db 761 AGCAGAGCTTTGATTAAGCTGCTGAGAAAGCTCAAGTCACTTGCCCAAGGCCGAGTGG 820  
 Qy 824 TGGCTTACTTCTGTGAGGAGATGACGATGAGAGCTCTGCTGATGAGGCTGAGGCTTGG 883  
 Db 821 TGGCTTACTTCTGTGAGGAGATGACGATGAGAGCTCTGCTGATGAGGCTGAGGCTTGG 880  
 Qy 884 GTCTAG 889  
 Db 881 GTCTAG 886  
 RESULT 11  
 AAC85787  
 ID AAC85787 standard; cDNA; 3129 BP.  
 XX  
 AC AAC85787;  
 XX  
 DT 18-JUL-2001 (first entry)

XX Human; metabotropic glutamate receptor; schizophrenia; GRM;   
 KW Alzheimer's; Parkinson's; stroke; depression; anxiety; pain; ds.   
 XX Homo sapiens.   
 OS MO200102566-A1.   
 PN 11-JAN-2001.   
 PD 27-JUN-2000; 2000MO-US17798.   
 PF 02-JUL-1999; 99US-0346326.   
 PR (NEUR-) NEUROCRINE BIOSCIENCES INC.   
 PA Schwarz DA, Maki RA;   
 PI WPI, 2001-123112/13.   
 DR Novel metabotropic glutamate receptor for prevention, treatment of   
 XX conditions associated with undesirable glutamate levels, e.g.   
 PT Alzheimer's; Parkinson's disease; stroke; depression, anxiety, pain and   
 PT schizophrenia -   
 PS Claim 2; Fig 6; 59pp; English.   
 XX The present invention relates to human metabotropic glutamate   
 CC receptor. An agent that decreases expression or activity of the   
 CC metabotropic glutamate receptor is useful for treating schizophrenia.   
 CC Metabotropic glutamate receptor polynucleotides, polypeptides   
 CC are useful for treating diseases associated with undesirable   
 CC levels of glutamate, such as Alzheimer's disease, Parkinson's   
 CC disease, stroke, depression, anxiety, pain and schizophrenia.   
 XX Sequence 2241 BP, 552 A, 516 C, 561 G, 612 T, 0 other;   
 SQ   
 Query Match 39.4%; Score 719; DB 22; Length 2241;   
 Best Local Similarity 99.9%; Pred. No. 5,1e-270;   
 Matches 769; Conservative 0; Mismatches 1; Indels 0; Gaps 0;   
 QY 1020 CAGAGTGAATCGCTGCTGTCGACATGCCCGCTCTGAAATCTAGAGTCAGTTCAAG 1079   
 DB 1450 CAGAGTGAATCGCTGCTGTCGACATGCCCGCTCTGAAATCTAGAGTCAGTTCAAG 1509   
 QY 1080 GCCCATCACTGAGCTGAGGAGCAAGCTCATCTAATCTGAGTGGATTTACTTGATTA 1139   
 DB 1510 GCCCATCACTGAGCTGAGGAGCAAGCTCATCTAATCTGAGTGGATTTACTTGATTA 1569   
 QY 1140 TAATGAAGCAACAGTCATATCTTCTGATGTGAGATTGAGAAAGATTGTATGGATG 1199   
 DB 1570 TAATGAAGCAACAGTCATATCTTCTGATGTGAGATTGAGAAAGATTGTATGGATG 1629   
 QY 1200 TGACCGTCAAAATGCGCCCATATCACTGCAACACCTCAAGTTTCTTGATGGGTCG 1259   
 DB 1630 TGACCGTCAAAATGCGCCCATATCACTGCAACACCTCAAGTTTCTTGATGGGTCG 1689   
 QY 1260 TGAGACTTTCACCTTCGCGCAAGTATCTGCGGAGGTCCATGCGGGGACTCTTGGAATG 1319   
 DB 1690 TGAGACTTTCACCTTCGCGCAAGTATCTGCGGAGGTCCATGCGGGGACTCTTGGAATG 1749   
 QY 1320 GGCTTCGGGTGTTTGAATTAAGTATGGAAGGGAAGATTCGAATGGCAATATATATG 1379   
 DB 1750 GGCTTCGGGTGTTTGAATTAAGTATGGAAGGGAAGATTCGAATGGCAATATATATG 1809   
 QY 1380 AAGAGGAGGACTTATGCTTGGATTTGTAAGACGACATTCAGTGCAGTCTCTTAC 1439   
 DB 1810 AAGAGGAGGACTTATGCTTGGATTTGTAAGACGACATTCAGTGCAGTCTCTTAC 1869   
 QY 1440 CACCTCCCAAGTTACCTGCAAGTATGCCAAGACCTCAACACATGATGATTTCTT 1499   
 DB 1870 CACCTCCCAAGTTACCTGCAAGTATGCCAAGACCTCAACACATGATGATTTCTT 1929

QY 1500 GGATTGTGAGCTAGAACTGTGAGCTTGTGATGTTAAATCAAAAGCTCCCTATATAC 1559   
 DB 1930 GGATTGTGAGCTAGAACTGTGAGCTTGTGATGTTAAATCAAAAGCTCCCTATATAC 1989   
 QY 1560 CATCCCTAATTTGCTCTTCTGACCTCTCTCAGGCTATCTTTTGTCTGATTTATCTCTG 1619   
 DB 1990 CATCCCTAATTTGCTCTTCTGACCTCTCTCAGGCTATCTTTTGTCTGATTTATCTCTG 2049   
 QY 1620 ACCAGAGCAAAATCAGAAATGTTTATCTGCTGAGGAAACCCCTTATCCCAATAAGCC 1679   
 DB 2050 ACCAGAGCAAAATCAGAAATGTTTATCTGCTGAGGAAACCCCTTATCCCAATAAGCC 2109   
 QY 1680 CTCTTCCTTGTGCTTATCAACAGCAAAATAGTTCTGTTTATGCTTGAATTCAT 1739   
 DB 2110 CTCTTCCTTATGCTTATCAACAGCAAAATAGTTCTGTTTATGCTTGAATTCAT 2169   
 QY 1740 TCTAATGTTATTAACCTCATTTATTTGTTACTATTAATGTGGTAAAA 1789   
 DB 2170 TCTAATGTTATTAACCTCATTTATTTGTTACTATTAATGTGGTAAAA 2219   
 RESULT 9   
 AAF29991   
 ID AAF29991 standard; DNA; 2326 BP.   
 XX AAF29991;   
 AC 06-APR-2001 (first entry)   
 DT Human GRM-1c DNA.   
 DE Human GRM-1c DNA.   
 XX Human; metabotropic glutamate receptor; schizophrenia; GRM;   
 KW Alzheimer's; Parkinson's; stroke; depression; anxiety; pain; ds.   
 XX Homo sapiens.   
 OS MO200102566-A1.   
 PN 11-JAN-2001.   
 PD 27-JUN-2000; 2000MO-US17798.   
 PF 02-JUL-1999; 99US-0346326.   
 PR (NEUR-) NEUROCRINE BIOSCIENCES INC.   
 PA Schwarz DA, Maki RA;   
 PI WPI, 2001-123112/13.   
 DR Novel metabotropic glutamate receptor for prevention, treatment of   
 PT conditions associated with undesirable glutamate levels, e.g.   
 PT Alzheimer's; Parkinson's disease; stroke; depression, anxiety, pain and   
 PT schizophrenia -   
 PS Claim 2; Fig 5; 59pp; English.   
 XX The present invention relates to human metabotropic glutamate   
 CC receptor. An agent that decreases expression or activity of the   
 CC metabotropic glutamate receptor is useful for treating schizophrenia.   
 CC Metabotropic glutamate receptor polynucleotides, polypeptides   
 CC are useful for treating diseases associated with undesirable   
 CC levels of glutamate, such as Alzheimer's disease, Parkinson's   
 CC disease, stroke, depression, anxiety, pain and schizophrenia.   
 XX Sequence 2326 BP, 581 A, 535 C, 580 G, 630 T, 0 other;   
 SQ   
 Query Match 39.4%; Score 719; DB 22; Length 2326;   
 Best Local Similarity 99.9%; Pred. No. 5,1e-270;   
 Matches 769; Conservative 0; Mismatches 1; Indels 0; Gaps 0;   
 QY 1020 CAGAGTGAATCGCTGCTGTCGACATGCCCGCTCTGAAATCTAGAGTCAGTTCAAG 1079

QY 721 ATTTCATGCGCCACTCTTACAAATCTACAGTAATGACGAGGAGGAGCTTTGATAG 780  
 Db 1082 ATTTCATGCGCCACTCTTACAAATCTACAGTAATGACGAGGAGGAGCTTTGATAG 1141  
 QY 781 CTCTGTAAGAGCTCAAGTCACTTGTCCCAAGCCCGGGTGGCTTACTTCTGTAG 840  
 Db 1142 CTCTGTAAGAGCTCAAGTCACTTGTCCCAAGCCCGGGTGGCTTACTTCTGTAG 1201  
 QY 841 GGCATGACGGTGAAGGCTGTCTGATGCGCATAGAGCGCTGGGTCTAGTGGAGAAATT 900  
 Db 1202 GGCATGACGGTGAAGGCTGTCTGATGCGCATAGAGCGCGCTGGGTCTAGTGGAGAAATT 1261  
 QY 901 CTCTCTTGGGCGGAGAACAGATGCCATCTTATGAGATCTCAAGAACAGATCCCTA 960  
 Db 1262 CTCTCTTGGGCGGAGAACAGATGCCATCTTATGAGATCTCAAGAACAGATCCCTA 1321  
 QY 961 TGGGAAGACAGAAAGAAATGCCAAGTCCGCTTCTGAG 999  
 Db 1322 TGGGAAGACAGAAAGAAATGCCAAGTCCGCTTCTGAG 1360

## RESULT 7

AAF29995  
 ID AAF29995 standard; DNA; 2064 BP.

AAF29995;

06-APR-2001 (first entry)

Human GRMX-1g DNA.

Human; metabotropic glutamate receptor; schizophrenia; GRMX;  
 Alzheimer's; Parkinson's; stroke; depression; anxiety; pain; ds.

Homo sapiens.

MO200102566-A1.

11-JAN-2001.

27-JUN-2000; 2000MO-US17798.

02-JUL-1999; 99US-0346326.

(NEUR-) NEUROCRINE BIOSCIENCES INC.

Schwarz DA, Maki RA;

WPI; 2001-123112/13.

Novel metabotropic glutamate receptor for prevention, treatment of  
 conditions associated with undesirable glutamate levels, e.g.  
 Alzheimer's, Parkinson's disease, stroke, depression, anxiety, pain and  
 schizophrenia -

Claim 2; Fig 11; 59pp; English.

The present invention relates to human metabotropic glutamate  
 receptor. An agent that decreases expression or activity of the  
 metabotropic glutamate receptor is useful for treating schizophrenia.  
 CC Metabotropic glutamate receptor polynucleotides, polypeptides  
 CC are useful for treating diseases associated with undesirable  
 CC levels of glutamate, such as Alzheimer's disease, Parkinson's  
 CC disease, stroke, depression, anxiety, pain and schizophrenia.

Sequence 2064 BP; 518 A; 466 C; 519 G; 561 T; 0 other;

Query Match 44.5%; Score 812; DB 22; Length 2064;

Best Local Similarity 99.8%; Pred. No. 3.7e-306;  
 Matches 912; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAAATGCTCTTGTGATCTCTAGTCTTACTTTTGAAGAAGATGTCGCGGAGT 60

Db 362 AAAATGCTCTTGTGATCTCTAGTCTTACTTTTGAAGAAGATGTCGCGGAGT 421  
 QY 61 GCACAGTCCAGTGAAGAGAGGGTGTGCTCAGATGCTGGTGAATCTTATTTAGAGCT 120  
 Db 422 GCACAGTCCAGTGAAGAGAGGGTGTGCTCAGATGCTGGTGAATCTTATTTAGAGCT 481  
 QY 121 CTCTTTCTGTTTATCAGACAGCTTACTGTGAGAGAGTTCATGAGAGAGAGTGGGCA 180  
 Db 482 CTCTTTCTGTTTATCAGACAGCTTACTGTGAGAGAGTTCATGAGAGAGAGTGGGCA 541  
 QY 181 GTCCGTGAACAGTATGAGATTCAAGAGTGAAGGCGCATGCTGATACCTTGAAGAGATC 240  
 Db 542 GTCCGTGAACAGTATGAGATTCAAGAGTGAAGGCGCATGCTGATACCTTGAAGAGATC 601  
 QY 241 AATTGACAGCCCACTCTTGGCCCAATCAGTCTGGCTGTGAGTAAAGGATTCCTGC 300  
 Db 602 AATTGACAGCCCACTCTTGGCCCAATCAGTCTGGCTGTGAGTAAAGGATTCCTGC 661  
 QY 301 TGGCATTGGGCTGTGGCCCTGAGAGAGAGATTGATTCATAGAGATTCCCTCATTTCT 360  
 Db 662 TGGCATTGGGCTGTGGCCCTGAGAGAGAGATTGATTCATAGAGATTCCCTCATTTCT 721  
 QY 361 TCGGAAGAGAGAGAGGCTTGTGATGCTGTGATGCTCTCTCTTCTTCCGCTCC 420  
 Db 722 TCGGAAGAGAGAGAGGCTTGTGATGCTGTGATGCTCTCTCTTCTTCCGCTCC 781  
 QY 421 AAGAGCCCATGATAGGGGTCAATTGGGCTGTGCTCAGATCTTTTACCATTCAGTCCAG 480  
 Db 782 AAGAGCCCATGATAGGGGTCAATTGGGCTGTGCTCAGATCTTTTACCATTCAGTCCAG 841  
 QY 481 AATTGCTCAGCTTTTCAACATACCTCAGATTGTTACTCAGACATCATGATCTG 540  
 Db 842 AATTGCTCAGCTTTTCAACATACCTCAGATTGTTACTCAGACATCATGATCTG 901  
 QY 541 AGTGAAGAGCTCTGTTCAAAATTTTCAATGAGGTTGTGCTTCAATGCTCAGAGCA 600  
 Db 902 AGTGAAGAGCTCTGTTCAAAATTTTCAATGAGGTTGTGCTTCAATGCTCAGAGCA 961  
 QY 601 AGTGAAGAGCTCTGTTCAAAATTTTCAATGAGGTTGTGCTTCAATGCTCAGAGCA 660  
 Db 962 AGTGAAGAGCTCTGTTCAAAATTTTCAATGAGGTTGTGCTTCAATGCTCAGAGCA 1021  
 QY 661 GAAGGCAACTATGAGAGAGAGTGGATGGAAGCTTCAAGATATGTCAAGGAAGAGAGG 720  
 Db 1022 GAAGGCAACTATGAGAGAGAGTGGATGGAAGCTTCAAGATATGTCAAGGAAGAGAGG 1081  
 QY 721 ATTTCATGCGCCACTCTTACAAATCTACAGTAATGACGAGGAGAGAGCTTTGATAG 780  
 Db 1082 ATTTCATGCGCCACTCTTACAAATCTACAGTAATGACGAGGAGAGAGCTTTGATAG 1141  
 QY 781 CTCTGTAAGAGCTCAAGTCACTTGTCCCAAGCCCGGGTGGCTTACTTCTGTAG 840  
 Db 1142 CTCTGTAAGAGCTCAAGTCACTTGTCCCAAGCCCGGGTGGCTTACTTCTGTAG 1201  
 QY 841 GGCATGACGGTGAAGGCTGTCTGATGCGCATAGAGCGCTGGGTCTAGTGGAGAAATT 900  
 Db 1202 GGCATGACGGTGAAGGCTGTCTGATGCGCATAGAGCGCGCTGGGTCTAGTGGAGAAATT 1261  
 QY 901 CTCTCTTGGGCGGAGAACAGATGCCATCTTATGAGATCTCAAGAACAGATCCCTA 960  
 Db 1262 CTCTCTTGGGCGGAGAACAGATGCCATCTTATGAGATCTCAAGAACAGATCCCTA 1321

## RESULT 8

AAF29992  
 ID AAF29992 standard; DNA; 2241 BP.

AAF29992;

06-APR-2001 (first entry)

Human GRMX-1d DNA.

QY 1083 CATCACTGAGCTGAGGAGAGGCTCATCTAATTCGAGTGATATTACTCTGCAATTATA 1142  
 DB 1823 CATCACTGAGCTGAGGAGAGGCTCATCTAATTCGAGTGATATTACTCTGCAATTATA 1882  
 QY 1143 TGAAGCCAAAGATCATCTTTCTGATGTGAGATTTGAGAGCATTTGTATTTGATGTGA 1202  
 DB 1883 TGAAGCCAAAGATCATCTTTCTGATGTGAGATTTGAGAGCATTTGTATTTGATGTGA 1942  
 QY 1203 CCGTCAAAATGCGCCCATATCACTGCAACACCTACAAAGTTTCTTGCAAGGGGTGCTCA 1262  
 DB 1943 CCGTCAAAATGCGCCCATATCACTGCAACACCTACAAAGTTTCTTGCAAGGGGTGCTCA 2002  
 QY 1263 GACTTTCACCTCTGAGCAAGTATTACTGAGAGTCCATGTGAGGAGCTTTGGAATTTGGG 1322  
 DB 2003 GACTTTCACCTCTGAGCAAGTATTACTGAGAGTCCATGTGAGGAGCTTTGGAATTTGGG 2062  
 QY 1323 TTTCCGTTTGTATTAAGTACTGAGAAAGGAGAAATCAGAAATGCAATATATATGAGGA 1382  
 DB 2063 TTTCCGTTTGTATTAAGTACTGAGAAAGGAGAAATCAGAAATGCAATATATATGAGGA 2122  
 QY 1383 GAGAGGAGCTTTAGTCTTGGGATTTGTAAGAACGACATTCAGTGCAGTCTTTTACAC 1442  
 DB 2123 GAGAGGAGCTTTAGTCTTGGGATTTGTAAGAACGACATTCAGTGCAGTCTTTTACAC 2182  
 QY 1443 CTCCTCCAGTTACACTGAGATATGCCAAGACCTACCAACATGTAGATTAATTCCTGGA 1502  
 DB 2183 CTCCTCCAGTTACACTGAGATATGCCAAGACCTACCAACATGTAGATTAATTCCTGGA 2242  
 QY 1503 TTTGTGAAGCTGAAAGCTGTAGCTTCTGTGATTTGTAATCAAAAGTCCCCCTATATACCAT 1562  
 DB 2243 TTTGTGAAGCTGAAAGCTGTAGCTTCTGTGATTTGTAATCAAAAGTCCCCCTATATACCAT 2302  
 QY 1563 CCGTAAATGCTCTCTCTCACTCTCTCAGAGCTATTTTGTGCTGATTAATTCCTGAGC 1622  
 DB 2303 CCGTAAATGCTCTCTCTCACTCTCTCAGAGCTATTTTGTGCTGATTAATTCCTGAGC 2362  
 QY 1623 AGAGACAAATCAGAAATGTGTTATCTGTGTGGAACCCCTTATCCATAAAGCCCTC 1682  
 DB 2363 AGAGACAAATCAGAAATGTGTTATCTGTGTGGAACCCCTTATCCATAAAGCCCTC 2422  
 QY 1683 TTTCTTGTGCTTATCAAAAGAGCAAAATAGTTCTGTTTATGTCTTGAATTCATTCT 1742  
 DB 2423 TTTCTTGTGCTTATCAAAAGAGCAAAATAGTTCTGTTTATGTCTTGAATTCATTCT 2482  
 QY 1743 AATGTTATTAATCACTATTAATGTGTTACTATTAATGTGTAATA 1789  
 DB 2483 AATGTTATTAATCACTATTAATGTGTTACTATTAATGTGTAATA 2529

RESULT 6  
 AAF29994  
 ID AAF29994 standard; DNA; 2149 BP.  
 XX AAF29994;  
 AC AAF29994;  
 DT 06-APR-2001 (first entry)  
 XX  
 DE Human GRMX-1f DNA.  
 XX  
 KW Human; metabotropic glutamate receptor; schizophrenia; GRMX;  
 KW Alzheimer's; Parkinson's; stroke; depression; anxiety; pain; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200102566-A1.  
 XX  
 PD 11-JAN-2001.  
 XX  
 PF 27-JUN-2000; 2000MO-US17798.  
 XX  
 PR 02-JUL-1999; 99US-0346326.  
 XX  
 PA (NEUR-) NEUROCRINE BIOSCIENCES INC.

XX  
 PI Schwarz DA, Maki RA;  
 XX  
 DR WPI; 2001-123112/13.  
 XX  
 PT Novel metabotropic glutamate receptor for prevention, treatment of  
 PT conditions associated with undesirable glutamate levels, e.g.  
 PT Alzheimer's, Parkinson's disease, stroke, depression, anxiety, pain and  
 PT schizophrenia -  
 XX  
 PS Claim 2, Fig 9; 59pp; English.  
 XX  
 CC The present invention relates to human metabotropic glutamate  
 CC receptor. An agent that decreases expression or activity of the  
 CC metabotropic glutamate receptor is useful for treating schizophrenia.  
 CC Metabotropic glutamate receptor polynucleotides, polypeptides  
 CC are useful for treating diseases associated with undesirable  
 CC levels of glutamate, such as Alzheimer's disease, Parkinson's  
 CC disease, stroke, depression, anxiety, pain and schizophrenia.  
 XX  
 SO Sequence 2149 BP; 547 A; 485 C; 538 G; 579 T; 0 other;

Query Match 49.2%; Score 897; DB 22; Length 2149;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 997; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAAATGCTCTCTGTGATTCCTGACGCTTACTTTGAAAGAAATGTCGAGGAGT 60  
 DB 362 AAAATGCTCTCTGTGATTCCTGACGCTTACTTTGAAAGAAATGTCGAGGAGT 421  
 QY 61 GCACAGTCCAGTGAAGAGAGGAGTGTGCTCAATGCTGGTGACATCAATTAATGAGCT 120  
 DB 422 GCACAGTCCAGTGAAGAGAGGAGTGTGCTCAATGCTGGTGACATCAATTAATGAGCT 481  
 QY 121 CTCTTTTCTGTTATCAACAAGCTTACTGTGAGCAAGTTCAATGAGAGAAAGTGGGCA 180  
 DB 482 CTCTTTTCTGTTATCAACAAGCTTACTGTGAGCAAGTTCAATGAGAGAAAGTGGGCA 541  
 QY 181 GTCCCGTGAACAGTATGAGCAATTCAGAGAGTGAAGGCGCATCTGATACCTGGAAGAAAGATC 240  
 DB 542 GTCCCGTGAACAGTATGAGCAATTCAGAGAGTGAAGGCGCATCTGATACCTGGAAGAAAGATC 601  
 QY 241 AATTGACACCCCACTCTTGGCCCAATCACTGAGGCTGTGAGATTAAGGATTCCTGC 300  
 DB 602 AATTGACACCCCACTCTTGGCCCAATCACTGAGGCTGTGAGATTAAGGATTCCTGC 661  
 QY 301 TGGCATTGCGCTGTGAGCCCTTGAAGCAGAGCATTAAGTCAATAAGATTCCTCATTTCT 360  
 DB 662 TGGCATTGCGCTGTGAGCCCTTGAAGCAGAGCATTAAGTCAATAAGATTCCTCATTTCT 721  
 QY 361 TCGGAAGAGAAAGAGGCTTGTGATGCTGTGTGAGATGAGTCTCTCTCTCTCTCTCC 420  
 DB 722 TCGGAAGAGAAAGAGGCTTGTGATGCTGTGTGAGATGAGTCTCTCTCTCTCTCTCC 781  
 QY 421 AAGAAGCCCATAGTGAAGGAGTCAATGAGGCTGTGATGCTCTTGAAGCAATTAAGTCCAG 480  
 DB 782 AAGAAGCCCATAGTGAAGGAGTCAATGAGGCTGTGATGCTCTTGAAGCAATTAAGTCCAG 841  
 QY 481 AATTGCTCAGCTTTCACAATCACTCAATGCTTACTCAAGCAACATCATGATGTCG 540  
 DB 842 AATTGCTCAGCTTTCACAATCACTCAATGCTTACTCAAGCAACATCATGATGTCG 901  
 QY 541 AGTGACAAAGCTCTGTTCAAATATTTCAATGAGGCTGTGATGCTCTTGAAGCAATTAAGTCCAG 600  
 DB 902 AGTGACAAAGCTCTGTTCAAATATTTCAATGAGGCTGTGATGCTCTTGAAGCAATTAAGTCCAG 961  
 QY 601 AGTGACAAAGCTCTGTTCAAATATTTCAATGAGGCTGTGATGCTCTTGAAGCAATTAAGTCCAG 660  
 DB 962 AGTGACAAAGCTCTGTTCAAATATTTCAATGAGGCTGTGATGCTCTTGAAGCAATTAAGTCCAG 1021  
 QY 661 GAAAGCACTATGAGAAAGTGGATGGAAGCTTCAAGATATGTCAGCGAAGAGAGG 720  
 DB 1022 GAAAGCACTATGAGAAAGTGGATGGAAGCTTCAAGATATGTCAGCGAAGAGAGG 1081



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Db 1321 GCTGAAGAACTCAACAGTCACTTCCCAAGCCCGGCTGCTTCTGTAGAGG 1380
QY 843 CATGACGGTGAAGGTCTGCTGATGAGCCGCTGGGTCTAGTGGAGAAATTTCT 902
Db 1381 CATGACGGTGAAGGTCTGCTGATGAGCCGCTGGGTCTAGTGGAGAAATTTCT 1440
QY 903 GCTTCTGGGCAAGGAAACCAATGCCATCTTTATTTGAGATCTCAAAACAGCATCTCTAG 962
Db 1441 GCTTCTGGGCAAGGAAACCAATGCCATCTTTATTTGAGATCTCAAAACAGCATCTCTAG 1500
QY 963 GGAAGACAGAGAAATGCAAGTGGCTTCTTCAAGGTTTGGAGACATATTACACAG 1022
Db 1501 GGAAGACAGAGAAATGCAAGTGGCTTCTTCAAGGTTTGGAGACATATTACACAG 1560
QY 1023 AAGTGAATCCGTCTGCTGTCACATGCCCAAGCTCTGATCTGAGTCAAGTCAAGGCC 1082
Db 1561 AAGTGAATCCGTCTGCTGTCACATGCCCAAGCTCTGATCTGAGTCAAGTCAAGGCC 1620
QY 1083 CATCACTGGACTGAGGAGCAGGCTCATCTTAATCTGATGATTTAATCTGATTA 1142
Db 1621 CATCACTGGACTGAGGAGCAGGCTCATCTTAATCTGATGATTTAATCTGATTA 1580
QY 1143 TGAAGCCAAAGTCAATCTTCTGATGATGAGATTTGAGAGATTTGATGATGATG 1202
Db 1681 TGAAGCCAAAGTCAATCTTCTGATGATGAGATTTGAGAGATTTGATGATGATG 1740
QY 1203 CCGTCAAAATGCGCCCAATATCACTGACACACCTACAAAGTTTCTTGATGAGGAGTCA 1262
Db 1741 CCGTCAAAATGCGCCCAATATCACTGACACACCTACAAAGTTTCTTGATGAGGAGTCA 1800
QY 1263 GACTTTCACTCTGGGAGATTTAATGAGGAGTCCATGAGGAGTCCCTGGAATGGGC 1322
Db 1801 GACTTTCACTCTGGGAGATTTAATGAGGAGTCCATGAGGAGTCCCTGGAATGGGC 1860
QY 1323 TTTCCGATTTGATTAATGATGAGAAAGGAAAGATCAAAATGCGCAATTAATGAGAGA 1382
Db 1861 TTTCCGATTTGATTAATGATGAGAAAGGAAAGATCAAAATGCGCAATTAATGAGAGA 1920
QY 1383 GGAAGGACTCTTAATGCTTGGGATTTGTAAGAACGACATTCAGTGCCTTTACAC 1442
Db 1921 GGAAGGACTCTTAATGCTTGGGATTTGTAAGAACGACATTCAGTGCCTTTACAC 1980
QY 1443 CTCCCCGATTACACTGAGATATGTCACCAACCTACCAACATGATAGATTAATCCCTGA 1502
Db 1981 CTCCCCGATTACACTGAGATATGTCACCAACCTACCAACATGATAGATTAATCCCTGA 2040
QY 1503 TTGTAAGCTAGAACTGAGACTCGTTGATGTTAATCAAAAGTCCCTTAATACACAT 1562
Db 2041 TTGTAAGCTAGAACTGAGACTCGTTGATGTTAATCAAAAGTCCCTTAATACACAT 2100
QY 1563 CCTTAATGCTCTTCTCACTCTCTCAAGGCTATCTTTGCTGTAATCATCTGAC 1622
Db 2101 CCTTAATGCTCTTCTCACTCTCTCAAGGCTATCTTTGCTGTAATCATCTGAC 2160
QY 1623 AGAGACAAATCAAGAAATGTTATCTGCTGAGGAAACCTTATCCCAATAAAGCCCTC 1682
Db 2161 AGAGACAAATCAAGAAATGTTATCTGCTGAGGAAACCTTATCCCAATAAAGCCCTC 2220
QY 1683 TTTCTTGGCTTATCAAAACAGACAAATAGTCTGTTTATGCTTGAATTCATCT 1742
Db 2221 TTTCTTGGCTTATCAAAACAGACAAATAGTCTGTTTATGCTTGAATTCATCT 2280
QY 1743 AATGTAATTAATCAATTAATGTTATGTTACTTAATTAATGTTGATAA 1789
Db 2281 AATGTAATTAATCAATTAATGTTATGTTACTTAATTAATGTTGATAA 2327

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RESULT 5  
AAF29989  
ID AAF29989 standard; DNA; 2551 BP.  
XX  
AC AAF29989;

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XX 06-APR-2001 (first entry)
XX Human GRM-X-1a DNA.
XX Human; metabotropic glutamate receptor; schizophrenia; GRM-X;
XX Alzheimer's; Parkinson's; stroke; depression; anxiety; pain; ds.
XX Homo sapiens.
XX WO200102566-A1.
XX 11-JAN-2001.
XX 27-JUN-2000; 2000MO-US17798.
XX 02-JUL-1999; 99US-0346326.
XX (NEUR-) NEUROCRINE BIOSCIENCES INC.
XX Schwarz DA, Maki RA;
XX WPI; 2001-123112/13.
XX Novel metabotropic glutamate receptor for prevention, treatment of
XX conditions associated with undesirable glutamate levels, e.g.
XX Alzheimer's, Parkinson's disease, stroke, depression, anxiety, pain and
XX schizophrenia -
XX Claim 2; Fig 1; 59pp; English.
XX The present invention relates to human metabotropic glutamate
XX receptor. An agent that decreases expression or activity of the
XX metabotropic glutamate receptor is useful for treating schizophrenia.
XX Metabotropic glutamate receptor polynucleotides, polypeptides
XX are useful for treating diseases associated with undesirable
XX levels of glutamate, such as Alzheimer's disease, Parkinson's
XX disease, stroke, depression, anxiety, pain and schizophrenia.
XX Sequence 2551 BP; 666 A; 566 C; 630 G; 689 T; 0 other;
SQ
Query Match 59.0%; Score 1076; DB 22; Length 2551;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1126; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 663 AGGCAACTATGAGAAAGTGGATGGAAGCTTCAAAAGATATGTCAGCCGAAGAGGAT 722
Db 1403 AGGCAACTATGAGAAAGTGGATGGAAGCTTCAAAAGATATGTCAGCCGAAGAGGAT 1462
QY 723 TTGCATGCGCCCACTTACAAATCTACAGTAATGAGGGGAGACAGCTTTGATAAGT 782
Db 1463 TTGCATGCGCCCACTTACAAATCTACAGTAATGAGGGGAGACAGCTTTGATAAGT 1522
QY 783 GCTGAAGAACTCAACAGTCACTTGCACCAAGCCCGGTGATGAGGCTTCTGTAGAGG 842
Db 1523 GCTGAAGAACTCAACAGTCACTTGCACCAAGCCCGGTGATGAGGCTTCTGTAGAGG 1582
QY 843 CATGACGGTGAAGGTCTGCTGATGAGCCGCTGGGTCTAGTGGAGAAATTTCT 902
Db 1583 CATGACGGTGAAGGTCTGCTGATGAGCCGCTGGGTCTAGTGGAGAAATTTCT 1642
QY 903 GCTTCTGGGCAAGGAAACCAATGCCATCTTTATTTGAGATCTCAAAACAGCATCTCTAG 962
Db 1643 GCTTCTGGGCAAGGAAACCAATGCCATCTTTATTTGAGATCTCAAAACAGCATCTCTAG 1702
QY 963 GGAAGACAGAGAAATGCAAGTGGCTTCTTCAAGGTTTGGAGACATATTACACAG 1022
Db 1703 GGAAGACAGAGAAATGCAAGTGGCTTCTTCAAGGTTTGGAGACATATTACACAG 1762
QY 1023 AAGTGAATCCGTCTGCTGTCACATGCCCAAGCTCTGATCTGAGTCAAGTCAAGGCC 1082
Db 1763 AAGTGAATCCGTCTGCTGTCACATGCCCAAGCTCTGATCTGAGTCAAGTCAAGGCC 1822

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Db      842 AATTGCTCAGCTTTTCAACATACCTCAGATTGCTTACTCAGAACCATCATCATGATCTG 901
Qy      541 AGTGAACAAGCTCTGTTCAATATTTGATGAGGGTGTGCTTCAGATGCTCAGCAGCA 600
Db      902 AGTGAACAAGCTCTGTTCAATATTTGATGAGGGTGTGCTTCAGATGCTCAGCAGCA 961
Qy      601 AGGTCCATGCTGATCATAGTGAAGAGTCACTGACCTATGATGACGCTGACACA 660
Db      962 AGGTCCATGCTGATCATAGTGAAGAGTCACTGACCTATGATGACGCTGACACA 1021
Qy      661 GAAGGCACTATGAGAAAGTGGGATGGAAGCTTCAAGATATGTCAGGAGAAAGG 720
Db      1022 GAAGGCACTATGAGAAAGTGGGATGGAAGCTTCAAGATATGTCAGGAGAAAGG 1081
Qy      721 ATTGTCATGCCCACTCTTCAAAATCTACAGTAATGTCAGGGAGCAGAGCTTGATAG 780
Db      1082 ATTGTCATGCCCACTCTTCAAAATCTACAGTAATGTCAGGGAGCAGAGCTTGATAG 1141
Qy      781 CTGCTGAAGAAGCTCACAGTCACTTGCCCAAGGCCGGGTGGTGGCTTCTGTGAG 840
Db      1142 CTGCTGAAGAAGCTCACAGTCACTTGCCCAAGGCCGGGTGGTGGCTTCTGTGAG 1201
Qy      841 GGCATACCGGTGAGAGGTCTGCTGATGCGCATGAGGCGCTGGGTCTAGTGGAGAAATTT 900
Db      1202 GGCATACCGGTGAGAGGTCTGCTGATGCGCATGAGGCGCTGGGTCTAGTGGAGAAATTT 1261
Qy      901 CTGCTTCTGGGGCAGGGAACAGATGCGCATCTTATGAGATCTCAAGAAACAGATCTTA 960
Db      1262 CTGCTTCTGGGGCAGGGAACAGATGCGCATCTTATGAGATCTCAAGAAACAGATCTTA 1321
Qy      961 TGGGAAGACAGAAAGAAATGCCAAGGTGCTTCTTCAGGGTTTTGAGACATATTAC 1020
Db      1322 TGGGAAGACAGAAAGAAATGCCAAGGTGCTTCTTCAGGGTTTTGAGACATATTAC 1381
Qy      1021 AGAAGTGAAGTCCGTGCTGTCACATGCCCAAGCTCTGATCTAGAGCTCAGTTCAGGG 1080
Db      1382 AGAAGTGAAGTCCGTGCTGTCACATGCCCAAGCTCTGATCTAGAGCTCAGTTCAGGG 1441
Qy      1081 CCCATCACTGAGCTGAGGGAAGGCTCATTAATCTGAGTGAATTAATCTGCAATTA 1140
Db      1442 CCCATCACTGAGCTGAGGGAAGGCTCATTAATCTGAGTGAATTAATCTGCAATTA 1501
Qy      1141 AATGAAGCCAAAGCATATCTTCTGATGAGATTTGAGAAATTTGATTTGATGATG 1200
Db      1502 AATGAAGCCAAAGCATATCTTCTGATGAGATTTGAGAAATTTGATTTGATGATG 1561
Qy      1201 GACCTGCAAAATGCGCCCATATCATGCAACCTTCAAGATTTCTTGATGGGGTCT 1260
Db      1562 GACCTGCAAAATGCGCCCATATCATGCAACCTTCAAGATTTCTTGATGGGGTCT 1621
Qy      1261 CAGACTTCACTCTGGCAAGTATTACTGGGAGGTCATGTTGGGGGACTTTTGGAAATGG 1320
Db      1622 CAGACTTCACTCTGGCAAGTATTACTGGGAGGTCATGTTGGGGGACTTTTGGAAATGG 1681
Qy      1321 GCTTTCGCTGTTTGTATATAGTACTGGAAGGAGAGATCAGATGCAATATATATGA 1380
Db      1682 GCTTTCGCTGTTTGTATATAGTACTGGAAGGAGAGATCAGATGCAATATATATGA 1741
Qy      1381 GAGGAGGAGCTCTTATAGTCTTGGATTTTGAAGAGCACTTCAAGTCACTCTTAC 1440
Db      1742 GAGGAGGAGCTCTTATAGTCTTGGATTTTGAAGAGCACTTCAAGTCACTCTTAC 1801
Qy      1441 AACTCCCAAGTTTCACTGCAAGTATGTCCTCAAGCACTTCAAGTCACTCTTAC 1500
Db      1802 AACTCCCAAGTTTCACTGCAAGTATGTCCTCAAGCACTTCAAGTCACTCTTAC 1861
Qy      1501 GATTGGAAGCTGAGACTGAGCTTCTGATGATTAATCAAGCTCCCTATATATAC 1560
Db      1862 GATTGGAAGCTGAGACTGAGCTTCTGATGATTAATCAAGCTCCCTATATATAC 1921
Qy      1561 ATCCCTAATTTGCTCTTCTCACTCTCTCAGGCTATCTTTTGTGATTAATCACTCTGA 1620
Db      1922 ATCCCTAATTTGCTCTTCTCACTCTCTCAGGCTATCTTTTGTGATTAATCACTCTGA 1981

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Qy      1621 CCAGAGCAAAATGAGAAATGTTTATCTGCTGGGAAACCCCTTATCCCATAAAGCCC 1680
Db      1982 CCAGAGCAAAATGAGAAATGTTTATCTGCTGGGAAACCCCTTATCCCATAAAGCCC 2041
Qy      1681 TCTTCTGCTGCTTATCAAAAGAGCAAAATAGGTTCTGTTTATGCTTGAATTCATT 1740
Db      2042 TCTTCTGCTGCTTATCAAAAGAGCAAAATAGGTTCTGTTTATGCTTGAATTCATT 2101
Qy      1741 CTATGTTATTAATCACTTATTTATGTTACTATTAATATGCTATAA 1789
Db      2102 CTATGTTATTAATCACTTATTTATGTTACTATTAATATGCTATAA 2150

RESULT 4
AAF29990
ID   AAF29990 standard; DNA; 2349 BP.
XX
AC   AAF29990;
XX
DT   06-APR-2001 (first entry)
XX
DE   Human GRMX-1b DNA.
XX
KW   Human; metabotropic glutamate receptor; schizophrenia; GRMX;
XX   Alzheimer's; Parkinson's; stroke; depression; anxiety; pain; ds.
XX
OS   Homo sapiens.
XX
PN   WO200102566-A1.
XX
PD   11-JAN-2001.
XX
PF   27-JUN-2000; 2000MO-US17798.
XX
PR   02-JUL-1999; 99US-0346326.
XX
PA   (NEUR-) NEUROCRINE BIOSCIENCES INC.
XX
PI   Schwarz DA, Maki RA;
XX
DR   WPI; 2001-123112/13.
XX
PT   Novel metabotropic glutamate receptor for prevention, treatment of
XX   conditions associated with undesirable glutamate levels, e.g.
PT   Alzheimer's, Parkinson's disease, stroke, depression, anxiety, pain and
XX   schizophrenia -
XX
PS   claim 2; Fig 3; 59pp; English.
XX
CC   The present invention relates to human metabotropic glutamate
XX   receptor. An agent that decreases expression or activity of the
XX   metabotropic glutamate receptor is useful for treating schizophrenia.
XX   Metabotropic glutamate receptor polynucleotides, polypeptides
XX   are useful for treating diseases associated with undesirable
XX   levels of glutamate, such as Alzheimer's disease, Parkinson's
XX   disease, stroke, depression, anxiety, pain and schizophrenia.
XX

SQ   Sequence 2349 BP; 588 A; 538 C; 586 G; 637 T; 0 other;
Query Match      59.0%; Score 1076; DB 22; Length 2349;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1166; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy      663 AGGCACTATGAGAAAGTGGATGGAAGCTTCAAGATATGTCAGCGAAGAAAGGAT 722
Db      1201 AGGCACTATGAGAAAGTGGATGGAAGCTTCAAGATATGTCAGCGAAGAAAGGAT 1260
Qy      723 TTGCAATGCCCACTCTTCAAAATCTACATGATGAGGGAGCAGAGCTTTGATTAAGCT 782
Db      1261 TTGCAATGCCCACTCTTCAAAATCTACATGATGAGGGAGCAGAGCTTTGATTAAGCT 1320
Qy      783 GCTGAAGAAAGCTCAAGTCACTTCCCAAGGCCGGGTGGTGGCTACTTCTGTAGGG 842

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QY 906 TCTGGGAGGGAACCGATGCCATCTTTATTGAGATCTCAAGAGACGATCTTATGGGA 965  
 DB 901 TCTGGGAGGGAACCGATGCCATCTTTATTGAGATCTCAAGAGACGATCTTATGGGA 960  
 QY 966 AGACAGAGAAAATGCGAAGGTGCTTCTTCAAGGTTTGAAGACATATTAACAGAAAG 1025  
 DB 961 AGACAGAGAAAATGCGAAGGTGCTTCTTCAAGGTTTGAAGACATATTAACAGAAAG 1020  
 QY 1026 TGAATCCGTGCTGTCGACATGCCCCAGCCTGGAATCTAGAGCTCAGTCAAGGCCCAT 1085  
 DB 1021 TGAATCCGTGCTGTCGACATGCCCCAGCCTGGAATCTAGAGCTCAGTCAAGGCCCAT 1080  
 QY 1086 CACTGAGCTAGAGGACAGGCTCATCTTAATCTGAGTGAATTAATCTGATTTAATGA 1145  
 DB 1081 CACTGAGCTAGAGGACAGGCTCATCTTAATCTGAGTGAATTAATCTGATTTAATGA 1140  
 QY 1146 AGCCAAACAGTCATATCTTCTGATGTGAGATTGAGAAAGCATTTGATGATGTGACCG 1205  
 DB 1141 AGCCAAACAGTCATATCTTCTGATGTGAGATTGAGAAAGCATTTGATGATGTGACCG 1200  
 QY 1206 TCAAAAATGCGCCCATATCACTGCAACACCTACAGTTTCTTGCAATGCGGTGCTCAGAC 1265  
 DB 1201 TCAAAAATGCGCCCATATCACTGCAACACCTACAGTTTCTTGCAATGCGGTGCTCAGAC 1260  
 QY 1266 TTTCACTCTGCGCAAGTATTAATCTGAGAGGTCCATGTGGGGGACTTTGGAATGGGCTTT 1325  
 DB 1261 TTTCACTCTGCGCAAGTATTAATCTGAGAGGTCCATGTGGGGGACTTTGGAATGGGCTTT 1320  
 QY 1326 CGGTGTTTGAATTAAGTATGAAAGGGAAGAAATCAGATGCGCAATTAATATGAGAGGA 1385  
 DB 1321 CGGTGTTTGAATTAAGTATGAAAGGGAAGAAATCAGATGCGCAATTAATATGAGAGGA 1380  
 QY 1386 GGGACCTTTAGTCTTGGGATTTGTAAGAAAGACATTCAGTGCAGTCTTTTACCACTTC 1445  
 DB 1381 GGGACCTTTAGTCTTGGGATTTGTAAGAAAGACATTCAGTGCAGTCTTTTACCACTTC 1440  
 QY 1446 CCCAGTTTACCTGACATGATGTCCCAAGACCTCAACACATGATGATTAATCTTGGATTTG 1505  
 DB 1441 CCCAGTTTACCTGACATGATGTCCCAAGACCTCAACACATGATGATTAATCTTGGATTTG 1500  
 QY 1506 TGAAGCTAGAACTGTGAGCTTGTGATGTTAATCAAGAGTCCCTTATATACACATCCC 1565  
 DB 1501 TGAAGCTAGAACTGTGAGCTTGTGATGTTAATCAAGAGTCCCTTATATACACATCCC 1560  
 QY 1566 TAAATGCTCTTCTCACTCTCTCAGAGCCTATCTTTGCTGATTCATCTTGAACGAGA 1625  
 DB 1561 TAAATGCTCTTCTCACTCTCTCAGAGCCTATCTTTGCTGATTCATCTTGAACGAGA 1620  
 QY 1626 GACAAATCAGAAATGTGTTATCTGCTGTGAGAAACCCCTTTATCCCATAAAGCCCTCTTC 1685  
 DB 1621 GACAAATCAGAAATGTGTTATCTGCTGTGAGAAACCCCTTTATCCCATAAAGCCCTCTTC 1680  
 QY 1686 CTGTGCTTATCAAAAGGAGCAAAATAGTCTGTTTATGCTTGAATGCAATTTAAT 1745  
 DB 1681 CTGTGCTTATCAAAAGGAGCAAAATAGTCTGTTTATGCTTGAATGCAATTTAAT 1740  
 QY 1746 GTTATTAATACTATTATTGTGTTACTATTAAATGTGTAAAA 1789  
 DB 1741 GTTATTAATACTATTATTGTGTTACTATTAAATGTGTAAAA 1784

## RESULT 3

AAF29993 standard; DNA; 2172 BP.

AAF29993;

06-APR-2001 (first entry)

Human GRM5-1e DNA.

Human; metabotropic glutamate receptor; schizophrenia; GRM5;

KM Alzheimer's; Parkinson's; stroke; depression; anxiety; pain; ds.  
 OS Homo sapiens.  
 PN WO200102566-A1.  
 XX 11-JAN-2001.  
 PD 27-JUN-2000; 2000MO-US17798.  
 PF 02-JUL-1999; 99US-0346326.  
 PR (NEUR-) NEUROCRINE BIOSCIENCES INC.  
 PA Schwarz DA, Maki RA;  
 PT WPI; 2001-123112/13.  
 PT Novel metabotropic glutamate receptor for prevention, treatment of  
 PT conditions associated with undesirable glutamate levels, e.g.  
 PT Alzheimer's; Parkinson's disease, stroke, depression, anxiety, pain and  
 PT schizophrenia.  
 PS Claim 2; Fig 7; 59pp; English.  
 XX The present invention relates to human metabotropic glutamate  
 CC receptor. An agent that decreases expression or activity of the  
 CC metabotropic glutamate receptor is useful for treating schizophrenia.  
 CC Metabotropic glutamate receptor polynucleotides, polypeptides  
 CC are useful for treating diseases associated with undesirable  
 CC levels of glutamate, such as Alzheimer's disease, Parkinson's  
 CC disease, stroke, depression, anxiety, pain and schizophrenia.  
 XX  
 SQ Sequence 2172 BP; 554 A; 488 C; 544 G; 586 T; 0 other;  
 Query Match 89.7%; Score 1636; DB 22; Length 2172;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 1786; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 AATAAGTCTCTTCTGTTGATCTGTGACGTTTCTTTGAAAGAGATGCTGGAGT 60  
 DB 362 AATAAGTCTCTTCTGTTGATCTGTGACGTTTCTTTGAAAGAGATGCTGGAGT 421  
 QY 61 GCACATGCCAGTGAAGAGAGAGGTGGTCAATGCTGGGATCATATTTAGAGT 120  
 DB 422 GCACATGCCAGTGAAGAGAGAGGTGGTCAATGCTGGGATCATATTTAGAGT 481  
 QY 121 CTCTTTTCTGTTATCAACAGCCTTACTGTGAGAGAAAGTTATGAGAGAGTGGGCA 180  
 DB 482 CTCTTTTCTGTTATCAACAGCCTTACTGTGAGAGAAAGTTATGAGAGAGTGGGCA 541  
 QY 181 GTCCGTGAACATGATGAGATTCAGAGATGAGAGCCATGCTGATACCTGGAAGATC 240  
 DB 542 GTCCGTGAACATGATGAGATTCAGAGATGAGAGCCATGCTGATACCTGGAAGATC 601  
 QY 241 AATTGAGACCCACATCTTGGCCCAATCACTGAGGCTGTGAGATTAAGGATTCCTGC 300  
 DB 602 AATTGAGACCCACATCTTGGCCCAATCACTGAGGCTGTGAGATTAAGGATTCCTGC 661  
 QY 301 TGGCATTGCGCTGAGCCCTAGAGAGAGATGAGTTCATTAAGATTCCTCATTTCT 360  
 DB 662 TGGCATTGCGCTGAGCCCTAGAGAGAGATGAGTTCATTAAGATTCCTCATTTCT 721  
 QY 361 TCGAAGAGAGAGAGGCTTGTATGCTGTGAGATGAGCTCTCTCTTCCGCTCC 420  
 DB 722 TCGAAGAGAGAGAGGCTTGTATGCTGTGAGATGAGCTCTCTCTTCCGCTCC 781  
 QY 421 AAGAAGCCATATAGAGGAGTTCAGGCGCTGTGAGATTCATTAAGATTCAGGTCAG 480  
 DB 782 AAGAAGCCATATAGAGGAGTTCAGGCGCTGTGAGATTCATTAAGATTCAGGTCAG 841  
 QY 481 AATTGCTCAGCTTTTCAACATACCTCAGATGCTTACTCAGCAACCATCATGATCTG 540

Db 1441 ACCTCCAGTACAGTATATGCCAAGACCTACCAACATGATATTCCTG 1500  
 Qy 1501 GATTGAGAGTACAGTATATGCCAAGACCTACCAACATGATATTCCTG 1500  
 Db 1501 GATTGAGAGTACAGTATATGCCAAGACCTACCAACATGATATTCCTG 1500  
 Qy 1561 ATCCCTATATGCTCTCTCACTCTCAAGGCTATATCTTCTGATTCATCTGGA 1620  
 Db 1561 ATCCCTATATGCTCTCTCACTCTCAAGGCTATATCTTCTGATTCATCTGGA 1620  
 Qy 1621 CCAGAGCAATTCAGAAATGTTATCTGTGTGGAAACCCCTTTATCCATAAGCCC 1680  
 Db 1621 CCAGAGCAATTCAGAAATGTTATCTGTGTGGAAACCCCTTTATCCATAAGCCC 1680  
 Qy 1681 TCTTCTGTGCTTATCAACAGACAAATAGGCTGTTTATGTCTGAATTCGAT 1740  
 Db 1681 TCTTCTGTGCTTATCAACAGACAAATAGGCTGTTTATGTCTGAATTCGAT 1740  
 Qy 1741 CTATGTTATTAATCACTTATTTATGTTACTATTAATGTGTAAAMCACAATAAA 1800  
 Db 1741 CTATGTTATTAATCACTTATTTATGTTACTATTAATGTGTAAAMCACAATAAA 1800  
 Qy 1801 AAAAAAAAAAAAAAAAAAAAAA 1823  
 Db 1801 AAAAAAAAAAAAAAAAAAAAAA 1823

## RESULT 2

ID AAS62274 standard; cDNA; 1788 BP.  
 AAS62274;

DT 14-FEB-2002 (first entry)  
 DE cDNA sequence #61 encoding novel human secreted protein.

KM Human secreted protein; hyperproliferative disorder; autoimmune disorder;  
 KM infectious disorder; gene therapy; antimicrobial; hepatotropic;  
 KM immunosuppressive; antineumatic; ss.

OS Homo sapiens.  
 PN MO200177291-A2.

PD 18-OCT-2001.

PF 29-MAR-2001; 2001MO-US10485.

PR 06-APR-2000; 2000US-195604P.

PA (GEMV) GENETICS INST INC.

PI Wong GG, Clark HF, Fechtel K, Agostino MJ, Howes SH, Resnick RJ;  
 PI Gulukota K, Graham JR.

DR WPI; 2002-010900/01.

PT New polynucleotides encoding secreted proteins useful for treating e.g.  
 PT asthma, HIV and Crohn's disease -

PS Claim 1; Page 106-107; 391pp; English.

CC The present invention relates to the isolation of novel cDNA sequences  
 CC which encode human secreted proteins. The cDNA sequences have been  
 CC derived from a variety of human tissues. The invention also provides  
 CC a method for producing proteins from these polynucleotide sequences.  
 CC The proteins are useful for identifying compounds that modulate their  
 CC activity and production, and the cell is also useful for identifying  
 CC compounds that modulate expression of the polynucleotide sequences  
 CC encoding the secreted proteins. The sequences of the invention are  
 CC useful for treating diseases such as hyperproliferative disorders

CC (e.g. cancer), immune deficiency disorders (e.g. severe combined  
 CC immunodeficiency (SCID)), autoimmune disorders (e.g. multiple  
 CC sclerosis), blood disorders (e.g. thrombocytopaenia), inflammatory  
 CC disorders (e.g. arthritis) and infectious disorders (e.g. hepatitis).  
 CC The polynucleotide sequences of the invention are also useful in gene  
 CC therapy. AAS62214-AAS62838 represent the cDNA sequences of the  
 CC invention that encode for novel human secreted proteins.

XX Sequence 1788 BP; 454 A; 398 C; 444 G; 492 T; 0 other;

Query Match 97.9%; Score 1784; DB 24; Length 1788;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1784; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GTCCTTCTGTATCTGTCAGTCTTACTTTGAAGAAGATGCGGAGTGACA 65  
 Db 1 GTCCTTCTGTATCTGTCAGTCTTACTTTGAAGAAGATGCGGAGTGACA 60  
 Qy 66 GTCAGTGAAGAGGCTGTGCTCAACATGCTGGGTGACATCATTTAGAGCTCTT 125  
 Db 61 GTCAGTGAAGAGGCTGTGCTCAACATGCTGGGTGACATCATTTAGAGCTCTT 120  
 Qy 126 TTTCTTCACTACCAAGCTTACTGTGACGAAGTTCAATGAGAGAGTGGGCAATC 185  
 Db 121 TTTCTTCACTACCAAGCTTACTGTGACGAAGTTCAATGAGAGAGTGGGCAATC 180  
 Qy 186 TGAACATATGAGATTCAGAGATGAGAGGCAATGCTGCAATCCCTGAAAGATCAATTC 245  
 Db 181 TGAACATATGAGATTCAGAGATGAGAGGCAATGCTGCAATCCCTGAAAGATCAATTC 240  
 Qy 246 AGACCCCACTCTTCCCAACATCAACATGCTGGGTGAGATTAAGGATTCCTGTGGCA 305  
 Db 241 AGACCCCACTCTTCCCAACATCAACATGCTGGGTGAGATTAAGGATTCCTGTGGCA 300  
 Qy 306 TTGCGCTGTGCGCTTGAAGAGAGCAATGATTCATTAAGATTCCTCATTTCTTGGGA 365  
 Db 301 TTGCGCTGTGCGCTTGAAGAGAGCAATGATTCATTAAGATTCCTCATTTCTTGGGA 360  
 Qy 366 AGAGGAAGAGGCTTGTGATCTGTGATGAGAGGCTCTCTCTTCCCTCCGCTCAAGAA 425  
 Db 361 AGAGGAAGAGGCTTGTGATCTGTGATGAGAGGCTCTCTCTTCCCTCCGCTCAAGAA 420  
 Qy 426 GCCCATATGAGGAGTATGAGGCTGCTGCTCAATTCCTTATAGCATTCAGGTCAGAAATTT 485  
 Db 421 GCCCATATGAGGAGTATGAGGCTGCTGCTCAATTCCTTATAGCATTCAGGTCAGAAATTT 480  
 Qy 486 GCTCAGCTTTTCAACATACCTGAGATTCCTTATCAGCAACCATCATGATCTGAGTGA 545  
 Db 481 GCTCAGCTTTTCAACATACCTGAGATTCCTTATCAGCAACCATCATGATCTGAGTGA 540  
 Qy 546 CAAGACTCTGTCAAAATATTTCAATGAGGCTGTGCTTCAAGATCTCAGAGGCAAGGTC 605  
 Db 541 CAAGACTCTGTCAAAATATTTCAATGAGGCTGTGCTTCAAGATCTCAGAGGCAAGGTC 600  
 Qy 606 CATGTGACATATGAGAGGATCACTGACCTATGATACAGCCGTACACAGAAAG 665  
 Db 601 CATGTGACATATGAGAGGATCACTGACCTATGATACAGCCGTACACAGAAAG 660  
 Qy 666 CAATATGAGAAAGTGGAGTGAAGCTTCAAGATATGTCAGCGAAGAGGAAATTTG 725  
 Db 661 CAATATGAGAAAGTGGAGTGAAGCTTCAAGATATGTCAGCGAAGAGGAAATTTG 720  
 Qy 726 CATGCGCCACTTCAAAATCTACAGTATGAGAGGAGCAGAGCTTTGATAGCTGCT 785  
 Db 721 CATGCGCCACTTCAAAATCTACAGTATGAGAGGAGCAGAGCTTTGATAGCTGCT 780  
 Qy 786 GAAGAAGCTCAAGGACCTGCGCAAGGCGGAGTGTGCTTCTTGTGAGGGCAT 845  
 Db 781 GAAGAAGCTCAAGGACCTGCGCAAGGCGGAGTGTGCTTCTTGTGAGGGCAT 840  
 Qy 846 GAGGTGAGAGGTCTGATGAGGCAATGAGGCGCTGAGTCTAGTGGAGAAATTTCTGCT 905  
 Db 841 GAGGTGAGAGGTCTGATGAGGCAATGAGGCGCTGAGTCTAGTGGAGAAATTTCTGCT 900

PD 12-SEP-2002.  
 XX 21-DEC-2001; 2001MO-US49817.  
 XX 22-DEC-2000; 2000US-257589P.  
 XX (AMHP) MYETH.  
 PA Bates BG, Xie Y, Gulukota K, Paulsen JB;  
 XX WPI; 2002-750462/81.  
 DR P-PSDB; ABP54921.  
 XX  
 PT New mglur5m nucleic acid molecules and proteins, useful for treating  
 PT neurological or psychiatric disorders such as schizophrenia,  
 PT schizoaffective disorder, bipolar or unipolar affective disorder, or  
 PT adolescent conduct disorder -  
 XX  
 PS Claim 11; Fig 1A; 99pp; English.  
 XX  
 CC The present sequence is that of cDNA clone Y1176 (deposited as  
 CC ATCC PTA-21715) encoding a novel human metabotropic glutamate  
 CC receptor subtype modulatory protein (mglur5m). The cDNA was  
 CC isolated from a human brain cDNA library. Expression of mglur5m  
 CC is predominant in cells and tissues of the central nervous system.  
 CC The gene maps to a region of chromosome 11 associated with  
 CC schizophrenia and related psychiatric disorders. The invention  
 CC provides mglur5m polypeptides and nucleic acids, and methods for  
 CC their detection, as well as methods for using them to identify  
 CC compounds that modulate metabotropic receptor (mglur) activity.  
 CC Such modulators include a mglur5m nucleic acid, a mglur5m antibody,  
 CC a ribozyme, an antisense oligonucleotide, a small molecule  
 CC modulator, a peptide and a peptidomimetic. They can be used in a  
 CC claimed method for treating a subject having a neurological  
 CC disorder, especially a psychiatric disorder selected from  
 CC schizophrenia, schizoaffective disorder, bipolar affective disorder,  
 CC unipolar affective disorder or adolescent conduct disorder (all  
 CC claimed). mglur5m polypeptides, nucleic acids and antipeptides are  
 CC also useful for screening assays, and in predictive medicine, e.g.  
 CC diagnostic assays (e.g. chromosome mapping and tissue typing),  
 CC prognostic assays, monitoring clinical trials, and pharmacogenomics.  
 CC  
 SQ Sequence 1823 BP; 488 A; 397 C; 444 G; 493 T; 1 other;  
 Query Match 100.0%; Score 1823; DB 24; Length 1823;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1823; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AAATGCTCTTCTGTTGATCTCTGATCTTACTTTTGAAGAAGATGTCGGAGT 60  
 DB 1 AAATGCTCTTCTGTTGATCTCTGATCTTACTTTTGAAGAAGATGTCGGAGT 60  
 QY 61 GCAAGTCCAGTGAAGAGAGGAGTGTGCTCAATGCTGAGTCAATCATTTATGAGCT 120  
 DB 61 GCAAGTCCAGTGAAGAGAGGAGTGTGCTCAATGCTGAGTCAATCATTTATGAGCT 120  
 QY 121 CTCTTTCTGTTTCAATCAACAGCTTACTGTGAGCAAGTTTCAAGAGAGTGTGGGCA 180  
 DB 121 CTCTTTCTGTTTCAATCAACAGCTTACTGTGAGCAAGTTTCAAGAGAGTGTGGGCA 180  
 QY 181 GTCCGTAAACAGTGTGATTCAGAGAGTGAAGGCATGTCATCCCTGGAAGATC 240  
 DB 181 GTCCGTAAACAGTGTGATTCAGAGAGTGAAGGCATGTCATCCCTGGAAGATC 240  
 QY 241 AATTGAGACCCCACTCTTCCCAACATCACTGAGCTGTGAGTAAGAGATTTCTGTC 300  
 DB 241 AATTGAGACCCCACTCTTCCCAACATCACTGAGCTGTGAGTAAGAGATTTCTGTC 300  
 QY 301 TGGCATTCGGCTGTGGGCTTGAAGAGACATTTGATTCATTAAGATTCCTCTATTTCT 360  
 DB 301 TGGCATTCGGCTGTGGGCTTGAAGAGACATTTGATTCATTAAGATTCCTCTATTTCT 360  
 QY 361 TCGAAGAGAGAGAGGCTTGTATGCTCTGTGATGAGTCTCTCTCTTCCGCTCC 420

DB 361 TCGAAGAGAGAGAGGCTTGTATGCTCTGTGATGAGTGGCTCTCTCTTCCGCTCC 420  
 QY 421 AAGAGCCCATGATGAGGGGTCAATGGGCTGGTTCAGATTCCTTACCATTCAGTTCAG 480  
 DB 421 AAGAGCCCATGATGAGGGGTCAATGGGCTGGTTCAGATTCCTTACCATTCAGTTCAG 480  
 QY 481 AATTGCTCAGCTTTTCAACATACCTCAGATTGCTTACAGCAACCATCATGATCTG 540  
 DB 481 AATTGCTCAGCTTTTCAACATACCTCAGATTGCTTACAGCAACCATCATGATCTG 540  
 QY 541 AGTGAACAGCTCTGTTCAAAATATTTCAATGAGGGTGTGCTTCAATGCTCAGAGCA 600  
 DB 541 AGTGAACAGCTCTGTTCAAAATATTTCAATGAGGGTGTGCTTCAATGCTCAGAGCA 600  
 QY 601 AGGTCCATGATGAGCATATGTAAGAGGTACATGCACTTATATACCCGTACACACA 660  
 DB 601 AGGTCCATGATGAGCATATGTAAGAGGTACATGCACTTATATACCCGTACACACA 660  
 QY 661 GAAGGCACTATGTAAGAAAGTGGAGTGAAGGCTTCAAAAGATATGTCAAGGAAGAGG 720  
 DB 661 GAAGGCACTATGTAAGAAAGTGGAGTGAAGGCTTCAAAAGATATGTCAAGGAAGAGG 720  
 QY 721 ATTGTCATGCGCCACTCTTCAAAATCTACATATGACAGGGAGAGAGCTTTGATTAAG 780  
 DB 721 ATTGTCATGCGCCACTCTTCAAAATCTACATATGACAGGGAGAGAGCTTTGATTAAG 780  
 QY 781 CTGCTGAAGAGTCAACAGTCACTTGGCCAGGCGCGGGTGTGCTTCTGTGAG 840  
 DB 781 CTGCTGAAGAGTCAACAGTCACTTGGCCAGGCGCGGGTGTGCTTCTGTGAG 840  
 QY 841 GGCATACGGTGAAGAGTCTGCTGATGAGGCAATGAGCGCTGGGTCTAGTGGAGAAATT 900  
 DB 841 GGCATACGGTGAAGAGTCTGCTGATGAGGCAATGAGCGCTGGGTCTAGTGGAGAAATT 900  
 QY 901 CTGCTTCTGGGCGAGGAACCAAGATGCACTTTATTTAGATCTCAAAAGACAGATCTTA 960  
 DB 901 CTGCTTCTGGGCGAGGAACCAAGATGCACTTTATTTAGATCTCAAAAGACAGATCTTA 960  
 QY 961 TGGGAAGACAGAAAGAAATGCAAGGTGCTTCTTCAAGGCTTTTGGAGACATTTACAC 1020  
 DB 961 TGGGAAGACAGAAAGAAATGCAAGGTGCTTCTTCAAGGCTTTTGGAGACATTTACAC 1020  
 QY 1021 AGAAGTGAAGTGGTGGCTGTCACATGCGCCAGCTCTGAATCTAAGAGTCAAGTTCAGG 1080  
 DB 1021 AGAAGTGAAGTGGTGGCTGTCACATGCGCCAGCTCTGAATCTAAGAGTCAAGTTCAGG 1080  
 QY 1081 CCCATCACTGAGTGAAGGAGCAGGCTCATCTAAATTCAGTGAATTAATCTGCAATTAT 1140  
 DB 1081 CCCATCACTGAGTGAAGGAGCAGGCTCATCTAAATTCAGTGAATTAATCTGCAATTAT 1140  
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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 14, 2003, 15:16:09 ; Search time 525.208 Seconds  
(without alignments)  
9369.765 Million cell updates/sec

Title: US-10-027-923-1

Sequence: 1 aaatgctctctctgtgat.....aaaaaaaaaaaaaaaaaa 1823

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 2552756 seqs, 1349719017 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	1784	97.9	1788	24	AA562274 CDNA sequence #61
3	1636	89.7	2172	22	AA299993 Human GRM5-1c DNA
4	1076	59.0	2349	22	AA299990 Human GRM5-1b DNA
5	1076	59.0	2351	22	AA299989 Human GRM5-1a DNA
6	897	49.2	2149	22	AA299994 Human GRM5-1f DNA
7	812	44.5	2064	22	AA299995 Human GRM5-1g DNA
8	719	39.4	2241	22	AA299992 Human GRM5-1d DNA

9	719	39.4	2326	22	AA299991 Human GRM5-1c DNA
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12	222	12.2	4078	25	AA299993 Human GRM5-1c DNA
13	222	12.2	4207	22	AA299990 Human GRM5-1b DNA
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15	222	12.2	4207	22	AA299994 Human GRM5-1f DNA
16	222	12.2	4207	22	AA299995 Human GRM5-1g DNA
17	222	12.2	4303	22	AA299991 Human GRM5-1c DNA
18	222	12.2	4303	22	AA299992 Human GRM5-1c DNA
19	222	12.2	4303	22	AA299993 Human GRM5-1c DNA
20	222	12.2	4303	22	AA299990 Human GRM5-1b DNA
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#### ALIGNMENTS

RESULT 1	ABV73899	standard; cDNA, 1823 BP.
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AC	ABV73899	
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DE	Human glutamate receptor modulatory protein mGluR5M cDNA.	
XX	Metabotropic glutamate receptor subtype 5 modulatory protein;	
KW	mGluR5M; human; G-protein coupled receptor; receptor; schizophrenia;	
KW	schizophrenia; bipolar affective disorder;	
KW	unipolar affective disorder; adolescent conduct disorder;	
KW	mood disorder; neuroprotective; neuroleptic; chromosome 11;	
KW	gene therapy; gene; 86.	
XX		
OS	Homo sapiens.	
XX		
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COMMENT On Jan 17, 2003 this sequence version replaced gi:27151430.

All repeats were identified using RepeatMasker:

Smith, A.P.A. & Green, P. (1996-1997)

<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: [sequence.submissions@genome.wi.mit.edu](mailto:sequence.submissions@genome.wi.mit.edu)

----- Project Information

Center project name: L28531

Center clone name: 114\_J\_20

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Only the first 152,3 kilobases of this clone are being submitted.  
The remainder overlaps accession number AC130364 [WICGR project  
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Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vasilev, H.,  
Viel, R., Vo, A., Wilson, B., Wu, X., Wymen, D., Young, G., Zaimoun, J.,  
Zemlek, U., Zimmer, A. and Zody, M.  
Direct Submission  
Submitted (27-MAR-2003) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Oct 10, 2002 this sequence version replaced gi:2477866.  
All repeats were identified using RepeatMasker:  
Smith, A.P.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence\_submissions@genome.wi.mit.edu  
----- Project Information  
Center project name: L27938  
Center clone name: 871\_G\_20

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\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 5 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1 3810: contig of 3810 bp in length  
\* 1 3911 3910: gap of 100 bp  
\* 3911 47222: contig of 43312 bp in length  
\* 47223 47323: gap of 100 bp  
\* 47323 54783: contig of 7461 bp in length  
\* 54784 54883: gap of 100 bp  
\* 54884 75151: contig of 20268 bp in length  
\* 75152 75251: gap of 100 bp  
\* 75252 173795: contig of 98544 bp in length.

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VERSION HTG; HTGS PHASE1; HTGS\_DRAFT.  
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SOURCE Homo sapiens  
ORGANISM

REFERENCE  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
TITLE 1 (bases 1 to 203298)  
JOURNAL The sequence of Homo sapiens clone  
REFERENCE 2 (bases 1 to 203298)  
AUTHORS Unpublished  
TITLE Direct Submission  
JOURNAL Submitted (08-JUN-2000) Genome Sequencing Center, Washington  
TITLE University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
MO 63108, USA  
On Aug 12, 2000 this sequence version replaced gi:8469033.

COMMENT

----- Genome Center -----  
Center: Washington University Genome Sequencing Center  
Center code: WUGSC  
Web site: http://genome.wustl.edu/gsc/index.shtml  
----- Project Information -----  
Center project name: H\_NH057D13  
----- Summary Statistics -----  
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Chemistry: Dye-terminator Big Dye; 0% of reads  
Assembly program: Phrap; version 0.990319  
Consensus quality: 180558 bases at least Q40  
Consensus quality: 188028 bases at least Q30  
Consensus quality: 192035 bases at least Q20  
Insert size: 16400; agarose-fp  
Insert size: 199798; sum-of-contigs  
Quality coverage: 4.42 in Q20 bases; agarose-fp  
Quality coverage: 3.69 in Q20 bases; sum-of-contigs  
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\* NOTE: This is a 'working draft' sequence. It currently

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Query Match 36.8%; Score 671; DB 9; Length 173032;

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Matches 671; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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ACCESSION
AC130336
VERSION
AC130336.3 GI:23683036
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HTG; HTGS_PHASE1; HTGS_FULFILL; HTGS_CANCELLED.
SOURCE
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ORGANISM
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 173795)
REFERENCE
Birren, B., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 11, clone RP13-871G20
Unpublished
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REFERENCE
Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,
Barra, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhgelter, B.,
Camata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A.,
Cook, A., Cooke, P., Deatrelano, K., Dewar, K., Diaz, J. S., Dodge, S.,
Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J.,
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Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C. H.,
O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K.,
Phunhahang, P., Pierre, N., Raymond, C., Retra, R., Rise, C., Rogov, P.,
Roman, J., Roy, A., Schauer, S., Schupbach, R., Seaman, S., Severy, P.,
Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J.,
Testaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J.,
Zemek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (09-AUG-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 173795)
REFERENCE
Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,
Barra, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhgelter, B.,
Camata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A.,
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Liu, G., Maclean, C., Macdonald, P., Major, J., Matthews, C.,
McCarthy, M., Meldrim, J., Menue, L., Mhova, T., Norman, C. H.,
Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C. H.,
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Center clone name: 707\_M.1

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TITLE  
JOURNAL  
COMMENT

Cook, A., Cooke, P., DeArrelano, K., Dewar, K., Diaz, J.S., Dodge, S.,  
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Liu, G., Maclean, C., MacDonald, P., Major, J., Matthews, C.,  
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Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J.,  
Testaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H.,  
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J.,  
Zembek, L., Zimmer, A. and Zody, M.

Submitted (14-SEP-2002) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA

On Sep 14, 2002 this sequence version replaced g1:22165292.  
All repeats were identified using RepeatMasker:

Smith, A.F.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence.submissions@genome.wi.mit.edu

Project Information

Center project name: L27963

Center clone name: 208 A\_14

Summary Statistics

Sequencing vector: Plasmid; n/a; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 145664 bases at least Q40

Consensus quality: 145694 bases at least Q30

Consensus quality: 145764 bases at least Q20

Insert size: 151000; agarose-fp

Insert size: 146721; sum-of-coverage

Quality coverage: 18.2 in Q20 bases; agarose-fp

Quality coverage: 18.7 in Q20 bases; sum-of-coverage

NOTE: This is a 'working draft' sequence. It currently

consists of 3 contigs. The true order of the pieces

is not known and their order in this sequence record is

arbitrary. Gaps between the contigs are represented as

runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence

as soon as it is available and the accession number will

be preserved.

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AC130364.5 GI:223683265  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 173032)  
Birren, B., Nusbaum, C. and Lander, E.  
Homo sapiens chromosome 11, clone RP11-707M1  
JOURNAL  
Unpublished  
2 (bases 1 to 173032)  
Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,  
Barna, N., Basteien, V., Bloom, T., Boguslavsky, L., Boukhalter, B.,



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ACCESSION AX068370
VERSION AX068370.1 GI:12578535
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SOURCE Homo sapiens (human)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Schwarz, D.A. and Maki, R.A.
TITLE Metabotropic glutamate receptors and methods of use therefor
JOURNAL Patent: WO 0102566-A 5 11-JAN-2001;
Neuroscience Biosciences, Inc. (US)
LOCATION/Qualifiers
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DEFINITION AC130357
ACCESSION AC130357
VERSION AC130357.2 GI:22857687
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Birren, B., Nusbaum, C. and Lander, E.
TITLE Homo sapiens chromosome 11, clone RP11-208A14
JOURNAL Unpublished
2 (bases 1 to 146921)
REFERENCE 2
AUTHORS Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,
Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Bouhassal, B.,
Camarda, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A.,
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Zembek, L., Zimmer, A. and Zody, M.
TITLE Direct Submission
JOURNAL Submitted (09-AUG-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 146921)
REFERENCE 3
AUTHORS Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,
Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Bouhassal, B.,
Camarda, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A.,
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VERSION AX068376.1 GI:12578539  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Schwarz, D.A. and Maki, R.A.  
TITLE Metabotropic glutamate receptors and methods of use therefor  
JOURNAL Patent: WO 0102566-A 11 JAN-2001;  
Neuroscience Biobiosciences, Inc. (US)  
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ACCESSION AX068371  
VERSION AX068371.1 GI:12578536  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Schwarz, D.A. and Maki, R.A.  
TITLE Metabotropic glutamate receptors and methods of use therefor  
JOURNAL Patent: WO 0102566-A 6 JAN-2001;  
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RESULT 6  
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DEFINITION AX068374  
ACCESSION AX068374.1 GI:12578538  
VERSION  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
1 Schwarz, D.A. and Maki, R.A.  
Metabotropic glutamate receptors and methods of use therefor  
Patent: WO 0102566-A 9 11-JAN-2001;  
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ACCESSION AX068376

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RESULT 5  
 AX068366 2551 bp DNA linear PAT 25-JAN-2001  
 LOCUS AX068366  
 DEFINITION Sequence 1 from Patent WO0102566.  
 ACCESSION AX068366  
 VERSION AX068366.1 GI:12578533  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 BUKARYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
 AUTHORS Schwarz,D.A. and Maki,R.A.  
 TITLE Metabotropic glutamate receptors and methods of use therefor  
 JOURNAL Patent: WO 0102566-A 1 11-JAN-2001;  
 Neurocrine Biosciences, Inc. (US)

FEATURES  
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 Location/Qualifiers  
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 /mol\_type="genomic DNA"  
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BASE COUNT 666 a 566 c 630 g 689 t

Query Match 59.0%; Score 1076; DB 6; Length 2551;  
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AX709349 1110 bp DNA linear PAT 04-APR-2003  
LOCUS Sequence 3 from Patent WO02070708.  
DEFINITION AX709349  
ACCESSION AX709349  
VERSION AX709349.1 GI:29564891  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS Bates,B.G., Xie,Y., Gulukota,K. and Paulsen,J.E.  
TITLE Glutamate receptor modulatory proteins and nucleic acids encoding  
them  
JOURNAL Patent: WO 02070708-A 3 12-SEP-2002;  
Myeth (US)  
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Db 301 CATTGGCTGTGGCTTGAAGACAGATTTAGTTCAATTAAGATTTCCCTCATTTCTTGG 360

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Db 361 GAAGAGAGAGAGGCTTGGTATGCTCTGATGAGATGAGCTCCCTCTTCCGCTCAAG 420  
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RESULT 4  
AX068368 2349 bp DNA linear PAT 25-JAN-2001  
LOCUS Sequence 3 from Patent WO0102566.  
DEFINITION AX068368  
ACCESSION AX068368  
VERSION AX068368.1 GI:12578534  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS Schwarz,D.A. and Maki,R.A.  
TITLE Metabotropic glutamate receptors and methods of use therefor  
JOURNAL Patent: WO 0102566-A 3 11-JAN-2001;  
Neuroscience Biotechnology, Inc. (US)  
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Source Location/Qualifiers  
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SOURCE	Homo sapiens (human)								
ORGANISM	Homo sapiens								
REFERENCE	Schwarz, D.A. and Maki, R.A.								
AUTHORS	Metabotropic glutamate receptors and methods of use therefor								
TITLE	Patent: WO 0102566-A 7 11-JAN-2001;								
JOURNAL	Neuroscience Bioscience, Inc. (US)								
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482	CTCTTTCTGTGATCCTGTCAGTCTTACTTTGAAAGAAGATGCGTGGAGT	541							
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542	GTCGCTGAAAGATGAGATGAGAGGCGATGTCATACCTTGAAAGATC	601							
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782	AAGAAGCCATAGTAGAGGATGATTTGGGCTGTGATGATTTTGAAGCATCAGATCAG	841							
481	AATTTGCTCAGCTTTTCAACATACCTGATGCTTACTGAGCAACCATCATGATGCTG	540							
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JOURNAL Patent: WO 02070708-A 1 12-SEP-2002;  
Wyeth (US)  
FEATURES Location/Qualifiers  
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QY 841 GGCATGACGGTGAAGAGTCTGCTGATGAGCCATGAGCGCTGGGTCTAGTGGAGATT 900  
DB 841 GGCATGACGGTGAAGAGTCTGCTGATGAGCCATGAGCGCTGGGTCTAGTGGAGATT 900  
QY 901 CTGCTTCTGGGGGAGAACAGATGCACTTATTTAGATCTCAAGAGACAGATCTTA 960  
DB 901 CTGCTTCTGGGGGAGAACAGATGCACTTATTTAGATCTCAAGAGACAGATCTTA 960  
QY 961 TGGGAAGACAGAAAGAAATGCCAAAGTGTCTTCCAGGGTTTGGAGACATATTAC 1020  
DB 961 TGGGAAGACAGAAAGAAATGCCAAAGTGTCTTCCAGGGTTTGGAGACATATTAC 1020  
QY 1021 AGAAGTGAAGTCCGTGCTGCTGACATGCCCCAGCTCTGATCTAGAGCTCAAGTCA 1080  
DB 1021 AGAAGTGAAGTCCGTGCTGCTGACATGCCCCAGCTCTGATCTAGAGCTCAAGTCA 1080  
QY 1081 CCCATGACGTGAGAGGAGCAGGCTCATCTAATTCGAGTGGATATTAATCTGCAATTAT 1140  
DB 1081 CCCATGACGTGAGAGGAGCAGGCTCATCTAATTCGAGTGGATATTAATCTGCAATTAT 1140  
QY 1141 AATGAAGCCAAAGTATCTTCTGATGAGATTTGAGAGCATTTGTATGTGATGT 1200  
DB 1141 AATGAAGCCAAAGTATCTTCTGATGAGATTTGAGAGCATTTGTATGTGATGT 1200  
QY 1201 GACCTGCAAAATGCGCCCATATCACTGCAACCTTCAAGTTTCTTGATGGGTGCT 1260  
DB 1201 GACCTGCAAAATGCGCCCATATCACTGCAACCTTCAAGTTTCTTGATGGGTGCT 1260  
QY 1261 CAGACTTCACTCTGCAAGATTAATCTGGAGAGTCAATGAGGAGCTTGGAAATTGG 1320  
DB 1261 CAGACTTCACTCTGCAAGATTAATCTGGAGAGTCAATGAGGAGCTTGGAAATTGG 1320  
QY 1321 GCTTTCGCTGTTTGTATTAAGTACTGAGAAAGGAGAAATGAGATGAGATATATGGA 1380  
DB 1321 GCTTTCGCTGTTTGTATTAAGTACTGAGAAAGGAGAAATGAGATGAGATATATGGA 1380  
QY 1381 GAGAGGAGACTTTTATGCTTGGGATTTGTAAGAAGCACTTCAAGTCACTCTTTACC 1440  
DB 1381 GAGAGGAGACTTTTATGCTTGGGATTTGTAAGAAGCACTTCAAGTCACTCTTTACC 1440  
QY 1441 ACCTCCCGATTACATGCGAGTATGTCCTCAAGACCTTACCAAGATGAGATTAATCCTG 1500  
DB 1441 ACCTCCCGATTACATGCGAGTATGTCCTCAAGACCTTACCAAGATGAGATTAATCCTG 1500  
QY 1501 GATTGTAAGCTTAAGACTGAGCTTCTGTGATGTTAATCAAGAGCTCCCTATATACCC 1560  
DB 1501 GATTGTAAGCTTAAGACTGAGCTTCTGTGATGTTAATCAAGAGCTCCCTATATACCC 1560  
QY 1561 ATCCCTTAATGCTCTTTCACCTCTCAGGCTTATCTTTGCTGATATCACTCTGA 1620  
DB 1561 ATCCCTTAATGCTCTTTCACCTCTCAGGCTTATCTTTGCTGATATCACTCTGA 1620  
QY 1621 CCAAGACAAATGAGAAATGTTTATGCTGCTGAGAACCCCTTAATCCATTAAGCCC 1680  
DB 1621 CCAAGACAAATGAGAAATGTTTATGCTGCTGAGAACCCCTTAATCCATTAAGCCC 1680  
QY 1681 TCTTCTGTGCTTATCAACAGAGCAATAGGTTCTGTTTATGCTTGAATTGCAAT 1740  
DB 1681 TCTTCTGTGCTTATCAACAGAGCAATAGGTTCTGTTTATGCTTGAATTGCAAT 1740  
QY 1741 CTATGTTATTAATACTCATTTATGTTGTTACTATTAATGCTTAATAACCAAAAAA 1800  
DB 1741 CTATGTTATTAATACTCATTTATGTTGTTACTATTAATGCTTAATAACCAAAAAA 1800



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 14, 2003, 15:19:23 ; Search time 6888.62 Seconds  
(without alignments)  
10826.305 Million cell updates/sec

Title: US-10-027-923-1

Perfect score: 1823

Sequence: 1 aaatggctctctctgtgat.....aaaaaaaaaaaaaaaaaaaaa 1823

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 2888711 seqs, 2045481386 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

GenBmb1.\*  
1: gb Da.\*  
2: gb Hcg.\*  
3: gb In.\*  
4: gb Om.\*  
5: gb Ov.\*  
6: gb Pat.\*  
7: gb Ph.\*  
8: gb Pl.\*  
9: gb Pr.\*  
10: gb Ro.\*  
11: gb Sts.\*  
12: gb Sts.\*  
13: gb Un.\*  
14: gb Vi.\*  
15: em Ba.\*  
16: em Fun.\*  
17: em Hum.\*  
18: em In.\*  
19: em Mu.\*  
20: em Om.\*  
21: em Or.\*  
22: em Ov.\*  
23: em Pac.\*  
24: em Ph.\*  
25: em Pl.\*  
26: em Ro.\*  
27: em Sts.\*  
28: em Un.\*  
29: em Vi.\*  
30: em Hcg\_hum.\*  
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32: em Hcg\_other.\*  
33: em Hcg\_mus.\*  
34: em Hcg\_pln.\*  
35: em Hcg\_rtd.\*  
36: em Hcg\_mam.\*  
37: em Hcg\_vtc.\*  
38: em Sv.\*  
39: em Htgo\_hum.\*  
40: em Htgo\_mus.\*  
41: em Htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1823	100.0	1823	6 AX709347	AX709347 Sequence
2	1636	89.7	2172	6 AX068372	AX068372 Sequence
3	1110	60.9	1110	6 AX709349	AX709349 Sequence
4	1076	59.0	2349	6 AX068368	AX068368 Sequence
5	1076	59.0	2551	6 AX068366	AX068366 Sequence
6	897	44.5	2149	6 AX068374	AX068374 Sequence
7	812	49.2	2064	6 AX068376	AX068376 Sequence
8	719	39.4	2241	6 AX068371	AX068371 Sequence
9	719	39.4	2326	6 AX068370	AX068370 Sequence
10	671	36.8	146921	2 AC130357	AC130357 Homo sapi
11	671	36.8	173032	9 AC130364	AC130364 Homo sapi
12	671	36.8	173795	2 AC130336	AC130336 Homo sapi
13	551	30.2	203298	2 AC073113	AC073113 Homo sapi
14	507	27.8	152269	9 AC136759	AC136759 Homo sapi
15	499	27.4	79253	9 AC107937	AC107937 Homo sapi
16	378	20.7	182701	2 AC026078	AC026078 Homo sapi
17	253	13.9	58560	2 AC131048	AC131048 Homo sapi
18	222	12.2	4078	6 AR270570	AR270570 Sequence
19	222	12.2	4207	6 AR145364	AR145364 Sequence
20	222	12.2	4207	6 AR145365	AR145365 Sequence
21	222	12.2	4303	6 AR145366	AR145366 Sequence
22	222	12.2	4303	6 AR145367	AR145367 Sequence
23	222	12.2	4518	6 AX548892	AX548892 Sequence
24	222	12.2	4518	9 HUMMGRS5A	D28538 Human mRNA
25	222	12.2	4614	9 HUMMGRS5B	D28539 Human mRNA
26	219	12.0	625	11 GS6623	GS6623 SHGC-102020
27	217	11.9	71127	2 AC131278	AC131278 Homo sapi
28	207	11.4	71127	2 AC131278	AC131278 Homo sapi
29	176	9.7	133278	2 AC034188	AC034188 Homo sapi
30	176	9.7	137384	9 AP001828	AP001828 Homo sapi
31	176	9.7	145299	2 AP000653	AP000653 Homo sapi
32	176	9.7	196373	2 AC022004	AC022004 Homo sapi
33	176	9.7	202218	9 AC026201	AC026201 Homo sapi
34	176	9.7	202864	2 AP003178	AP003178 Homo sapi
35	171	9.4	3282	6 AR038828	AR038828 Sequence
36	171	9.4	3282	6 AR038845	AR038845 Sequence
37	171	9.4	3282	6 AR256861	AR256861 Sequence
38	171	9.4	3282	6 AR256861	AR256861 Sequence
39	171	9.4	4085	6 AR038826	AR038826 Sequence
40	171	9.4	4085	6 AR038843	AR038843 Sequence
41	171	9.4	4085	6 AR256859	AR256859 Sequence
42	171	9.4	4085	6 AR256859	AR256859 Sequence
43	171	9.4	4085	6 AR256859	AR256859 Sequence
44	171	9.4	4181	6 AR038827	AR038827 Sequence
45	171	9.4	4181	6 AR038844	AR038844 Sequence
				6 AR256860	AR256860 Sequence

#### ALIGNMENTS

RESULT 1	AX709347	1823 bp	DNA	linear	PAT 04-APR-2003
LOCUS	AX709347				
DEFINITION	Sequence 1 from Patent WO02070708.				
ACCESSION	AX709347				
VERSION	AX709347.1	GI:29564889			
KEYWORDS					
SOURCE					
ORGANISM	Homo sapiens (human)				
REFERENCE	Bukacynski, Metazoa; Chordata; Vertebrata; Euteleostomi;				
AUTHORS	Bates, B.G., Xie, Y., Gulukota, K. and Paulsen, J.E.				
TITLE	Glutamate receptor modulatory proteins and nucleic acids encoding them				



DB 1040 CAGATGCTCAGCAGCAGGCGCATGATGACATAGTGAAGAGTCAAACTGGAACCTTATG 1099  
 QY 641 TATCAGCCCGTACACAGAAAGGCACTATGAGAAAGTGGATGGAAGCCTTAAAGATA 700  
 DB 1100 TATCAGCCCGTACACAGAAAGGCACTATGAGAAAGTGGATGGAAGCCTTAAAGATA 1159  
 QY 701 TGTCAAGGAAAGGAAATTTGATGCGCCACTCTTACAAATCTACATATGACAGGG 760  
 DB 1160 TGTCAAGGAAAGGAAATTTGATGCGCCACTCTTACAAATCTACATATGACAGGG 1219  
 QY 761 AGCAGAGCTTTGATTAAGCTGCTGAAGAGCTCAAGTCACTTCCCAAGGCCCGGATG 820  
 DB 1220 AGCAGAGCTTTGATTAAGCTGCTGAAGAGCTCAAGTCACTTCCCAAGGCCCGGATG 1279  
 QY 821 TGGCCATCTTCTGTAGAGGCGATGACGCTGCTGATGAGCCATGAGGCGGCTG 880  
 DB 1280 TGGCCATCTTCTGTAGAGGCGATGACGCTGCTGATGAGCCATGAGGCGGCTG 1339  
 QY 881 GTCTAG 886  
 DB 1340 GTCTAG 1345

RESULT 15  
 AAD05030  
 ID AAD05030 standard; mRNA; 4207 BP.  
 AC AAD05030;  
 DT 17-JUL-2001 (first entry)  
 DE Human metabotropic glutamate receptor, mGluR5A mRNA.  
 KW Human; metabotropic glutamate receptor; mGluR5A; excitatory amino acid;  
 KW EAA; central nervous system; CNS; presynaptic release; neurotransmitter;  
 KW postsynaptic sensitivity; glutamate excitation; ss.  
 OS Homo sapiens.  
 FT Key Location/Qualifiers  
 FT CDS 460..4002  
 FT /\*tag= a  
 FT /product= "Human metabotropic glutamate receptor,  
 FT mGluR5A"

US6211353-B1.  
 03-APR-2001.  
 07-JUN-1996; 96US-0660148.  
 29-JUL-1994; 94US-0282853.  
 (ELIL ) LILLY & CO ELI.  
 Burnett JP, Wayne NG, Sharp RL, Snyder YM;  
 WPI, 2001-289639/30.  
 P-PSDB; AAB01156.

New isolated nucleic acids for producing human metabotropic glutamate  
 PT receptors, which are useful for modulating the presynaptic release of  
 PT glutamate or the postsynaptic sensitivity of the neuronal cell to  
 PT glutamate excitation -  
 Claim 2; Column 43-46; 53p; English.

The present sequence is a mRNA encoding human metabotropic glutamate  
 CC receptor, mGluR5A. L-glutamate, the most abundant neurotransmitter in  
 CC the central nervous system (CNS), mediates excitatory pathway in  
 CC mammals. L-glutamate is referred to as excitatory amino acid (EAA) and  
 CC the receptors that respond to glutamate are EAA receptors. The receptors  
 CC are useful for modulating the presynaptic release of glutamate and the

CC postsynaptic sensitivity of the neuronal cell to glutamate excitation.  
 XX  
 SQ Sequence 4207 BP; 1010 A; 1121 C; 1112 G; 964 U; 0 other;  
 Query Match 20.0%; Score 222; DB 22; Length 4207;  
 Best Local Similarity 76.3%; Pred. No. 4e-102;  
 Matches 325; Conservative 97; Mismatches 4; Indels 0; Gaps 0;

QY 461 TGGCCATCTTCTGTAGAGGCGATGACGCTGCTGATGAGCCATGAGGCGGCTG 520  
 DB 920 UAGCCATCTTCTGTAGAGGCGATGACGCTGCTGATGAGCCATGAGGCGGCTG 979  
 QY 521 CAACCATCATGATCTGATGAGCAAGACTCTGTTCAAAATATTTATGAGGGTTGCTT 580  
 DB 980 CAACCATCATGATCTGATGAGCAAGACTCTGTTCAAAATATTTATGAGGGTTGCTT 1039  
 QY 581 CAGATGCTCAGCAGCAGGCGCATGATGAGCAATGATGAGAGTCAAACTGGAACCTATG 640  
 DB 1040 CAGATGCTCAGCAGCAGGCGCATGATGAGCAATGATGAGAGTCAAACTGGAACCTATG 1099  
 QY 641 TATCAGCCCGTACACAGAAAGGCACTATGAGAAAGTGGATGGAAGCCTTAAAGATA 700  
 DB 1100 TATCAGCCCGTACACAGAAAGGCACTATGAGAAAGTGGATGGAAGCCTTAAAGATA 1159  
 QY 701 TGTCAAGGAAAGGAAATTTGATGCGCCACTCTTACAAATCTACATATGACAGGG 760  
 DB 1160 TGTCAAGGAAAGGAAATTTGATGCGCCACTCTTACAAATCTACATATGACAGGG 1219  
 QY 761 AGCAGAGCTTTGATTAAGCTGCTGAAGAGCTCAAGTCACTTCCCAAGGCCCGGATG 820  
 DB 1220 AGCAGAGCTTTGATTAAGCTGCTGAAGAGCTCAAGTCACTTCCCAAGGCCCGGATG 1279  
 QY 821 TGGCCATCTTCTGTAGAGGCGATGACGCTGCTGATGAGCCATGAGGCGGCTG 880  
 DB 1280 TGGCCATCTTCTGTAGAGGCGATGACGCTGCTGATGAGCCATGAGGCGGCTG 1339  
 QY 881 GTCTAG 886  
 DB 1340 GTCTAG 1345

Search completed: December 14, 2003, 18:46:52  
 Job time : 324.792 secs

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FT mutation replace (425, A)
XX /+tag= b
XX
XX US6211353-B1.
XX
XX 03-APR-2001.
XX
XX 07-JUN-1996; 96US-0660148.
XX
XX 29-JUL-1994; 94US-0282853.
XX
XX (ELIL ) LILLY & CO ELI.
XX
XX Burnett JP, Mayne NG, Sharp RL, Snyder YM;
XX
XX WPI; 2001-289639/30.
XX
XX New isolated nucleic acids for producing human metabotropic glutamate
XX receptors, which are useful for modulating the presynaptic release of
XX glutamate or the postsynaptic sensitivity of the neuronal cell to
XX glutamate excitation -
XX
XX Disclosure; Column -, 53pp; English.
XX
XX The present sequence is a cDNA mutant encoding human metabotropic
XX glutamate receptor, mGluR5A. L-glutamate, the most abundant
XX neurotransmitter in the central nervous system (CNS), mediates excitatory
XX pathway in mammals. L-glutamate is referred to as excitatory amino acid
XX (EAA) and the receptors that respond to glutamate are EAA receptors. The
XX receptors are useful for modulating the presynaptic release of glutamate
XX and the postsynaptic sensitivity of the neuronal cell to glutamate
XX excitation.
XX Note: The present sequence is not shown in the specification, but is
XX derived from the sequence referred as SEQ ID NO:1, shown in column
XX 59-68 (AABD05029) of the specification.
XX
XX Sequence 4207 BP; 1010 A; 1121 C; 1112 G; 964 T; 0 other;
SQ
Query Match 20.0%; Score 222; DB 22; Length 4207;
Best Local Similarity 99.1%; Pred. No. 4e-102;
Matches 422; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 461 TAGCCATTGAGTCCAGAAATTGCTCCAGCTTTTCAACATACCTCAGATTGTTACTCAG 520
DB 920 TAGCCATTGAGTCCAGAAATTGCTCCAGCTTTTCAACATACCTCAGATTGTTACTCAG 979
QY 521 CAACCATCATGATCTGATGACAGAACTCTGTTCAAAATATTTTCATGAGGTTGTCCTT 580
DB 980 CAACCATCATGATCTGATGACAGAACTCTGTTCAAAATATTTTCATGAGGTTGTCCTT 1039
QY 581 CAGATGCTCAGAGGAGGAGTTCATGATGACATAGTGAAGAGTACCACTGAGCCTTAG 640
DB 1040 CAGATGCTCAGAGGAGGAGTTCATGATGACATAGTGAAGAGTACCACTGAGCCTTAG 1099
QY 641 TATCAGCCCTTACACAGAAAGCACTATGAGAAAGTGGAGTGAAGCTTCAAGATA 700
DB 1100 TATCAGCCCTTACACAGAAAGCACTATGAGAAAGTGGAGTGAAGCTTCAAGATA 1159
QY 701 TGTGACGGAAGAGGAGTTCATGATGACCTCTTACAAATCTACAGTAATGACGGG 760
DB 1160 TGTGACGGAAGAGGAGTTCATGATGACCTCTTACAAATCTACAGTAATGACGGG 1219
QY 761 AGCAGAGCTTTGATTAAGCTGCTGAAGAAGTCAAGTCACTTGCCCAAGGCCGGGTG 820
DB 1220 AGCAGAGCTTTGATTAAGCTGCTGAAGAAGTCAAGTCACTTGCCCAAGGCCGGGTG 1279
QY 821 TGGCCCTACTTCTGTGAGGGATGACGGTGAAGAGTCTGCTGATGAGGCGCTCG 880
DB 1280 TGGCCCTACTTCTGTGAGGGATGACGGTGAAGAGTCTGCTGATGAGGCGCTCG 1339
QY 881 GTCTAG 886
DB 1340 GTCTAG 1345

```

```

RESULT 14
AABD05029
ID AABD05029 standard; cDNA; 4207 BP.
XX
XX AABD05029;
XX
XX 17-JUL-2001 (first entry)
XX
XX Human metabotropic glutamate receptor, mGluR5A cDNA.
XX
XX Human; metabotropic glutamate receptor; mGluR5A; excitatory amino acid;
XX EAA; central nervous system; CNS; presynaptic release; neurotransmitter;
XX postsynaptic sensitivity; glutamate excitation; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 460..4002
XX /+tag= a
XX /product= "Human metabotropic glutamate receptor,
XX mGluR5A"
XX
XX US6211353-B1.
XX
XX 03-APR-2001.
XX
XX 07-JUN-1996; 96US-0660148.
XX
XX 29-JUL-1994; 94US-0282853.
XX
XX (ELIL ) LILLY & CO ELI.
XX
XX Burnett JP, Mayne NG, Sharp RL, Snyder YM;
XX
XX WPI; 2001-289639/30.
XX
XX P-PSDB; AAB01156.
XX
XX New isolated nucleic acids for producing human metabotropic glutamate
XX receptors, which are useful for modulating the presynaptic release of
XX glutamate or the postsynaptic sensitivity of the neuronal cell to
XX glutamate excitation -
XX
XX Claim 2; Column 59-68; 53pp; English.
XX
XX The present sequence is a cDNA encoding human metabotropic glutamate
XX receptor, mGluR5A. L-glutamate, the most abundant neurotransmitter in
XX the central nervous system (CNS), mediates excitatory pathway in
XX mammals. L-glutamate is referred to as excitatory amino acid (EAA) and
XX the receptors that respond to glutamate are EAA receptors. The receptors
XX are useful for modulating the presynaptic release of glutamate and the
XX postsynaptic sensitivity of the neuronal cell to glutamate excitation.
XX Note: The present sequence is stated as being the same as that shown as
XX SEQ ID NO:1 (AABD05029) in column 7-18 of the specification. However the
XX sequences differ at several positions.
XX
XX Sequence 4207 BP; 1011 A; 1120 C; 1112 G; 964 T; 0 other;
SQ
Query Match 20.0%; Score 222; DB 22; Length 4207;
Best Local Similarity 99.1%; Pred. No. 4e-102;
Matches 422; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 461 TAGCCATTGAGTCCAGAAATTGCTCCAGCTTTTCAACATACCTCAGATTGTTACTCAG 520
DB 920 TAGCCATTGAGTCCAGAAATTGCTCCAGCTTTTCAACATACCTCAGATTGTTACTCAG 979
QY 521 CAACCATCATGATCTGATGACAGAACTCTGTTCAAAATATTTTCATGAGGTTGTCCTT 580
DB 980 CAACCATCATGATCTGATGACAGAACTCTGTTCAAAATATTTTCATGAGGTTGTCCTT 1039
QY 581 CAGATGCTCAGAGGAGGAGTTCATGATGACATAGTGAAGAGTACCACTGAGCCTTAG 640

```

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Db      521 CAACGAGCATGATCGAGTGAACAAGCTCTGTTCAAAATTTTCATGAGGTTGTGCTT 580
Qy      581 CAGATCTCAGCAGGCGAAGTTCATGTCAGTCACTAGTAAAGAGTCAACTGACCTTATG 640
Db      581 CAGATCTCAGCAGGCGAAGTTCATGTCAGTCACTAGTAAAGAGTCAACTGACCTTATG 640
Qy      641 TATCAGCCGTGACACAGAAAGCACTATGGAAGAAAGTGGGATGGAAGCTTCAAAAGAT 700
Db      641 TATCAGCCGTGACACAGAAAGCACTATGGAAGAAAGTGGGATGGAAGCTTCAAAAGAT 700
Qy      701 TGTCAAGCAGAAAGGAGATTGTCATGCCCACTTTACAAATCTACAGTATATGACGAG 760
Db      701 TGTCAAGCAGAAAGGAGATTGTCATGCCCACTTTACAAATCTACAGTATATGACGAG 760
Qy      761 AGCAGAGCTTTGTAAGCTGCTGAAGAAGTCAAGTCACTTGGCCCAAGGCCCGGCTG 820
Db      821 TGCCCTACTTCTGTGAGGGCATGACGGTGAAGAGTCTGCTGATGCGCATGAGGCGCTG 880
Qy      881 GTCTAG 886
Db      881 GTCTAG 886

```

RESULT 12  
ACAS6535  
ID ACAS6535 standard; cDNA; 4078 BP.

ACAS6535;  
06-JUN-2003 (first entry)  
Human signalling pathway polynucleotide probe SEQ ID NO 1133.

Human; probe; ss; array element; Parkinson's disease;  
signalling pathway population; cancer; adenocarcinoma; leukaemia;  
immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.

Homo sapiens.  
US6500938-B1.  
31-DEC-2002.  
30-JAN-1998; 98US-0016434.  
30-JAN-1998; 98US-0016434.  
(INCY-) INCYTE GENOMICS INC.  
Au-Young J, Seilhamer Jf;  
WPI; 2003-352189/33.

Combination of polynucleotide probes, useful as array elements in a  
microarray for monitoring the expression of a number of target  
polynucleotides.

Claim 1; SEQ ID NO 1133; 65bp; English.

The invention relates to a combination which comprises a number of  
polynucleotide probes comprising a sequence selected from one of the 1490  
sequences mentioned in the specification. The combination is useful as an  
array element in a microarray for monitoring the expression of a number  
of target polynucleotides. The microarray is particularly useful in the  
diagnosis and treatment of cancer and immunopathology and neuropathology.  
The microarray is useful in diagnostic and treatment regimens, drug  
discovery and development, toxicological and carcinogenicity studies,  
forensics and pharmacogenomics. The microarray is also useful for

monitoring progression of diseases and for developing sophisticated  
profiles for the effects of currently available therapeutic drugs. The  
combination is also useful for purifying a subpopulation of mRNAs, cDNAs  
and genomic fragments and in research and diagnostic applications. The  
array can detect changes in expression in a large number of genes coding  
for different signalling pathway populations which can be used to diagnose  
various diseases including cancer e.g. adenocarcinoma and leukaemia,  
immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease  
and Parkinson's disease. The present sequence represents a polynucleotide  
probe of the invention.  
Note: The sequence data for this patent did not form part of the printed  
specification but was obtained in electronic format directly from USPTO  
at [seqdata.uspto.gov/sequence.html?docid=06500938B1](http://seqdata.uspto.gov/sequence.html?docid=06500938B1).

SO Sequence 4078 BP; 994 A; 1074 C; 1076 G; 934 T; 0 other;

Query Match 20.0%; Score 222; DB 25; Length 4078;  
Best Local Similarity 99.1%; Pred. No. 4e-102;  
Matches 422; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy      461 TAGCCATTGAGTCCAGAAATTTGCTCCAGCTTTTCAACATACCTCAGATTGCTTACAG 520
Db      611 TAGCCATTGAGTCCAGAAATTTGCTCCAGCTTTTCAACATACCTCAGATTGCTTACAG 670
Qy      521 CAACCATCATGATCTGATGACAAGACTCTGTTCAATATTTTCATGAGGTTGTGCTT 580
Db      671 CAACCATCATGATCTGATGACAAGACTCTGTTCAATATTTTCATGAGGTTGTGCTT 730
Qy      581 CAGATCTCAGCAGGCGAAGGCTTCATGTCAGTCACTAGTAAAGAGTCAACTGACCTATG 640
Db      731 CAGATCTCAGCAGGCGAAGGCTTCATGTCAGTCACTAGTAAAGAGTCAACTGACCTATG 790
Qy      641 TATCAGCCGTGACACAGAAAGCACTATGGAAGAAAGTGGGATGGAAGCTTCAAAAGAT 700
Db      791 TATCAGCCGTGACACAGAAAGCACTATGGAAGAAAGTGGGATGGAAGCTTCAAAAGAT 850
Qy      701 TGTCAAGCAGAAAGGAGATTGTCATGCCCACTTTACAAATCTACAGTATATGACGAG 760
Db      851 TGTCAAGCAGAAAGGAGATTGTCATGCCCACTTTACAAATCTACAGTATATGACGAG 910
Qy      761 AGCAGAGCTTTGTAAGCTGCTGAAGAAGTCAAGTCACTTGGCCCAAGGCCCGGCTG 820
Db      911 AGCAGAGCTTTGTAAGCTGCTGAAGAAGTCAAGTCACTTGGCCCAAGGCCCGGCTG 970
Qy      821 TGCCCTACTTCTGTGAGGGCATGACGGTGAAGAGTCTGCTGATGCGCATGAGGCGCTG 880
Db      971 TGCCCTACTTCTGTGAGGGCATGACGGTGAAGAGTCTGCTGATGCGCATGAGGCGCTG 1030
Qy      881 GTCTAG 886
Db      1031 GTCTAG 1036

```

RESULT 13  
AAD04990  
ID AAD04990 standard; cDNA; 4207 BP.

AAD04990;

17-JUL-2001 (first entry)

Human metabotropic glutamate receptor, mGluR5A cDNA mutant.

Human; metabotropic glutamate receptor; mGluR5A; excitatory amino acid;  
EAA; central nervous system; CNS; presynaptic release; neurotransmitter;  
postsynaptic sensitivity; glutamate excitation; mutant; ss.

Homo sapiens.  
Synthetic.

Key Location/Qualifiers  
mutation replace (416, T)  
/\*tag= a

```

XX AAC85785;
AC 18-JUL-2001 (first entry)
DT 18-JUL-2001 (first entry)
XX
XX cDNA encoding metabotropic glutamate receptor.
DE
XX Human; metabotropic glutamate receptor; mglur; splice variant;
XX mglur5; G-protein-coupled receptor; glutamate; neurological disorder;
XX anticonvulsant; neuroprotectant; analgesic; cognitive enhancer;
XX muscle relaxant; ss.
XX Homo sapiens.
XX MO200130829-A1.
XX
XX 03-MAY-2001.
XX
XX 25-OCT-2000; 2000MO-US29356.
XX
XX 25-OCT-1999; 99US-0161481.
XX PR 24-OCT-2000; 2000US-0695481.
XX (NPSP-) NPS PHARM INC.
XX
XX Krapcho K, Stormann T, Levinthal C, Hammerland L, Storjohann L;
XX
XX WPI: 2001-308615/32.
XX P-PSDB; AAB47217.
XX
XX New nucleic acid encoding an isoform of human metabotropic glutamate
XX receptor, for identifying potential therapeutic agents for neurological
XX disease
XX
XX Claim 2; Page 51-56; 86pp; English.
XX
XX This sequence encodes a human metabotropic glutamate receptor (mglur).
XX mglur is a splice variant of human metabotropic glutamate receptor 5
XX (mglur5). mglur's are G-protein-coupled receptors capable of activating
XX a variety of intracellular second messenger systems following the
XX binding of glutamate. Recombinant mglur DNA and compounds that bind to,
XX or modulate activity of mglur are useful for diagnosing or treating
XX neurological disorders, e.g. as anticonvulsants, neuroprotectants,
XX analgesics, cognitive enhancers and muscle relaxants.
XX
XX Sequence 2826 BP; 729 A; 679 C; 712 G; 706 T; 0 other;
XX
XX
XX Query Match 20.0%; Score 222; DB 22; Length 2826;
XX Best Local Similarity 99.1%; Pred. No. 4e-102;
XX Matches 422; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX 461 TAGCCATTGAGTCCAGAAATTTGCTCCAGTTTTCACATACCTCGATTGCTTACTCAG 520
DB 461 TAGCCATTGAGTCCAGAAATTTGCTCCAGTTTTCACATACCTCGATTGCTTACTCAG 520
XX
XX 521 CAACCATCATGATCTGATGACACAGACTCTGTTCAATATTTTCAAGGGTTGCGCTT 580
DB 521 CAACCATCATGATCTGATGACACAGACTCTGTTCAATATTTTCAAGGGTTGCGCTT 580
XX
XX 581 CAGATGCTCAGCAGGCAAGGTCATGATGACATAGTGAAGAGTCAATGCACTTATG 640
DB 581 CAGATGCTCAGCAGGCAAGGTCATGATGACATAGTGAAGAGTCAATGCACTTATG 640
XX
XX 641 TATCAGCCGTACACACAGAAAGCAATATGAGAGAAAGTGGATGAAAGCCTTCAAGATA 700
DB 641 TATCAGCCGTACACACAGAAAGCAATATGAGAGAAAGTGGATGAAAGCCTTCAAGATA 700
XX
XX 701 TGTCAAGCAAGGAGGATTTGATGCCACTCTTACAAATCTACATTAATGCAAGGG 760
DB 701 TGTCAAGCAAGGAGGATTTGATGCCACTCTTACAAATCTACATTAATGCAAGGG 760
XX
XX 761 AGCAGAGCTTTGATAGTGTGTAAGAAAGTCAAGTCACTTGCCCAAGGCCCGGGTGG 820
XX

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DB 761 AGCAGAGCTTTGATAGTGTGTAAGAAAGTCAAGTCACTTGCCCAAGGCCCGGGTGG 820
XX
XX 821 TGGCTTACTTCTGTGAGGGCATGAGGTGCGTGCATGAGGCATGAGGCGCTTG 880
DB 821 TGGCTTACTTCTGTGAGGGCATGAGGTGCGTGCATGAGGCATGAGGCGCTTG 880
XX
XX 881 GTCTAG 886
DB 881 GTCTAG 886
XX
XX
XX RESULT 11
XX AAC85787
XX ID AAC85787 standard; cDNA; 3129 BP.
XX
XX AAC85787;
XX
XX 18-JUL-2001 (first entry)
XX
XX cDNA encoding chimeric receptor containing hmglur5d portion.
XX
XX Human; metabotropic glutamate receptor; mglur; splice variant;
XX mglur5; G-protein-coupled receptor; glutamate; neurological disorder;
XX anticonvulsant; neuroprotectant; analgesic; cognitive enhancer;
XX muscle relaxant; calcium receptor; Car; mglur5d; ss.
XX
XX Chimeric - Homo sapiens.
XX
XX MO200130829-A1.
XX
XX 03-MAY-2001.
XX
XX 25-OCT-2000; 2000MO-US29356.
XX
XX 25-OCT-1999; 99US-0161481.
XX PR 24-OCT-2000; 2000US-0695481.
XX
XX (NPSP-) NPS PHARM INC.
XX
XX Krapcho K, Stormann T, Levinthal C, Hammerland L, Storjohann L;
XX
XX WPI: 2001-308615/32.
XX P-PSDB; AAB47219.
XX
XX New nucleic acid encoding an isoform of human metabotropic glutamate
XX receptor, for identifying potential therapeutic agents for neurological
XX disease
XX
XX Claim 18; Page 70-75; 86pp; English.
XX
XX This sequence encodes a chimeric receptor comprising the intracellular
XX cytoplasmic tail of the human calcium receptor (Car) and the extra-
XX cellular and seven transmembrane domains of the human metabotropic
XX glutamate receptor (mglur) splice variant of human metabotropic
XX glutamate receptor 5 (mglur5). mglur5d. mglur's are G-protein-coupled
XX receptors capable of activating a variety of intracellular second
XX messenger systems following the binding of glutamate. Recombinant
XX mglur5d DNA and compounds that bind to, or modulate activity of it
XX are useful for diagnosing or treating neurological disorders, e.g.
XX as anticonvulsants, neuroprotectants, analgesics, cognitive enhancers
XX and muscle relaxants.
XX
XX Sequence 3129 BP; 806 A; 782 C; 804 G; 737 T; 0 other;
XX
XX
XX Query Match 20.0%; Score 222; DB 22; Length 3129;
XX Best Local Similarity 99.1%; Pred. No. 4e-102;
XX Matches 422; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX 461 TAGCCATTGAGTCCAGAAATTTGCTCCAGTTTTCACATACCTCGATTGCTTACTCAG 520
DB 461 TAGCCATTGAGTCCAGAAATTTGCTCCAGTTTTCACATACCTCGATTGCTTACTCAG 520
XX
XX 521 CAACCATCATGATCTGATGACACAGACTCTGTTCAATATTTTCAAGGGTTGCGCTT 580
XX

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Db      425 CAGTCCAGTGAAGAGAGGGGTGGCTCAGATCTGGGTGACATCTATTGAGCTCTC 484
Qy      121 TTTTCTGTTCAATCAGCAGCTACTGTGAGAGAAATTATGAGAGAAAGTGGGGAGTC 180
Db      485 TTTTCTGTTCAATCAGCAGCTACTGTGAGAGAAATTATGAGAGAAAGTGGGGAGTC 544
Qy      181 CGTGAACAGTATGGCATTTCAAGAGTGGAGGCCATGTCTGATACCTTGGAAAAGATCAAT 240
Db      545 CGGAACAGTATGGCATTTCAAGAGTGGAGGCCATGTCTGATACCTTGGAAAAGATCAAT 604
Qy      241 TCAGACCCCACTCTTTGGCCCAATCACTGGGCTGGAGATTAAGGATTCCTGCTGG 300
Db      605 TCAGACCCCACTCTTTGGCCCAATCACTGGGCTGGAGATTAAGGATTCCTGCTGG 664
Qy      301 CATTGGCTGTGGCCCTAGAGCAGAGCATTTAGTTCATTAAGATTCCTCATTTCTTGG 360
Db      665 CATTGGCTGTGGCCCTAGAGCAGAGCATTTAGTTCATTAAGATTCCTCATTTCTTGG 724
Qy      361 GAAGAGAGAGAGGGCTTGGTATGCTGTGGAGTGGCTCTCTCTTCTTCCGCTCCAG 420
Db      725 GAAGAGAGAGAGGGCTTGGTATGCTGTGGAGTGGCTCTCTCTTCTTCCGCTCCAG 784
Qy      421 AAGCCCATATGATAGGGGCTATTTGGGCTGTTCCAGTCTTTAGCCATTGAGTCCAGAA 480
Db      785 AAGCCCATATGATAGGGGCTATTTGGGCTGTTCCAGTCTTTAGCCATTGAGTCCAGAA 844
Qy      481 TTGCTCAGCTTTTCAACATACCTCAGATTGCTTACTCAGCAACCATCATGATGATGAT 540
Db      845 TTGCTCAGCTTTTCAACATACCTCAGATTGCTTACTCAGCAACCATCATGATGATGAT 904
Qy      541 GACAAAGCTCTGTTCAAAATTTTTCATGAGGGTGTGGCTTCAAGTGTCTCAGCAGGCAAG 600
Db      905 GACAAAGCTCTGTTCAAAATTTTTCATGAGGGTGTGGCTTCAAGTGTCTCAGCAGGCAAG 964
Qy      601 TCATGATGAGCATATGAGAGAGGTACAACATGAGCTATGATCAGCCGTACACAGAA 660
Db      965 TCATGATGAGCATATGAGAGAGGTACAACATGAGCTATGATCAGCCGTACACAGAA 1024
Qy      661 GG 662
Db      1025 GG 1026

```

RESULT 9  
AAFP2989  
ID AAFP2989 standard; DNA; 2551 BP.  
XX

AC AAFP2989;

DT 06-APR-2001 (first entry)

DE Human GRMx-1a DNA.

KW Human; metabotropic glutamate receptor; schizophrenia; GRMx;  
KW Alzheimer's; Parkinson's; stroke; depression; anxiety; pain; de.

XX Homo sapiens.

OS WO200102566-A1.

PN 11-JAN-2001.

PD 27-JUN-2000; 2000WO-US17798.

XX 02-JUL-1999; 99US-0346326.

PR (NEUR-) NEUROCRINE BIOSCIENCES INC.

XX Schwarz DA, Maki RA;

PI WPI; 2001-123112/13.

XX

PT Novel metabotropic glutamate receptor for prevention, treatment of  
PT conditions associated with undesirable glutamate levels, e.g.  
PT Alzheimer's, Parkinson's disease, stroke, depression, anxiety, pain and  
PT schizophrenia -  
XX  
XX Claim 2; Fig 1; 59pp; English.

CC The present invention relates to human metabotropic glutamate  
CC receptor. An agent that decreases expression or activity of the  
CC metabotropic glutamate receptor is useful for treating schizophrenia.  
CC Metabotropic glutamate receptor polymucleotides, polypeptides  
CC are useful for treating diseases associated with undesirable  
CC levels of glutamate, such as Alzheimer's disease, Parkinson's  
CC disease, stroke, depression, anxiety, pain and schizophrenia.

XX Sequence 2551 BP; 666 A; 566 C; 630 G; 689 T; 0 other;

Qy Query Match 50.4%; Score 559; DB 22; Length 2551;  
Best Local Similarity 99.7%; Pred. No. 3.5e-273;  
Matches 659; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy      1 ATGCTCTTCTGTTGATCTGTGATCTTACTTCTTGAAGAAAGATGCTGGAGATGCA 60
Db      365 ATGCTCTTCTGTTGATCTGTGATCTTACTTCTTGAAGAAAGATGCTGGAGATGCA 424
Qy      61 CAGTCCAGTGAAGAGAGGGGTGGGCTCAATGCTGGGTGACATCTTATTGAGCTCTC 120
Db      425 CAGTCCAGTGAAGAGAGGGGTGGGCTCAATGCTGGGTGACATCTTATTGAGCTCTC 484
Qy      121 TTTTCTGTTCAATCAGCAGCTACTGTGAGAGAAATTATGAGAGAAAGTGGGGAGTC 180
Db      485 TTTTCTGTTCAATCAGCAGCTACTGTGAGAGAAATTATGAGAGAAAGTGGGGAGTC 544
Qy      181 CGTGAACAGTATGGCATTTCAAGAGTGGAGGCCATGTCTGATACCTTGGAAAAGATCAAT 240
Db      545 CGGAACAGTATGGCATTTCAAGAGTGGAGGCCATGTCTGATACCTTGGAAAAGATCAAT 604
Qy      241 TCAGACCCCACTCTTTGGCCCAATCACTGGGCTGGAGATTAAGGATTCCTGCTGG 300
Db      605 TCAGACCCCACTCTTTGGCCCAATCACTGGGCTGGAGATTAAGGATTCCTGCTGG 664
Qy      301 CATTGGCTGTGGCCCTAGAGCAGAGCATTTAGTTCATTAAGATTCCTCATTTCTTGG 360
Db      665 CATTGGCTGTGGCCCTAGAGCAGAGCATTTAGTTCATTAAGATTCCTCATTTCTTGG 724
Qy      361 GAAGAGAGAGAGGGCTTGGTATGCTGTGGAGTGGCTCTCTCTTCTTCCGCTCCAG 420
Db      725 GAAGAGAGAGAGGGCTTGGTATGCTGTGGAGTGGCTCTCTCTTCTTCCGCTCCAG 784
Qy      421 AAGCCCATATGATAGGGGCTATTTGGGCTGTTCCAGTCTTTAGCCATTGAGTCCAGAA 480
Db      785 AAGCCCATATGATAGGGGCTATTTGGGCTGTTCCAGTCTTTAGCCATTGAGTCCAGAA 844
Qy      481 TTGCTCAGCTTTTCAACATACCTCAGATTGCTTACTCAGCAACCATCATGATGATGAT 540
Db      845 TTGCTCAGCTTTTCAACATACCTCAGATTGCTTACTCAGCAACCATCATGATGATGAT 904
Qy      541 GACAAAGCTCTGTTCAAAATTTTTCATGAGGGTGTGGCTTCAAGTGTCTCAGCAGGCAAG 600
Db      905 GACAAAGCTCTGTTCAAAATTTTTCATGAGGGTGTGGCTTCAAGTGTCTCAGCAGGCAAG 964
Qy      601 TCATGATGAGCATATGAGAGAGGTACAACATGAGCTATGATCAGCCGTACACAGAA 660
Db      965 TCATGATGAGCATATGAGAGAGGTACAACATGAGCTATGATCAGCCGTACACAGAA 1024
Qy      661 G 661
Db      1025 G 1025

```

RESULT 10  
AAC85785  
ID AAC85785 standard; cDNA; 2826 BP.

DE Human GRMX-1c DNA.  
 XX Human; metabotropic glutamate receptor; schizophrenia; GRMX;  
 KM Alzheimer's; Parkinson's; stroke; depression; anxiety; pain; ds.  
 XX  
 OS Homo sapiens.  
 XX MO200102566-A1.  
 XX PN  
 XX PD 11-JAN-2001.  
 XX PF 27-JUN-2000; 2000MO-US17798.  
 XX PR 02-JUL-1999; 99US-0346326.  
 XX (NEUR-) NEUROCRINE BIOSCIENCES INC.  
 XX PI Schwarz DA, Maki RA;  
 XX WPI; 2001-123112/13.  
 XX Novel metabotropic glutamate receptor for prevention, treatment of  
 PT conditions associated with undesirable glutamate levels, e.g.  
 PT Alzheimer's, Parkinson's disease, stroke, depression, anxiety, pain and  
 PT schizophrenia.  
 XX  
 PS Claim 2; Fig 5; 59pp; English.  
 XX  
 CC The present invention relates to human metabotropic glutamate  
 CC receptor. An agent that decreases expression or activity of the  
 CC metabotropic glutamate receptor is useful for treating schizophrenia.  
 CC Metabotropic glutamate receptor polynucleotides, polypeptides  
 CC are useful for treating diseases associated with undesirable  
 CC levels of glutamate, such as Alzheimer's disease, Parkinson's  
 CC disease, stroke, depression, anxiety, pain and schizophrenia.  
 XX  
 SQ Sequence 2326 BP; 581 A; 535 C; 580 G; 630 T; 0 other;  
 Query Match 50.5%; Score 560; DB 22; Length 2326;  
 Best Local Similarity 99.7%; Pred. No. 1.1e-273;  
 Matches 660; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 ATGGTCTTCTGTGATCTGTGATCTTGTGAAAGAGATGTCGGGAGATGCA 60  
 DB 365 ATGGTCTTCTGTGATCTGTGATCTTGTGAAAGAGATGTCGGGAGATGCA 424  
 QY 61 CAGTCCAGTGAAGAGAGGTGTGCTCACATGCTGGGTGACATCATTTAGAGCTCTC 120  
 DB 425 CAGTCCAGTGAAGAGAGGTGTGCTCACATGCTGGGTGACATCATTTAGAGCTCTC 484  
 QY 121 TTTTCTGTTCAATACAGAGCTTGTGAGAGAGATTCATAGAGAGAGTGTGGGCAATC 180  
 DB 485 TTTTCTGTTCAATACAGAGCTTGTGAGAGAGATTCATAGAGAGAGTGTGGGCAATC 544  
 QY 181 CCGTGAACAGATGAGATTCAGAGAGAGAGAGAGATGTCATGCTGAGAGAGATCAAT 240  
 DB 545 CCGTGAACAGATGAGATTCAGAGAGAGAGAGAGATGTCATGCTGAGAGAGATCAAT 604  
 QY 241 TCAGACCCCACTCTTGGCCCAATCACTGAGGTGTGAGATTAAGAGATTCCTGCTGG 300  
 DB 605 TCAGACCCCACTCTTGGCCCAATCACTGAGGTGTGAGATTAAGAGATTCCTGCTGG 664  
 QY 301 CATTGGCTGTGGCCCTAGAGAGAGATTCATTAAGAGATTCCTGATTTCTTTCG 360  
 DB 665 CATTGGCTGTGGCCCTAGAGAGAGATTCATTAAGAGATTCCTGATTTCTTTCG 724  
 QY 361 GAAGAGAGAGAGAGGTGTGATGCTGTGAGATGAGCTCTCTTCTTCCGCTCAAG 420  
 DB 725 GAAGAGAGAGAGAGGTGTGATGCTGTGAGATGAGCTCTCTTCTTCCGCTCAAG 784  
 QY 421 AAGCCCATAGTAGAGGTGTGATGAGGTGTGATGAGGTGTGATGAGGTGTGATGAGGT 480  
 DB 785 AAGCCCATAGTAGAGGTGTGATGAGGTGTGATGAGGTGTGATGAGGTGTGATGAGGT 844

QY 481 TTGCTCAGCTTTTCAACATACCTCAGATTTGCTTACTCAGCAACATCATGATCTGAGT 540  
 DB 845 TTGCTCAGCTTTTCAACATACCTCAGATTTGCTTACTCAGCAACATCATGATCTGAGT 904  
 QY 541 GACAGACTCTGTCAAAATATTTTCATGAGAGGTGTGCTTCAATGCTCAGAGCAAGG 600  
 DB 905 GACAGACTCTGTCAAAATATTTTCATGAGAGGTGTGCTTCAATGCTCAGAGCAAGG 964  
 QY 601 TCCATGCTGACATAGTGAAGAGGTACACTGACCTATGATACGCCGTACACAGGAA 660  
 DB 965 TCCATGCTGACATAGTGAAGAGGTACACTGACCTATGATACGCCGTACACAGGAA 1024  
 QY 661 GG 662  
 DB 1025 GG 1026  
 RESULT 8  
 ID AAF29990 standard; DNA; 2349 BP.  
 AC AAF29990;  
 XX 06-APR-2001 (first entry)  
 DT  
 XX  
 DE Human GRMX-1b DNA.  
 XX  
 KM Human; metabotropic glutamate receptor; schizophrenia; GRMX;  
 KM Alzheimer's; Parkinson's; stroke; depression; anxiety; pain; ds.  
 XX  
 OS Homo sapiens.  
 XX MO200102566-A1.  
 XX PN  
 XX PD 11-JAN-2001.  
 XX PF 27-JUN-2000; 2000MO-US17798.  
 XX PR 02-JUL-1999; 99US-0346326.  
 XX (NEUR-) NEUROCRINE BIOSCIENCES INC.  
 XX PI Schwarz DA, Maki RA;  
 XX WPI; 2001-123112/13.  
 XX Novel metabotropic glutamate receptor for prevention, treatment of  
 PT conditions associated with undesirable glutamate levels, e.g.  
 PT Alzheimer's, Parkinson's disease, stroke, depression, anxiety, pain and  
 PT schizophrenia.  
 XX  
 PS Claim 2; Fig 3; 59pp; English.  
 XX  
 CC The present invention relates to human metabotropic glutamate  
 CC receptor. An agent that decreases expression or activity of the  
 CC metabotropic glutamate receptor is useful for treating schizophrenia.  
 CC Metabotropic glutamate receptor polynucleotides, polypeptides  
 CC are useful for treating diseases associated with undesirable  
 CC levels of glutamate, such as Alzheimer's disease, Parkinson's  
 CC disease, stroke, depression, anxiety, pain and schizophrenia.  
 XX  
 SQ Sequence 2349 BP; 588 A; 538 C; 586 G; 637 T; 0 other;  
 Query Match 50.5%; Score 560; DB 22; Length 2349;  
 Best Local Similarity 99.7%; Pred. No. 1.1e-273;  
 Matches 660; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 ATGGTCTTCTGTGATCTGTGATCTTGTGAAAGAGATGTCGGGAGATGCA 60  
 DB 365 ATGGTCTTCTGTGATCTGTGATCTTGTGAAAGAGATGTCGGGAGATGCA 424  
 QY 61 CAGTCCAGTGAAGAGAGGTGTGCTCACATGCTGGGTGACATCATTTAGAGCTCTC 120

```
Db 725 GAAGAGAAAGGGCTTGGTGTGCTGTGATGGCTCTCTCTTCCGCTCCAAAG 784
Qy 421 AAGCCATAGTAGGGGTCAATGGGCTGTGTTCCAGTTCTTTAGCCATTGAGTCCGAAT 480
Db 785 AAGCCATAGTAGGGGTCAATGGGCTGTGTTCCAGTTCTTTAGCCATTGAGTCCGAAT 844
Qy 481 TTGCTCCAGCTTTTCAACATCTGATGATGCTTACGACCAATCATGATGATGATG 540
Db 845 TTGCTCCAGCTTTTCAACATCTGATGATGCTTACGACCAATCATGATGATGATG 904
Qy 541 GACAAAGCTCTGTCTTCAATATTTTCAATGAGGGTGTGCTTCAATGCTCAGAGCAAG 600
Db 905 GACAAAGCTCTGTCTTCAATATTTTCAATGAGGGTGTGCTTCAATGCTCAGAGCAAG 964
Qy 601 TCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
Db 965 TCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1024
Qy 661 GGGCACTATGAGAAAGTGGAGTGAAGAGCTTCAAGATATGTCAGGGAAGAGGAT 720
Db 1025 GGGCACTATGAGAAAGTGGAGTGAAGAGCTTCAAGATATGTCAGGGAAGAGGAT 1084
Qy 721 TGCATGCGCCACTCTTACAAATCTACATGATGAGAGGAGAGAGCTTGTATAGCTG 780
Db 1085 TGCATGCGCCACTCTTACAAATCTACATGATGAGAGGAGAGAGCTTGTATAGCTG 1144
Qy 781 CTGAAGAGCTCAAGAGTCACTTGGCCAGAGCCCGGGTGTGCTTACTTGTGAGGGC 840
Db 1145 CTGAAGAGCTCAAGAGTCACTTGGCCAGAGCCCGGGTGTGCTTACTTGTGAGGGC 1204
Qy 841 ATGACGCTGAGAGAGTCTGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900
Db 1205 ATGACGCTGAGAGAGTCTGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1264
Qy 901 CTCTGGGCGAG 911
Db 1265 CTCTGGGCGAG 1275

RESULT 6
AAF29992
ID .AAF29992 standard; DNA; 2241 BP.
XX
AC AAF29992;
XX
DT 06-APR-2001 (first entry)
XX
DE Human GRMX-Id DNA.
XX
KW Human; metabotropic glutamate receptor; schizophrenia; GRMX;
KW Alzheimer's; Parkinson's; stroke; depression; anxiety; pain; ds.
XX
OS Homo sapiens.
XX
PN W0200102566-A1.
XX
PD 11-JAN-2001.
XX
PF 27-JUN-2000; 2000MO-US17798.
XX
PR 02-JUL-1999; 99US-0346326.
XX
PA (NEUR-) NEUROCRINE BIOSCIENCES INC.
XX
PI Schwarz DA, Maki RA;
XX
DR WPI; 2001-123112/13.
XX
PT Novel metabotropic glutamate receptor for prevention, treatment of
PT conditions associated with undesirable glutamate levels, e.g.
PT Alzheimer's, Parkinson's disease, stroke, depression, anxiety, pain and
PT schizophrenia -
XX
```

```
PS Claim 2; Fig 6; 59pp; English.
XX
CC The present invention relates to human metabotropic glutamate
CC receptor. An agent that decreases expression or activity of the
CC metabotropic glutamate receptor is useful for treating schizophrenia.
CC - Metabotropic glutamate receptor polynucleotides, polypeptides
CC are useful for treating diseases associated with undesirable
CC levels of glutamate, such as Alzheimer's disease, Parkinson's
CC disease, stroke, depression, anxiety, pain and schizophrenia.
XX
SQ Sequence 2241 BP; 552 A; 516 C; 561 G; 612 T; 0 other;
XX
Query Match 50.5%; Score 560; DB 22; Length 2241;
Best Local Similarity 99.7%; Pred. No. 1.1e-273;
Matches 660; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 ATGCTCTCTGTGATGCTGCTGATGCTTACTTGTGAAAGAGATGCGTGGAGTGCA 60
Db 365 ATGCTCTCTGTGATGCTGCTGATGCTTACTTGTGAAAGAGATGCGTGGAGTGCA 424
Qy 61 CAGTCCAGTGAAGAGAGGCTGTGCTTCAATGCTGCTGATGATGATGATGATGATG 120
Db 425 CAGTCCAGTGAAGAGAGGCTGTGCTTCAATGCTGCTGATGATGATGATGATGATG 484
Qy 121 TTTTCTGTTCAATCAGGCTACTGATGAGAGAGTTCATGAGAGAGAGTGGGAGTC 180
Db 485 TTTTCTGTTCAATCAGGCTACTGATGAGAGAGTTCATGAGAGAGAGTGGGAGTC 544
Qy 181 CGTGAACATATGAGATTCATGAGAGAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGG 240
Db 545 CGTGAACATATGAGATTCATGAGAGAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGG 604
Qy 241 TCAGACCCCACTCTTGGCCCAATCAGACAGTGGCTGTGAGATTAAGGATTCCTGCTG 300
Db 605 TCAGACCCCACTCTTGGCCCAATCAGACAGTGGCTGTGAGATTAAGGATTCCTGCTG 664
Qy 301 CATTCGGCTGTGAGGCTTGAAGAGAGATGATGATGATGATGATGATGATGATGATG 360
Db 665 CATTCGGCTGTGAGGCTTGAAGAGAGATGATGATGATGATGATGATGATGATGATG 724
Qy 361 GAAGAGAAAGAGGCTGTGATGCTGCTGATGAGGCTCTCTCTTCCGCTCCAG 420
Db 725 GAAGAGAAAGAGGCTGTGATGCTGCTGATGAGGCTCTCTCTTCCGCTCCAG 784
Qy 421 AAGCCATAGTAGGGGTCAATGGGCTGTGTTCCAGTTCTTTAGCCATTGAGTCCGAAT 480
Db 785 AAGCCATAGTAGGGGTCAATGGGCTGTGTTCCAGTTCTTTAGCCATTGAGTCCGAAT 844
Qy 481 TTGCTCCAGCTTTTCAACATCTGATGATGCTTACGACCAATCATGATGATGATG 540
Db 845 TTGCTCCAGCTTTTCAACATCTGATGATGCTTACGACCAATCATGATGATGATG 904
Qy 541 GACAAAGCTCTGTCTTCAATATTTTCAATGAGGGTGTGCTTCAATGCTCAGAGCAAG 600
Db 905 GACAAAGCTCTGTCTTCAATATTTTCAATGAGGGTGTGCTTCAATGCTCAGAGCAAG 964
Qy 601 TCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
Db 965 TCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1024
Qy 661 GG 662
Db 1025 GG 1026

RESULT 7
AAF29991
ID .AAF29991 standard; DNA; 2326 BP.
XX
AC AAF29991;
XX
DT 06-APR-2001 (first entry)
XX
```

Oy	1	ATGCTCTCTCTGTATCTGTCAGCTTACTTTTGAAGAAGATGTCGTGGAGTGA	60
Db	365	ATGCTCTCTCTGTATCTGTCAGCTTACTTTTGAAGAAGATGTCGTGGAGTGA	424
Oy	61	CAGTCCAGTGAAGAGGGGTGGCTCAATGCTGGTGACATTAATTGAGCTTTC	120
Db	425	CAGTCCAGTGAAGAGGGGTGGCTCAATGCTGGTGACATTAATTGAGCTTTC	484
Oy	121	TTTTCTGTTCATCAACAGCTTACTGTGACGAAAGTTCATGAAAGAAAGTGTGGGCACTC	180
Db	485	TTTTCTGTTCATCAACAGCTTACTGTGACGAAAGTTCATGAAAGAAAGTGTGGGCACTC	544
Oy	181	CGTGAACAGTATGSGCATTCAGAGATGAGGCGCATGCTGCATACCTGGAAAGATCAAT	240
Db	545	CGTGAACAGTATGSGCATTCAGAGATGAGGCGCATGCTGCATACCTGGAAAGATCAAT	604
Oy	241	TCAGACCCCAACACTTTGGCCCAATCACTAGGCTGTGAGATTAAGGATTTCTGTGG	300
Db	605	TCAGACCCCAACACTTTGGCCCAATCACTAGGCTGTGAGATTAAGGATTTCTGTGG	664
Oy	301	CATTGGCGTGGGCCCTTAGAGAGAGCATGAGTTCAATAAGATATTCCTCATTTCTTGG	360
Db	665	CATTGGCGTGGGCCCTTAGAGAGAGCATGAGTTCAATAAGATATTCCTCATTTCTTGG	724
Oy	361	GAAGAGGAAGAGGGCTTGGTATGCTCTGTGAGATGGCTCCTCTTCTCTTCGCTCCAG	420
Db	725	GAAGAGGAAGAGGGCTTGGTATGCTCTGTGAGATGGCTCCTCTTCTCTTCGCTCCAG	784
Oy	421	AAGCCCATATGTAAGGGGTCAATTGGGCTGGTTCAGTCTTTTAGCCATTCAGGTCAGAAAT	480
Db	785	AAGCCCATATGTAAGGGGTCAATTGGGCTGGTTCAGTCTTTTAGCCATTCAGGTCAGAAAT	844
Oy	481	TTGCTCCAGCTTTTCAATACCTAGATGTCATCTAGAACATATGATGATTCGAT	540
Db	845	TTGCTCCAGCTTTTCAATACCTAGATGTCATCTAGAACATATGATGATTCGAT	904
Oy	541	GACAAAGACTCTGTTCAAAATATTTCAATGAGGGTGTGCTTCAGATGCTCAGCAGGCAAG	600
Db	905	GACAAAGACTCTGTTCAAAATATTTCAATGAGGGTGTGCTTCAGATGCTCAGCAGGCAAG	964
Oy	601	TCCATGTGTGACATATGTAAGAGGTCAACTGAGACCTATGTAATGCATCCGTAACAAGAA	660
Db	965	TCCATGTGTGACATATGTAAGAGGTCAACTGAGACCTATGTAATGCATCCGTAACAAGAA	1024
Oy	661	GGCAACTATGGAAGAAAGTGGAGTGAAGCCTTCAAAAGATATGTCGCGAAGGAAGGGATT	720
Db	1025	GGCAACTATGGAAGAAAGTGGAGTGAAGCCTTCAAAAGATATGTCGCGAAGGAAGGGATT	1084
Oy	721	TGCATGCGCCACTCTTACAAATCTTACAGTATATGCAAGGGAGCAGAGCTTTGATTAAGCTG	780
Db	1085	TGCATGCGCCACTCTTACAAATCTTACAGTATATGCAAGGGAGCAGAGCTTTGATTAAGCTG	1144
Oy	781	CTGAAAGAGCTCACAAGTCACTTGGCCCAAGGCGGGGTGTGGCTTACTTCTGTGAGGGC	840
Db	1145	CTGAAAGAGCTCACAAGTCACTTGGCCCAAGGCGGGGTGTGGCTTACTTCTGTGAGGGC	1204
Oy	841	ATGACGGGTGAGAGGCTGTGCTATATGCTCATATGAGCGCTGGGTCTATGTGGGAATTTCTG	900
Db	1205	ATGACGGGTGAGAGGCTGTGCTATATGCTCATATGAGCGCTGGGTCTATGTGGGAATTTCTG	1264
Oy	901	CTTCTGGGCAAGGAACAGATGCACTTTTATGATCTCAAAAGAACAGATCCTATG	960
Db	1265	CTTCTGGGCAAGGAACAGATGCACTTTTATGATCTCAAAAGAACAGATCCTATG	1324
Oy	961	GAAGAAGAAAGAAATGCCAAGGTGCTTCTTCAAG	996
Db	1325	GAAGAAGAAAGAAATGCCAAGGTGCTTCTTCAAG	1360

Query Match	72.9%	Score 809	DB 22	Length 2064
Best Local Similarity	99.8%	Pred. No. 0		
Matches 909	Conservative 0	Mismatches 2	Indels 0	Gaps 0
QY	1	ATGCTCTCTGCTGATCCTGTCAGTCTTCTTTGAAAGAGATGCCGCGGAGTGC	60	
DB	365	ATGCTCTCTGCTGATCCTGTCAGTCTTCTTTGAAAGAGATGCCGCGGAGTGC	424	
QY	61	CAGTCAGTGAAGAGAGAGGAGTGGCTCACATGCTGGGTGACATTTATGAGCTTC	120	
DB	425	CAGTCAGTGAAGAGAGAGGAGTGGCTCACATGCTGGGTGACATTTATGAGCTTC	484	
QY	121	TTTTCTGTTATCAACAGCTACTGTGAGCGAAGTTATGAGAGAAATGTGGGCACTC	180	
DB	485	TTTTCTGTTATCAACAGCTACTGTGAGCGAAGTTATGAGAGAAATGTGGGCACTC	544	
QY	181	CGTGAACAGTATGTCATTCAAGAGTGAAGGCCATGCTGCATACCTTGGAAAGATCAAT	240	
DB	545	CGTGAACAGTATGTCATTCAAGAGTGAAGGCCATGCTGCATACCTTGGAAAGATCAAT	604	
QY	241	TTCGAGCCCAACATCTTGGCCCAACATCACTGGGGCTGTGAGATTAAGGAAATCTCGTGG	300	
DB	605	TTCGAGCCCAACATCTTGGCCCAACATCACTGGGGCTGTGAGATTAAGGAAATCTCGTGG	664	
QY	301	CATTGGCTGTGGCCCTAGAGCAGAGCATTAAGATTTCCCTCATTTCTTCG	360	
DB	665	CATTGGCTGTGGCCCTAGAGCAGAGCATTAAGATTTCCCTCATTTCTTCG	724	
QY	361	GAAAGGAGAGAGGCTTGTATGCTCTGTGAGATGCTCTCTCTTCTTCCGCTCAAG	420	



PT conditions associated with undesirable glutamate levels, e.g.  
 PT Alzheimer's, Parkinson's disease, stroke, depression, anxiety, pain and  
 PT schizophrenia -  
 PS Claim 2; Fig 7; 59pp; English.  
 XX  
 CC The present invention relates to human metabotropic glutamate  
 CC receptor. An agent that decreases expression or activity of the  
 CC metabotropic glutamate receptor is useful for treating schizophrenia.  
 CC Metabotropic glutamate receptor polynucleotides, polypeptides  
 CC are useful for treating diseases associated with undesirable  
 CC levels of glutamate, such as Alzheimer's disease, Parkinson's  
 CC disease, stroke, depression, anxiety, pain and schizophrenia.  
 XX  
 SQ Sequence 2172 BP; 554 A; 488 C; 544 G; 586 T; 0 other;

Query Match 90.8%; Score 1008; DB 22; Length 2172;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 1108; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCTCTTCTGTGATCCCTGTCAGTCTTACTTTTGAAGAAGATGCCGTGGAGTGA 60  
 DB ATGGCTCTTCTGTGATCCCTGTCAGTCTTACTTTTGAAGAAGATGCCGTGGAGTGA 424  
 QY 61 CAGTCCAGTGAAG 120  
 DB CAGTCCAGTGAAG 425  
 QY 121 TTTTCTGTTTCATCCAGCCTACTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180  
 DB TTTTCTGTTTCATCCAGCCTACTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 485  
 QY 181 CGTGAAGATGATGAGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 240  
 DB CGTGAAGATGATGAGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 545  
 QY 241 TCAGACCCCACTCTTGGCCCAATCACTGGGCTGTGAGATGAAGAGATTCCTGCTGG 300  
 DB TCAGACCCCACTCTTGGCCCAATCACTGGGCTGTGAGATGAAGAGATTCCTGCTGG 605  
 QY 301 CATTGCGCTGTGGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATTC 360  
 DB CATTGCGCTGTGGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATTC 665  
 QY 665 CATTGCGCTGTGGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATTC 724  
 DB CATTGCGCTGTGGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATTC 361  
 QY 361 GAAAG 420  
 DB GAAAG 725  
 QY 421 AAGCCCATGATGAT 480  
 DB AAGCCCATGATGAT 785  
 QY 785 AAGCCCATGATGAT 844  
 DB AAGCCCATGATGAT 481  
 QY 481 TTGCTCAGCTTTTCAACATACCTCAGATTGCTTACTCAGAACATCATAGATCTAGT 540  
 DB TTGCTCAGCTTTTCAACATACCTCAGATTGCTTACTCAGAACATCATAGATCTAGT 845  
 QY 845 TTGCTCAGCTTTTCAACATACCTCAGATTGCTTACTCAGAACATCATAGATCTAGT 904  
 DB TTGCTCAGCTTTTCAACATACCTCAGATTGCTTACTCAGAACATCATAGATCTAGT 541  
 QY 541 GACAAAGCTCTGTTCAATATTTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600  
 DB GACAAAGCTCTGTTCAATATTTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 905  
 QY 905 GACAAAGCTCTGTTCAATATTTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 601  
 DB GACAAAGCTCTGTTCAATATTTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 661  
 QY 661 GCGCAATATGAT 720  
 DB GCGCAATATGAT 1025  
 QY 1025 GCGCAATATGAT 721  
 DB GCGCAATATGAT 1085  
 QY 1085 TGCAATGCCCACTCTTCAAAATCTACAGTATATCAGAGAGAGAGAGAGATTTGATTA 1144  
 DB TGCAATGCCCACTCTTCAAAATCTACAGTATATCAGAGAGAGAGAGAGATTTGATTA 781  
 QY 781 CTGAAGAAGGTCACAAAGTCACTTGCCCAAGGCCCGGGTGTGGCTTCTGTGAGAGGC 840

DB 1145 CTGAAGAAGGTCACAAAGTCACTTGCCCAAGGCCCGGGTGTGGCTTCTGTGAGAGGC 1204  
 QY 841 ATGACGGTGAAGAGTCTGTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 900  
 DB ATGACGGTGAAGAGTCTGTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1205  
 QY 901 CTTCTGGAT 960  
 DB CTTCTGGAT 1265  
 QY 1265 CTTCTGGAT 961  
 DB GAAAGAT 1325  
 QY 1325 GAAAGAT 1021  
 DB AGTGAATCCGTGCTGCTGCAATGCCAGAGCTCTGATATCTAAGCTCAAGTCAAGGCC 1080  
 QY 1081 AGTGAATCCGTGCTGCTGCAATGCCAGAGCTCTGATATCTAAGCTCAAGTCAAGGCC 1385  
 DB AGTGAATCCGTGCTGCTGCAATGCCAGAGCTCTGATATCTAAGCTCAAGTCAAGGCC 1445  
 QY 1445 ATCACTGAGACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1474  
 DB ATCACTGAGACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1474

RESULT 4  
 AAF29994  
 ID AAF29994 standard; DNA; 2149 BP.  
 XX  
 AC AAF29994;  
 XX  
 DT 06-APR-2001 (first entry)  
 XX  
 DE Human GRMX-1f DNA.  
 XX  
 KW Human; metabotropic glutamate receptor; schizophrenia; GRMX;  
 KW Alzheimer's; Parkinson's; stroke; depression; anxiety; pain; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 FN W0200102566-A1.  
 XX  
 PD 11-JAN-2001.  
 XX  
 PF 27-JUN-2000; 2000MO-US17798.  
 XX  
 PR 02-JUL-1999; 99US-0346326.  
 XX  
 PA (NEUR-) NEUROCRINE BIOSCIENCES INC.  
 XX  
 PI Schwarz DA, Maki RA;  
 XX  
 DR WPI, 2001-123112/13.  
 XX  
 PT Novel metabotropic glutamate receptor for prevention, treatment of  
 PT conditions associated with undesirable glutamate levels, e.g.  
 PT Alzheimer's, Parkinson's disease, stroke, depression, anxiety, pain and  
 PT schizophrenia -  
 PS Claim 2; Fig 9; 59pp; English.  
 XX  
 CC The present invention relates to human metabotropic glutamate  
 CC receptor. An agent that decreases expression or activity of the  
 CC metabotropic glutamate receptor is useful for treating schizophrenia.  
 CC Metabotropic glutamate receptor polynucleotides, polypeptides  
 CC are useful for treating diseases associated with undesirable  
 CC levels of glutamate, such as Alzheimer's disease, Parkinson's  
 CC disease, stroke, depression, anxiety, pain and schizophrenia.  
 XX  
 SQ Sequence 2149 BP; 547 A; 485 C; 538 G; 579 T; 0 other;

Query Match 80.5%; Score 894; DB 22; Length 2149;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 994; Conservative 0; Mismatches 2; Indels 0; Gaps 0;



12-SEP-2002.

XX 21-DEC-2001; 2001MO-US49817.

XX 22-DEC-2000; 2000US-257589P.

PA (AMHP) MYETH.

PI Bates BG, Xie Y, Gulukota K, Paulsen JR,

XX MPI; 2002-750462/81.

DR P-PSDB; ABP54921.

PT New mglu5m nucleic acid molecules and proteins, useful for treating

PT neurological or psychiatric disorders such as schizophrenia,

PT schizoaffective disorder, bipolar or unipolar affective disorder, or

PT adolescent conduct disorder.

PS Claim 11; Fig 1A; 99pp; English.

XX The present sequence is that of cDNA clone Y1176 (deposited as

CC ATCC PTA-2775) encoding a novel human metabotropic glutamate

CC receptor subtype modulatory protein (mglu5m). The cDNA was

CC isolated from a human brain cDNA library. Expression of mglu5m

CC is predominant in cells and tissues of the central nervous system.

CC The gene maps to a region of chromosome 11 associated with

CC schizophrenia and related psychiatric disorders. The invention

CC provides mglu5m polypeptides and nucleic acids, and methods for

CC their detection, as well as methods for using them to identify

CC compounds that modulate metabotropic receptor (mglu5m) activity.

CC Such modulators include a mglu5m nucleic acid, a mglu5m antibody,

CC a ribozyme, an antisense oligonucleotide, a small molecule

CC modulator, a peptide and a peptidomimetic. They can be used in a

CC claimed method for treating a subject having a neurological

CC disorder, especially a psychiatric disorder selected from

CC schizophrenia, schizoaffective disorder, bipolar affective disorder,

CC unipolar affective disorder or adolescent conduct disorder (all

CC claimed). mglu5m polypeptides, nucleic acids and antibodies are

CC also useful for screening assays, and in predictive medicine, e.g.

CC diagnostic assays (e.g. chromosome mapping and tissue typing),

CC prognostic assays, monitoring clinical trials, and pharmacogenomics.

XX

SQ Sequence 1823 BP; 488 A; 397 C; 444 G; 493 T; 1 other;

Query Match 100.0%; Score 1110; DB 24; Length 1823;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTCTTCTGTTGATCTGTCAGTCTTACTTTTGAAGAAGATGCCGTGGAGTGA 60

DB 4 ATGGTCTTCTGTTGATCTGTCAGTCTTACTTTTGAAGAAGATGCCGTGGAGTGA 63

QY 61 CAGTCCAGTGAAGAGAGGAGTGGTCTCAATGCTGGGTGATCATTTATTTGAGCTCTC 120

DB 64 CAGTCCAGTGAAGAGAGGAGTGGTCTCAATGCTGGGTGATCATTTATTTGAGCTCTC 123

QY 121 TTTTCTGTTTATCCACGCTTACTGTGAGCAAGTTTCAATGAGAGAAAGTGTGGCAGTC 180

DB 124 TTTTCTGTTTATCCACGCTTACTGTGAGCAAGTTTCAATGAGAGAAAGTGTGGCAGTC 183

QY 181 CGTGAACAGTATGATTCAGAGAGTGAAGGCGCAATGCTGATCCCTGGAAGATCAAT 240

DB 184 CGTGAACAGTATGATTCAGAGAGTGAAGGCGCAATGCTGATCCCTGGAAGATCAAT 243

QY 241 TCAGACCCCACTCTTGGCCCAATCACTAGGCTGTGAGATTAAGGATTTCTGTCTGG 300

DB 244 TCAGACCCCACTCTTGGCCCAATCACTAGGCTGTGAGATTAAGGATTTCTGTCTGG 303

QY 301 CATTGGCTGTGGCCCTTGAAGAGAGCATTTGATTTCAATGAAGATTTCTTATTTCTTG 360

DB 304 CATTGGCTGTGGCCCTTGAAGAGAGCATTTGATTTCAATGAAGATTTCTTATTTCTTG 363

QY 361 GAAGAGGAAGAGGCTTGTATGCTCTGTGATGAGCTTCCTCTTCTTCCGCTCCAG 420

DB 364 GAAGAGGAAGAGGCTTGTATGCTCTGTGAGTGGCTCTCTCTCTCTCTCTCTCTCAAG 423

QY 421 AAGCCATAGTAGGGGTCAATTTGGGCTGTGCTTCAAGTTCTTTAGCCATTTAGTCCAGAT 480

DB 424 AAGCCATAGTAGGGGTCAATTTGGGCTGTGCTTCAAGTTCTTTAGCCATTTAGTCCAGAT 483

QY 481 TTGCTCAGCTTTTCAACATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 540

DB 484 TTGCTCAGCTTTTCAACATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 543

QY 541 GACAAAGCTCTGTTCAATATTTTCAATGAGGTTGCTTCAAGTCTCAAGAGCAAG 600

DB 544 GACAAAGCTCTGTTCAATATTTTCAATGAGGTTGCTTCAAGTCTCAAGAGCAAG 603

QY 601 TCCATGTTGACATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 660

DB 604 TCCATGTTGACATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 663

QY 661 GGCACCTATGAGAAAGTGGATGAGAGCTTCAAGATTAATGTCAGCGAAGAGGATTT 720

DB 664 GGCACCTATGAGAAAGTGGATGAGAGCTTCAAGATTAATGTCAGCGAAGAGGATTT 723

QY 721 TGCATGCCCCACTCTTCAAAATCTACAGTATGACAGGAGAGAGAGCTTTGATTAAGCTG 780

DB 724 TGCATGCCCCACTCTTCAAAATCTACAGTATGACAGGAGAGAGAGCTTTGATTAAGCTG 783

QY 781 CTGAAGAAGTCAAGATCACTTGGCCCAAGCCCGGCTGTGCTTCTGTGAGGCT 840

DB 784 CTGAAGAAGTCAAGATCACTTGGCCCAAGCCCGGCTGTGCTTCTGTGAGGCT 843

QY 841 ATGACGTTGAGAGTGTGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900

DB 844 ATGACGTTGAGAGTGTGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 903

QY 901 CTTCTGGGAGGAGAACAGATGCTTATTTGATGATCTCAAGATCTCAAGATCTCAAGAT 960

DB 904 CTTCTGGGAGGAGAACAGATGCTTATTTGATGATCTCAAGATCTCAAGATCTCAAGAT 963

QY 961 GAAGACGAAGAAATGCAAGGCTCTTCTTCAAGGCTTTTGAAGATTTTACACAGA 1020

DB 964 GAAGACGAAGAAATGCAAGGCTCTTCTTCAAGGCTTTTGAAGATTTTACACAGA 1023

QY 1021 AGTGAAGTGGTGTGCTGACATGCCCCAGGCTCTGAATCTAAGTCAAGTCAAGGCTCC 1080

DB 1024 AGTGAAGTGGTGTGCTGACATGCCCCAGGCTCTGAATCTAAGTCAAGTCAAGGCTCC 1083

QY 1081 ATCACTGAGTGAAGGACAGGCTCATCTAA 1110

DB 1084 ATCACTGAGTGAAGGACAGGCTCATCTAA 1113

RESULT 2

AAS62274

ID AAS62274 standard; cDNA; 1788 BP.

XX AAS62274;

XX 14-FEB-2002 (first entry)

XX cDNA sequence #61 encoding novel human secreted protein.

XX Human secreted protein; hyperproliferative disorder; autoimmune disorder;

XX immune deficiency disorder; blood disorder; inflammatory disorder;

XX infectious disorder; gene therapy; antimicrobial; hepatotropic;

XX immunosuppressive; antineumatic; ss.

OS Homo sapiens.

XX W020017291-A2.

PN 18-OCT-2001.

PD





QY 61 ArgGluGlnTyrGlyIleGlnArgValGluAlaMetLeuHisThrLeuGluArgIleAsn 80  
 DB 640 CGTGAACAGATGGCATTCAGAGAGTGGAGCCATGCTGATACCTCGGAAGATCAAT 639  
 QY 81 SerAspProThrLeuLeuProAsnIleThrLeuGlyCysGluIleArgAspSerCysTrp 100  
 DB 700 TCAGACCCCACTCTTGGCCCAACATCACTGGGCTGTAGATTAAGGAGCTCCTGCTGG 759  
 QY 101 HisSerAlaValAlaLeuGluGlnSerIleGluPheIleArgAspSerLeuIleSerSer 120  
 DB 760 CATTGGCTGTGGCCCTAGAGCAGAGCATTAAGTTCATTAAGATTCCTCATTTCTTCA 819  
 QY 121 GluGluGluGluGlyLeuValCysSerValAspGlySerSerSerSerPheArgSerIle 140  
 DB 820 GAAGAGGAAGAAGGCTTGTACCGCTGTGTGATGGCTCTCTCTCTCTCTCCGCTCAAG 879  
 QY 141 LysProIleValGlyValIleGlyProGlySerSerSerSerLeuAlaIleGlnValGlnAsn 160  
 DB 880 AACCCCATAGTAGGGGCTCATTTGGGCTGGCTCCAGTTCTTACCATTCAGTCCAGAAAT 939  
 QY 161 LeuLeuGluLeuPheAsnIleProGlnIleAlaIleThrSerIleAlaThrIleMetAspLeuSer 180  
 DB 940 TTGCTCCAGCTTTTCAACATACCTCAGATTCCTTACCTCAGCAACAGCATGATCTGAGT 999  
 QY 181 AspLysThrLeuPheLysTyrPheMetArgValValProSerAspAlaGlnIleAlaArg 200  
 DB 1000 GACAAAGCTCTGTTCAAAATTTTCATGAGGCTGTGCTTCATAGTCTCAGCAGGCAAG 1059  
 QY 201 SerMetValAspIleValIleValArgTyrAsnTrpThrTyrValSerAlaValHisThrGlu 220  
 DB 1060 GCCATGCTGAGCATATGAGAGAGTGAACCTGACCTATATACAGCCGTCGACACAGAA 1119  
 QY 221 GlyAsnTyrGlyGluSerGlyMetGluAlaPheLeuAspMetSerAlaValGluGlyIle 240  
 DB 1120 GGCAACTATGGAAGAAAGTGGATGGAAGCTTCAMAAATATGTCAGCGAAGAGGAGATT 1179  
 QY 241 CysAlaAlaHisSerTyrLysIleTyrSerAsnAlaGlyGluGlnSerPheAspLysLeu 260  
 DB 1180 TGCATGCGCCACTCTTCAAAATCTACAGTAAATGACGGAGGAGCACTTTGATTAAGCTG 1239  
 QY 261 LeuLysLeuLeuThrSerHisLeuProLysAlaArgValAlaIleTyrPheCysGluGly 280  
 DB 1240 CTGAAGAGCTCAAGTCACTTGGCCCAAGCCCGGGTGTGGCTGCTTCTGTGAGGGC 1299  
 QY 281 MetThrValArgGlyLeuLeuMetAlaMetArgThrLeuGlyLeuValGlyGluPheLeu 300  
 DB 1300 ATGACGCTGAGAGGCTGTGCTGATGCGCATGAGCGCTGCTGCTAGCGGAGAAATTTCTG 1359  
 QY 301 LeuLeuGlyArgGluProAspAlaIlePheIleGluIleSerLysAsnSerIleLeuTrp 320  
 DB 1360 CTTCTGGGCGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380  
 QY 321 GluAspArgArgLysCys-GlnGlyArgPheLeuGlnGlyPheGlyAspIleLeuHisArg 340  
 DB 1381 GCTGACAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1410  
 QY 340 gSerGluSerValLeuLeuHisMetProGlnProLeuAsnLeuGluLeuSerSerGly 359  
 DB 1411 CAGCGAGAGAGCTGTGTGGCATCACATCAATCAAGCTCCATCTCCGATGCAAGTGGT 1468  
 RESULT 15  
 AAD05030 standard; mRNA; 4207 BP.  
 ID AAD05030;  
 AC AAD05030;  
 XX 17-JUL-2001 (first entry)  
 DT 17-JUL-2001 (first entry)  
 XX Human metabotropic glutamate receptor, mGluR5A mRNA.  
 DE Human metabotropic glutamate receptor; mGluR5A; excitatory amino acid;  
 XX Human; metabotropic glutamate receptor; mGluR5A; excitatory amino acid;  
 KM Human; metabotropic glutamate receptor; mGluR5A; excitatory amino acid;  
 EA; central nervous system; CNS; presynaptic release; neurotransmitter;

KW post synaptic sensitivity; glutamate excitation; ss.  
 XX Homo sapiens.  
 OS Homo sapiens.  
 PH Key  
 FT CDS  
 FT Location/Qualifiers  
 FT 460..4002  
 FT /\*tag= a  
 FT /product= "Human metabotropic glutamate receptor,  
 FT mGluR5A"  
 XX US6211353-B1.  
 PN US6211353-B1.  
 XX 03-APR-2001.  
 PD 03-APR-2001.  
 XX 07-JUN-1996; 96US-0660148.  
 PF 07-JUN-1996; 96US-0660148.  
 XX 29-JUL-1994; 94US-0282853.  
 PR 29-JUL-1994; 94US-0282853.  
 XX (BLIL ) LILLY & CO ELI.  
 PA (BLIL ) LILLY & CO ELI.  
 XX Burnet JP, Wayne NG, Sharp RL, Snyder YM;  
 PI Burnet JP, Wayne NG, Sharp RL, Snyder YM;  
 XX WPI, 2001-289639/30.  
 DR P-PSDB; AAE01156.  
 XX New isolated nucleic acids for producing human metabotropic glutamate  
 PT receptors, which are useful for modulating the presynaptic release of  
 PT glutamate or the post synaptic sensitivity of the neuronal cell to  
 PT glutamate excitation -  
 PS Claim 2; Column 43-46; 53pp; English.  
 XX The present sequence is a mRNA encoding human metabotropic glutamate  
 CC receptor, mGluR5A. L-glutamate, the most abundant neurotransmitter in  
 CC the central nervous system (CNS), mediates excitatory pathway in  
 CC mammals. L-glutamate is referred to as excitatory amino acid (EAA) and  
 CC the receptors that respond to glutamate are EAA receptors. The receptors  
 CC are useful for modulating the presynaptic release of glutamate and the  
 CC post synaptic sensitivity of the neuronal cell to glutamate excitation.  
 XX Sequence 4207 BP; 1010 A; 1121 C; 1112 G; 964 U; 0 other;  
 SQ  
 Alignment Scores:  
 Pred. No.: 1,5e-158 Length: 4207  
 Score: 1484.50 Matches: 306  
 Percent Similarity: 87.228 Conservative: 8  
 Best Local Similarity: 85.008 Mismatches: 22  
 Query Match: 79.264 Indels: 24  
 DB: 22 Gaps: 2  
 US-10-027-923-2 (1-369) x AAD05030 (1-4207)  
 QY 1 MetValLeuLeuLeuIleLeuSerValLeuLeuLeuGluAspValArgLysSerAla 20  
 DB 460 AUGGUCUCUCUGUAGUCCUGACAGUCUUAUUUAAAGAAUUGUCCUGUGGAGUUGCA 519  
 QY 21 GlnSerSerGluArgArgValAlaHisMetLeuGlyAspIleIleIleGlyAlaLeu 40  
 DB 520 CAGUCCAGUGAGAGAGGUGUGUGUGUCACAGUCCGAGUGACUUAUUGGAGUCUCC 579  
 QY 41 PheSerValHisHisGlnProThrValAspGluValHisGluArgLysCysGlyAlaVal 60  
 DB 580 UUUUCUGUUCACUCCAGGCUUACUGUGGCAAAAGUUCAGAGAGAGAGUGUGGCGGUC 639  
 QY 61 ArgGluGlnTyrGlyIleGlnArgValGluAlaMetLeuHisThrLeuGluArgIleAsn 80  
 DB 640 CGUGAAGAGUAGGCAUUCAGAGAGGAGGCAUUCUCCUAGAAAGUAGUCAAU 699  
 QY 81 SerAspProThrLeuLeuProAsnIleThrLeuGlyCysGluIleArgAspSerCysTrp 100  
 DB 700 UCAGACCCCACTCTTGGCCCAACATCACTGGGCTGTAGATTAAGGAGCTCCTGCTGG 759  
 QY 101 HisSerAlaValAlaLeuGluGlnSerIleGluPheIleArgAspSerLeuIleSerSer 120



us-10-027-923-2 (1-369) x ACA56535 (1-4078)

QY 1 MetValLeuLeuLeuLeuSerValLeuLeuLeuGluAspValArgGlySerAla 20  
 Db 151 ATGGTCTCTCTGTTGATCTGTGACGCTTCTTTGAAAGAAAGATGCTGGGAGTGA 210  
 QY 21 GlnSerSerGluArgArgValAlaAlaMetLeuGlyAspIleIleIleGlyAlaLeu 40  
 Db 211 CAGTCCAGAGAGAGAGGGGTGGTGGCTCAATGCCGGGTGACATCTATTATGAGGCTTC 270  
 QY 41 PheSerValHisIleGlnProThrValAspGluValHisGluArgGlyCysGlyAlaVal 60  
 Db 271 TTTTCTGTTTCATACCACTGCTGAGCAAGATTCATAGAGAAAGTGTGGGGCGGTC 330  
 QY 61 ArgGluGlnThrGlyIleGlnArgValGluAlaMetLeuHisIleLeuGluValAlaLeu 80  
 Db 331 CGTGAACAGATGACATTCAGAGAGAGAGCCATGCTGATACCTCGAAGAGATCAAT 390  
 QY 81 SerAspProThrLeuLeuProAsnIleThrLeuGlyCysGluIleArgAspSerCysTrp 100  
 Db 391 TCAGACCCCACTCTTGGCCCAATCACTGCGGTGATGATTAAGGAGCTCTGCTGG 450  
 QY 101 HisSerAlaValAlaLeuGluGlnSerIleGlnPheIleArgAspSerLeuIleSerSer 120  
 Db 451 CATTCGGCTGTGGCCCTAGAGCAGAGCATTTGATCAATAGATTCCTCATTTCTTCA 510  
 QY 121 GluGluGluGluGluLeuValCysSerValAspGlySerSerSerSerPheArgSerIys 140  
 Db 511 GAAGAGAGAGAGAGGCTGTGACCGCTGTGAGATGAGCTCTCTCTCTCTCTCTCCAG 570  
 QY 141 LysProIleValGlyValIleGlyProGlySerSerSerSerLeuAlaIleGlnValGlnAsn 160  
 Db 571 AAGCCCATAGTAGGGGTGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 630  
 QY 161 LeuLeuGlnLeuPheLeuIleProGlnIleAlaIleThrSerAlaThrIleMetAspLeuSer 180  
 Db 631 TTGCTCAGCTTTTCAACATCACTCAGATTTGTTACTCAGCAACAGCATGATCTGAGT 690  
 QY 181 AspLeuThrLeuPheLeuIlePheMetArgValValProSerAspAlaGlnGlnAlaArg 200  
 Db 691 GAAAGAACTCTGTTCAAAATATTTTCATGAGGGTGTGCTTCAATGCTCAGCGGAGAG 750  
 QY 201 SerMetValAspIleValIleValArgIleArgIleThrValSerAlaValHisIleGln 220  
 Db 751 GCATGTGTGACATAGTGAAGAGGTACATGACCTATATATACGCCGTCACACAGAA 810  
 QY 221 GlyAsnTrpGlyGluSerGlyMetGluAlaPheLeuAspMetSerAlaIleGluGlyIle 240  
 Db 811 GGCACCTATGAGAAAGTGGATGGAAGCTTCAAGATATGTCAAGGAAAGAGGATTT 870  
 QY 241 CysIleAlaHisSerTrpIleIleIleIleIleIleIleIleIleIleIleIleIleIle 260  
 Db 871 TGCATGCCCACTTACAAATCTACATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGG 930  
 QY 261 LeuIleValLeuThrSerHisLeuProIleValAlaArgValAlaIleIlePheCysGly 280  
 Db 931 CTGAAAGAGCTCAAGATCACTTGGCCCAAGGCCCGGGTGTGGCTCTCTCTGTAGG 990  
 QY 281 MetThrValArgGlyLeuLeuMetAlaMetArgArgLeuGlyLeuValGlyIlePheLeu 300  
 Db 991 ATGACGGTGAAGAGTGTGCTGATGCGCATGAGCGCTGGGTCTAAGGGGAGAAATTTCT 1050  
 QY 301 LeuLeuGlyArgGluProAspAlaIlePheIleGluIleSerIleAsnSerIleLeuTrp 320  
 Db 1051 CTTCTGGGAGTATGAGC-----TTGG 1071  
 QY 321 GluAspArgArgIysCysGlnGlyArgPheLeuGlnGlyPheGlyAspIleLeuHisIle 340  
 Db 1072 GCTGACAGGTATATGTGACAG-----ATGATAT 1101  
 QY 340 gSerGluSerValLeuLeuHisMetProGlnProLeuAsnLeuGluLeuSerSerGly 359  
 Db 1102 CAGCGAAGAGCTGTGTGTGATCAATCAATCAAGCTCAATCTCCGATGTCAAGTGT 1159

# RESULT 13

AAD04990 ID AAD04990 standard; cDNA; 4207 BP.

AC AAD04990;

DT 17-JUL-2001 (first entry)

DE Human metabotropic glutamate receptor; mGluR5A cDNA mutant.

KW Human; metabotropic glutamate receptor; mGluR5A; excitatory amino acid; BAA; central nervous system; CNS; presynaptic release; neurotransmitter; postsynaptic sensitivity; glutamate excitation; mutant; ss.

KX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT mutation replace (416, T)

FT mutation /tag= a

FT mutation /tag= b

PN US6211353-B1.

PD 03-APR-2001.

PP 07-JUN-1996; 96US-0660148.

PR 29-JUL-1994; 94US-0282853.

DA (BLU) DINDY-6-66-BLZ.

XX Burnett JP, Wayne NG, Sharp RL, Snyder YM;

XX WPI; 2001-289639/30.

PT New isolated nucleic acids for producing human metabotropic glutamate receptors, which are useful for modulating the presynaptic release of glutamate or the postsynaptic sensitivity of the neuronal cell to glutamate excitation.

PS disclosure; Column -; 53pp; English.

XX The present sequence is a cDNA mutant encoding human metabotropic glutamate receptor, mGluR5A, L-glutamate, the most abundant neurotransmitter in the central nervous system (CNS), mediates excitatory pathway in mammals. L-glutamate is referred to as excitatory amino acid (EAA) and the receptors that respond to glutamate are EAA receptors. The CC receptors are useful for modulating the presynaptic release of glutamate and the postsynaptic sensitivity of the neuronal cell to glutamate excitation.

CC Note: The present sequence is not shown in the specification, but is CC derived from the sequence referred as SEQ ID NO.1, shown in column CC 59-68 (AAD05029) of the specification.

XX Sequence 4207 BP; 1010 A; 1121 C; 1112 G; 964 T; 0 other;

SQ Alignment Scores:

Pred. No.: 1.5e-158 Length: 4207

Score: 1484.50 Matches: 306

Percent Similarity: 87.22% Conservativity: 8

Best Local Similarity: 85.00% Mismatches: 22

Query Match: 79.26% Indels: 24

DB: Gaps: 2

US-10-027-923-2 (1-369) x AAD04990 (1-4207)

QY 1 MetValLeuLeuLeuLeuSerValLeuLeuLeuGluAspValArgGlySerAla 20  
 Db 460 ATGGTCTCTCTGTTGATCTGTGACGCTTCTTTGAAAGAAAGATGCTGGGAGTGA 519



Query Match: 79.26% Indels: 24  
 DB: 22 Gaps: 2  
 US-10-027-923-2 (1-369) x AAC85787 (1-3129)

QY 1 MetValLeuLeuLeuLeuLeuSerValLeuLeuLeuLeuValArgGlySerAla 20  
 DB 1 ATGGTCTTCTGTGATCCGTCAAGTCTTCTTTGAAAGAAATGTCCTGGAGAGCA 60  
 QY 21 GlnSerSerGluArgArgValValAlaHisMetLeuGlyAspIleIleIleGlyAlaLeu 40  
 DB 61 CAGTCCAGTGAAGAGGGGTGGTGGCTCACATGCCGGGTACATCATTTATGAGCTCTC 120  
 QY 41 PheSerValHisIleGlnProThrValAspGluValHisGluArgGlyCysGlyAlaVal 60  
 DB 121 TTTTCTGTTCATACCAAGCTTACTGTGAGCAAGTTTCATAGAGAGAGTGTGGCGGTG 180  
 QY 61 ArgGluGlnTyrGlyIleGlnArgValGluAlaMetLeuHisThrLeuGluArgIleAsn 80  
 DB 181 CGTGAACAGTATGGCATTGAGAGAGTGAAGGCCATGCTGATACCTCGAAAGATCAAT 240  
 QY 81 SerAspProThrLeuLeuProAsnIleThrLeuGlyCysGluIleArgAspSerCysTrp 100  
 DB 241 TCAGACCCCACTCTTGCCCAATCATCACTGGGTGTGAGATTAAGGAGCTCTGCTGG 300  
 QY 101 HisSerAlaValAlaLeuGluGlnSerIleGluPheIleArgAspSerLeuIleSerSer 120  
 DB 301 CATTCGGCTGTGGCCCTTGAAGAGCATTGATTCATTAAGATTCCTCATTTCTTCA 360  
 QY 121 GluGluGluGluGlyLeuValCysSerValAspGlySerSerSerPheArgSerIys 140  
 DB 361 GAAGAGAAAGAGGCTTGTGATGCTGTGTGATGCTCTCTCTCTCTCTCTCTCTCAAG 420  
 QY 141 LysProIleValGlyValIleGlyProGlySerSerSerLeuAlaIleGlnValGlnAsn 160  
 DB 421 AACCCCATAGTAGGGGTCAATGGGCTGGCTCCAGTCTCTAGCATTGACATTCAGCAAT 480  
 QY 161 LeuLeuGlnLeuPheAsnIleProGlnIleAlaTyrSerValThrIleMetAspLeuSer 180  
 DB 481 TTCTCTCAAGCTTTTCAACATACCTCAGATTGCTTACACACACAGCATGAGATCTGAGT 540  
 QY 181 AspLysThrLeuPheLysTyrPheMetArgValValProSerAspAlaGlnIleAlaArg 200  
 DB 541 GACAAAGCTCTGTTCAAATATTTTCATGAGGTTGTGCTTCAGATGCTCAGCAGCAGG 600  
 QY 201 SerMetValAspIleValIleValArgTyrAsnTrpThrTyrValSerAlaValHisThrGlu 220  
 DB 601 GCCATGTGTGACATAGTGAAGAGGTACACTGACCTATGATATCAGCCGTGCACACAGAA 660  
 QY 221 GlyAsnTrpGlyGluSerGlyMetGluAlaPheLysAspMetSerAlaLysGluGlyIle 240  
 DB 661 GGCAACTATGAGAAAGTGGAGTGAAGCCCTTCAAAGATATGTCAGGAAAGAGGAGATT 720  
 QY 241 CysIleAlaHisSerTyrLysIleTyrSerAsnAlaGlyGlnSerPheAspLysLeu 260  
 DB 721 TGCATGCCCACTTTCACAAATATTCAGTAATGACAGGAGCAGACTTTGATAGCTG 780  
 QY 261 LeuLysLeuLeuThrSerHisLeuProLysAlaArgValAlaAlaTyrPheCysGluGly 280  
 DB 781 CTGAAAGAGCTCAAGATCTCACTTGGCCCAAGCCCGGGTGGTGGCTCTCTGTGAGGGC 840  
 QY 281 MetThrValArgGlyLeuLeuMetAlaMetArgArgLeuGlyLeuValGlyGluPheLeu 300  
 DB 841 ATGACGGTGAAGGTCTGTGATGAGCCATGAGCGCTGGGTCTGAGCGGAGAAATTTCTG 900  
 QY 301 LeuLeuGlyArgGluProAspAlaIlePheIleGluIleSerLysAsnSerIleLeuTrp 320  
 DB 901 CTTCCTGGGAGTATGGC-----TGG 921  
 QY 321 GluAspArgArgLysCys-GlnGlyArgPheLeuGlnGlyPheGlyAspIleLeuHisArg 340  
 DB 922 GCTGACAGGTATGATGATGACAG-----ATGATAT 951

QY 340 gSerGluSerValLeuLeuHisMetProGlnProLeuAsnLeuGluLeuSerSerGly 359  
 DB 952 CAGCGAAGAGCTGTTGTGTGGCATCACATCAAGCTCCATCTCCGATGTCAAGTGT 1009

RESULT 12  
 ID ACAS6535 standard; cDNA; 4078 BP.  
 ACAS6535;  
 06-JUN-2003 (first entry)  
 Human signalling pathway polynucleotide probe SEQ ID NO 1133.  
 Human; probe; ss; array element; Parkinson's disease;  
 signalling pathway population; cancer; adenocarcinoma; leukaemia;  
 immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.  
 Homo sapiens.  
 US650938-B1.  
 31-DEC-2002.  
 30-JAN-1998; 98US-0016434.  
 30-JUN-1998; 98US-0016434.  
 (INCYTE GENOMICS INC.  
 Au-Young J, Selthamer JJ;  
 WPI; 2003-352189/33.  
 Combination of polynucleotide probes, useful as array elements in a  
 microarray for monitoring the expression of a number of target  
 polynucleotides -  
 Claim 1, SEQ ID NO 1133; 65pp; English.

The invention relates to a combination which comprises a number of  
 polynucleotide probes comprising a sequence selected from one of the 1490  
 sequences mentioned in the specification. The combination is useful as an  
 array element in a microarray for monitoring the expression of a number  
 of target polynucleotides. The microarray is particularly useful in the  
 diagnosis and treatment of cancer and immunopathology and neuropathology.  
 The microarray is useful in diagnostics and treatment regimens, drug  
 discovery and development, toxicological and carcinogenicity studies,  
 forensics and pharmacogenomics. The microarray is also useful for  
 monitoring progression of diseases and for developing sophisticated  
 profiles for the effects of currently available therapeutic drugs. The  
 combination is also useful for purifying a subpopulation of mRNA, cDNA  
 and genomic fragments and in research and diagnostic applications. The  
 array can detect changes in expression in a large number of genes coding  
 for different signalling pathway populations which can be used to diagnose  
 various diseases including cancer e.g. adenocarcinoma and leukaemia,  
 immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease  
 and Parkinson's disease. The present sequence represents a polynucleotide  
 probe of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification but was obtained in electronic format directly from USPTO  
 CC at seqdata.uspto.gov/sequence.html?docId=650938B1.

Sequence 4078 BP; 994 A; 1074 C; 1076 G; 934 T; 0 other;  
 SQ

Alignment Scores:  
 Pred. No.: 1,43e-158 Length: 4078  
 Score: 1484.50 Matches: 306  
 Percent Similarity: 87.22% Conservative: 8  
 Best Local Similarity: 85.00% Mismatches: 22  
 Query Match: 79.26% Indels: 24  
 DB: 25 Gaps: 2

CC or modulate activity of mglur are useful for diagnosing or treating  
CC neurological disorders, e.g. as anticonvulsants, neuroprotectants,  
CC analgesics, cognitive enhancers and muscle relaxants.

XX Sequence 2826 BP; 729 A; 679 C; 712 G; 706 T; 0 other;

# Alignment Scores:

Pred. No.: 8.2e-159 Length: 2826  
Score: 1484.50 Matches: 306  
Percent Similarity: 87.22% Conservative: 8  
Best Local Similarity: 85.00% Mismatches: 22  
Query Match: 79.26% Indels: 24  
DB: 22 Gaps: 2

US-10-027-923-2 (1-369) x AAC85785 (1-2826)

QY 1 MetValLeuLeuLeuLeuLeuSerValLeuLeuLeuGluValAlaArgGlySerAla 20  
DB 1 ATGGTCTCTGTGATCTGTCAGTCTTACTTTGAAAGAGATGCTCGGAGAGTGA 60  
QY 21 GlnSerSerGluArgValValAlaHisMetLeuGlyAspIleIleIleGlyAlaLeu 40  
DB 61 CAGTCAG 120  
QY 41 PheSerValHisGlnProThrValAspGluValHisGluArgGlySerGlyAlaVal 60  
DB 121 TTTTCTGTCATCAGCAGGCTTACTGTGACAAAGTTTCAATGAGAGAGAGAGAG 180  
QY 61 ArgGluGlnTyrGlyIleGlnAlaValGluAlaMetLeuHisThrLeuGluArgIleAsn 80  
DB 181 CGTGAACAGATGAGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 240  
QY 81 SerAspProThrLeuLeuProAsnIleThrLeuGlyCysGluIleArgAspSerCysTrp 100  
DB 241 TCGACCCCACTCTTGGCCCAATCACTGGCGTGAAGTAAAGAGAGAGAGAGAG 300  
QY 101 HisSerAlaValAlaLeuGluGlnSerIleGluPheIleArgAspSerLeuIleSerSer 120  
DB 301 CATTGGCGTGTGGCCCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360  
QY 121 GluGluGluGluGluValCysSerValAspGlySerSerSerSerSerPheArgSerIys 140  
DB 361 GAAG 420  
QY 141 LysProIleValGlyValIleGlyProGlySerSerSerSerLeuAlaIleGlnValGlnAsn 160  
DB 421 AAGCCCATAGTAAAG 480  
QY 161 LeuLeuGlnLeuPheAsnIleProGlnIleAlaTyrSerAlaThrIleMetAspLeuSer 180  
DB 481 TTGCTCCAGCTTTTCAACATCACTGAGATTGCTTACTAGCAACAGCATGATCGAGT 540  
QY 181 AspIleThrLeuPheIleTyrPheMetArgValAlaProSerAspAlaGlnGlnAlaArg 200  
DB 541 GACAG 600  
QY 201 SerMetValAspIleValIleValysArgTyrAsnTrpThrTyrValSerAlaHisIleTrpGlu 220  
DB 601 GCCATGTGAGACATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660  
QY 221 GlyAsnTyrGlyGluSerGlyMetGluAlaPheIleAspMetSerAlaIleGluGlyIle 240  
DB 661 GGCAATTAAGAT 720  
QY 241 CysIleAlaHisSerTyrIleTyrSerAsnAlaGlyGluGlnSerPheAspIleLeu 260  
DB 721 TGCATGCGCCAGCTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780  
QY 261 LeuIleValLeuThrSerHisLeuProIleAlaArgValAlaAlaTyrPheCysGluGly 280  
DB 781 CTGAAG 840  
QY 281 MetThrValArgGlyLeuLeuMetAlaMetArgArgLeuGlyLeuValGlyGluPheLeu 300

DB 841 ATGACGGTAGAGAGTGTGATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900  
QY 301 LeuLeuGlyArgGluProAspAlaIlePheIleGluIleSerIleValAsnIleLeuTrp 320  
DB 901 CTTCTGGGAGAGTATGAGC-----TGG 921  
QY 321 GluAspArgArgCysGlyGlnGlyArgPheLeuGlnGlyPheGlyAspIleLeuHisArg 340  
DB 922 GCTGACAGATGATGATGACAG-----ATGATAT 951  
QY 340 gSerGluSerValLeuLeuHisMetProGlnProLeuAlaLeuGluLeuSerSerGly 359  
DB 952 CAGCGAGAGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1009

RESULT 11  
AAC85787  
ID AAC85787 standard; cDNA, 3129 BP.  
XX  
AC AAC85787;  
XX  
DT 18-JUL-2001 (first entry)  
XX  
DE cDNA encoding chimeric receptor containing hmglur5d portion.  
XX  
KW Human; metabotropic glutamate receptor; mglur; splice variant;  
KW mglur5; G-protein-coupled receptor; glutamate; neurological disorder;  
KW anticonvulsant; neuroprotectant; analgesic; cognitive enhancer;  
KW muscle relaxant; calcium receptor; Ca<sub>v</sub>; mglur5d; ss.  
XX  
OS Chimeric - Homo sapiens.  
XX  
PN MO200130829-A1.  
XX  
PD 03-MAY-2001.  
XX  
PF 25-OCT-2000; 2000WO-US29356.  
XX  
PR 25-OCT-1999; 99US-0161481.  
PR 24-OCT-2000; 2000US-0695481.  
XX  
PA (NPSF-) NPS PHARM INC.  
PI Kratocho K, Stormann T, Levinthal C, Hammerland L, Storchmann L;  
XX WPI, 2001-308615/32.  
DR F-PSDB; AAB47219.  
XX  
PT New nucleic acid encoding an isoform of human metabotropic glutamate  
PT receptor, for identifying potential therapeutic agents for neurological  
PT disease.  
XX  
PS Claim 18; Page 70-75; 86pp; English.  
XX  
XX This sequence encodes a chimeric receptor comprising the intracellular  
XX cytoplasmic tail of the human calcium receptor (CaR) and the extra-  
XX cellular and seven transmembrane domains of the human metabotropic  
XX glutamate receptor (mglur) splice variant of human metabotropic  
XX glutamate receptor 5 (mglur5), mglur5d. mglur's are G-protein-coupled  
XX receptors capable of activating a variety of intracellular second  
XX messenger systems following the binding of glutamate. Recombinant  
XX mglur5d DNA and compounds that bind to, or modulate activity of it  
XX are useful for diagnosing or treating neurological disorders, e.g.,  
XX as anticonvulsants, neuroprotectants, analgesics, cognitive enhancers  
XX and muscle relaxants.

SO Sequence 3129 BP; 806 A; 782 C; 804 G; 737 T; 0 other;

Alignment Scores:  
Pred. No.: 9.57e-159 Length: 3129  
Score: 1484.50 Matches: 306  
Percent Similarity: 87.22% Conservative: 8  
Best Local Similarity: 85.00% Mismatches: 22

CC disease, stroke, depression, anxiety, pain and schizophrenia.  
 XX Sequence 2241 BP; 552 A; 516 C; 561 G; 612 T; 0 other;

## Alignment Scores:

Pred. No.:	Length:	2241
Score:	Matches:	332
Percent Similarity:	Conservative:	1
Best Local Similarity:	Mismatches:	0
Query Match:	Indels:	95
DB:	Gaps:	2

US-10-027-923-2 (1-369) x AAF29992 (1-2241)

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QY 1 MetValLeuLeuLeuLeuSerValLeuLeuLeuLeuValArgGlySerAla 20
DB 365 ATGGCTCTTGTGTGATCCCTGACGCTTACTTTGAAAGAAATGCCGTGGAGGCA 424
QY 21 GlnSerSerGluArgArgValAlaAlaHisMetLeuGlyAspIleIleIleGlyAlaLeu 40
DB 425 CAGTCCAGTAGAGAGAGGGGTGGTGCACATGCTGGGTGACATCATTAATGGAGCTCTC 484
QY 41 PheSerValHisHisGlnProthrValAspGluValHisGluArgGlySerGlyAlaVal 60
DB 485 TTTTCTGTTCAATCAGCAGCTTACTGTGACGAAGTTCAAGAGAAAGTGTGGGAGCTC 544
QY 61 ArgGluGlnIleArgIleGlnIleArgValGluAlaMetLeuHisThrLeuGluArgIleAsn 80
DB 545 CGTGAACAGATGAGCATTCAGAGAGGAGCCATGCTGATACCCCTGGAAAGATCAAT 604
QY 81 SerAspProthrLeuLeuProAsnIleThrLeuGlyCysGluIleArgAspSerCysTrp 100
DB 605 TCGAGCCCACTCTTCCCAACATCAGCTGGGCTGTGAAGTAAAGGATTCCTGCTGG 664
QY 101 HisSerAlaValAlaLeuGlnGlnSerIleGluPheIleArgAspSerLeuIleSerSer 120
DB 665 CATTGGCTGTGGCCCTAGAGCAGAGCATTTAGATTCAAGAGATTCCTCATTTCTTGC 724
QY 121 GluGluGluGluGluLeuValCysSerValAspGlySerSerSerSerPheArgSerIle 140
DB 725 GAAGAGAGAAAGGGCTGTGTGCTCTGTGAATGGCTCCCTCTTCTTCCCTCCAG 784
QY 141 LysProIleValGlyValIleGlyProGlySerSerSerSerLeuAlaIleGlnValGlnAsn 160
DB 785 AAGCCCATGATAGGGGCTATTGGGCTGTTCAGTTCTGTAGCCATTACAGTCCAGAT 844
QY 161 LeuLeuGlnLeuPheAsnIleProGlnIleAlaIleSerAlaThrIleMetAspLeuSer 180
DB 845 TTGCTCCAGCTTTTCAACATACCTCAGATTGCTTACTCAGCAACCATCATGATCTGAGT 904
QY 181 AspLysThrLeuPheLeuValIlePheMetArgValAlaProSerSerAlaGlnGlnAlaArg 200
DB 905 GACAAAGACTCTGTTCAAATATTTTCATAGAGGTGTGTGCTTCAGATGCTCAGCAGG 964
QY 201 SerMetValAspIleValIleValArgIleAsnTrpThrIleValIleSerAlaValHisThrGlu 220
DB 965 TCCATGTTGACATGATGAAGAGGTACACTGACCTATGATATCAGCCGTACACACAGAA 1024
QY 220 ----- 220
DB 1025 GGTTCAAAGTATTCTCATGCTCAGCTCCAGAGAGACTAGGCTGTTCATCACTTTGG 1084
QY 220 ----- 220
DB 1085 CCTCAAGTATCTGCTTGTGGCTTCCTCAAAATTTGCTGGGATTATGGAGTACGCCACC 1144
QY 221 -----Gly 221
DB 1145 ACAAGACCCGGCCAGTCCGCAATCTTAGAACACTCTTGAGTGTCTTCTGATTTTATGGC 1204
QY 222 AsnTrpGlyGlnSerGlyMetGluAlaPheLysAspMetSerAlaValGluGlyIleCys 241
DB 1205 AACTATGAGAAAGTGGAGTGAAGCTCTCAAGATATGTTCAGGAGAAAGGAGATTGGC 1264
  
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QY 242 IleAlaHisSerTrpIleValIleTyrSerAsnAlaGlyGluGlnSerPheAspLysLeuLeu 261
DB 1265 ATGCCCCACTCTTCAAAATCTACACTATGACAGGGAGACAGACTTTATTAAGTGTGCTG 1324
QY 262 LysLysLeuThrSerHisLeuProLysAlaArgValAlaIleTyrPheCysGluGlyMet 281
DB 1325 AAGAACTCACAAGTCACTTGCCTCAAGGCCCGGGGTGTGGCTTACTTGTGAGGGCAGT 1384
QY 282 ThrValArgGlyLeuLeuMetAlaMetArgArgLeuGlyLeuValGlyGluPheLeuLeu 301
DB 1385 ACGGTGAGAGGTCTGTGTATGAGCCATGAGCCGCTGGGTCTGTGTGTGGAATTTCTGCTT 1444
QY 302 LeuGlyArgGluProAspAlaIlePheIleGluIleSerLysAsnSerIleLeuTrpGlu 321
DB 1445 CTGGGC----- 1450
QY 322 AspArgArgLysCysGlnGlyArgPheLeuGlnGlyPheGlyAspIleLeuHisArgSer 341
DB 1451 -----AGAAAT 1456
QY 342 GluSerValLeuLeuHisMetProGlnProLeuAsnLeuGluLeuSerSerGlyProIle 361
DB 1457 GAGTCCGTGCTGTGCACATGCCCGCCCTCTGAATCTGAGCTCAGTTCAGGGCCCATC 1516
QY 362 ThrGlyLeuArgAspArgLeuIle 369
DB 1517 ACTGACTGAGGAGCAGGCTCATC 1540

RESULT 10
ID AAC85785 standard; cDNA; 2826 BP.
XX AAC85785;
AC AAC85785;
XX 18-JUL-2001 (first entry)
DT XX
XX
DE cDNA encoding metabotropic glutamate receptor.
XX Human; metabotropic glutamate receptor; mGluR; splice variant;
XX mGluR5; G-protein-coupled receptor; glutamate; neurological disorder;
XX anticonvulsant; neuroprotectant; analgesic; cognitive enhancer;
XX muscle relaxant; ss.
OS Homo sapiens.
XX
XX WO200130829-A1.
PN
XX 03-MAY-2001.
PD
XX
XX 25-OCT-2000; 2000MO-US29356.
PF
XX 25-OCT-1999; 99US-0161481.
PR 24-OCT-2000; 2000US-0695481.
XX
XX (NPSP-) NPS PHARM INC.
PA
XX Krapcho K, Stormann T, Levinthal C, Hammettland L, Storchmann L;
PT WPI; 2001-308615/32.
DR P-PSDB; AAB47217.
XX
XX New nucleic acid encoding an isoform of human metabotropic glutamate
PT receptor, for identifying potential therapeutic agents for neurological
PT disease.
XX
XX Claim 2; Page 51-56; 86pp; English.
XX
XX This sequence encodes a human metabotropic glutamate receptor (mGluR).
XX mGluR is a splice variant of human metabotropic glutamate receptor 5
XX (mGluR5). mGluR5 are G-protein-coupled receptors capable of activating
XX a variety of intracellular second messenger systems following the
XX binding of glutamate. Recombinant mGluR DNA and compounds that bind to,
  
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DE Human GRMx-ID DNA.  
XX Human; metabotropic glutamate receptor; schizophrenia; GRMx;  
KW Alzheimer's; Parkinson's; stroke; depression; anxiety; pain; ds.  
XX Homo sapiens;  
XX MO200102566-A1.  
XX 11-JAN-2001.  
XX 27-JUN-2000; 2000MO-US17798.  
XX 02-JUL-1999; 99US-0346326.  
XX (NEUR-) NEUROCRINE BIOSCIENCES INC.  
XX Schwarz DA, Maki RA;  
XX MPI; 2001-123112/13.  
XX Novel metabotropic glutamate receptor for prevention, treatment of  
XX conditions associated with undesirable glutamate levels, e.g.  
XX Alzheimer's, Parkinson's disease, stroke, depression, anxiety, pain and  
XX schizophrenia -  
XX Claim 2; Fig 6; 59pp; English.  
XX The present invention relates to human metabotropic glutamate  
XX receptor. An agent that decreases expression or activity of the  
XX metabotropic glutamate receptor is useful for treating schizophrenia.  
XX Metabotropic glutamate receptor polynucleotides, polypeptides  
XX are useful for treating diseases associated with undesirable  
XX levels of glutamate, such as Alzheimer's disease, Parkinson's  
XX disease, stroke, depression, anxiety, pain and schizophrenia.  
SQ Sequence 2241 BP; 552 A; 516 C; 561 G; 612 T; 0 other;  
Query Match 76.2%; Score 1389.6; DB 22; Length 2241;  
Best Local Similarity 85.4%; Pred. No. 0;  
Matches 1697; Conservative 1; Mismatches 5; Indels 285; Gaps 2;  
QY 1 AAAATGTCCTTCCTGTCATCTGTCAGTCTTACTTTGAAAGAAATGTCGGAGT 60  
DB 362 AAAATGTCCTTCCTGTCATCTGTCAGTCTTACTTTGAAAGAAATGTCGGAGT 421  
QY 61 GCACAGTCACAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 120  
DB 422 GCACAGTCACAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 481  
QY 121 CTCCTTTCTGTTTCATCACCAGCTTCTGTGAGAGAGAGAGAGAGAGAGAGT 180  
DB 482 CTCCTTTCTGTTTCATCACCAGCTTCTGTGAGAGAGAGAGAGAGAGAGAGT 541  
QY 181 GTCGCGTGAAGATGTCATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 240  
DB 542 GTCGCGTGAAGATGTCATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 601  
QY 241 AATTCAAGACCCACACTCTTCCCAATCACTGAGAGAGAGAGAGAGAGAGAGT 300  
DB 602 AATTCAAGACCCACACTCTTCCCAATCACTGAGAGAGAGAGAGAGAGAGAGT 661  
QY 301 TGGCATTCGGCTGTGGCCCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGT 360  
DB 662 TGGCATTCGGCTGTGGCCCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGT 721  
QY 361 TCGGAAGT 420  
DB 722 TCGGAAGT 781  
QY 421 AAGAAGCCATAGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 480  
DB 782 AAGAAGCCATAGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 841

QY 481 AATTGCTCCAGCTTTTCAACATACCTGATGTTGCTTACTCAGCAACCATATGATCTG 540  
DB 842 AATTGCTCCAGCTTTTCAACATACCTGATGTTGCTTACTCAGCAACCATATGATCTG 901  
QY 541 AGTGAACAAGACTCTGTTCAAAATATTTTCATGAGAGAGAGAGAGAGAGAGAGT 600  
DB 902 AGTGAACAAGACTCTGTTCAAAATATTTTCATGAGAGAGAGAGAGAGAGAGAGT 961  
QY 601 AGTTCATGAGT 660  
DB 962 AGTTCATGAGT 1021  
QY 661 GA----- 662  
DB 1022 GAAGGTTCAAGCTATTCTATGCTCAGCTCCAGAGAGAGAGAGAGAGAGT 1081  
QY 663 ----- 662  
DB 1082 TGGCTCAAGTATGTCCTGCTTTGGCCTTCCAAATTTGCTGGAGATTATGGAGTACG 1141  
QY 663 -----A 663  
DB 1142 ACCACAGCACCCGCGCAGTGCAGCTTGAACACTCTTGAAGTCTTTGATTTTGA 1201  
QY 664 GCGAATATGAGT 723  
DB 1202 GCGAATATGAGT 1261  
QY 724 TGCATGCGCCACTCTTCAAAATCTACAGTAAATGACAGAGAGAGAGAGAGT 783  
DB 1262 TGCATGCGCCACTCTTCAAAATCTACAGTAAATGACAGAGAGAGAGAGAGT 1321  
QY 784 CTGAAGAGCTCAAGAGTCACTTGCACAGAGAGAGAGAGAGAGAGAGAGAGT 843  
DB 1322 CTGAAGAGCTCAAGAGTCACTTGCACAGAGAGAGAGAGAGAGAGAGAGAGT 1381  
QY 844 ATGACGATGAGT 903  
DB 1382 ATGACGATGAGT 1441  
QY 904 CTTCTGGGAGT 963  
DB 1442 CTTCTGGG----- 1449  
QY 964 GAAAGCAAGT 1023  
DB 1450 -----CAGA 1453  
QY 1024 AGTGAATCCGTCGTGTCGACATGCCCCAGAGCTCTGAATCTAGAGTCAAGTCAAGGCCC 1083  
DB 1454 AGTGAATCCGTCGTGTCGACATGCCCCAGAGCTCTGAATCTAGAGTCAAGTCAAGGCCC 1513  
QY 1084 ATCACTGAGT 1143  
DB 1514 ATCACTGAGT 1573  
QY 1144 GAAAGCAAGTCAATCTTGAATGAGAGAGAGAGAGAGAGAGAGAGAGAGT 1203  
DB 1574 GAAAGCAAGTCAATCTTGAATGAGAGAGAGAGAGAGAGAGAGAGAGAGT 1633  
QY 1204 CGTCAAAATGCGCCCATATCACTGCAAGACCTTCAAAATTTCTTGGATGAGAGAGT 1263  
DB 1634 CGTCAAAATGCGCCCATATCACTGCAAGACCTTCAAAATTTCTTGGATGAGAGAGT 1693  
QY 1264 ACTTCACTCTGAGCAATTAATCTGAGAGAGTCAATGAGAGAGAGAGAGT 1323  
DB 1694 ACTTCACTCTGAGCAATTAATCTGAGAGAGTCAATGAGAGAGAGAGAGT 1753  
QY 1324 TTCGGTGTGTAATTAAGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGT 1383  
DB 1754 TTCGGTGTGTAATTAAGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGT 1813

OY	181	GTCCGGAAACAGTAATGGCAATTCAGAGAGTGGAGGCCATGCTGCATATCCCTGGAAAGATC	240
Db	542	GTCCGTGAACAGTAATGGCAATTCAGAGAGTGGAGGCCATGCTGCATATCCCTGGAAAGATC	601
OY	241	AATTGAGACCCCACTCTTGTGCCCAATCACACTGGGCTGTGAATGAAGGATTCCTGC	300
Db	602	AATTGAGACCCCACTCTTGTGCCCAATCACACTGGGCTGTGAATGAAGGATTCCTGC	661
OY	301	TGGCATTTGGGCTGTGGCCCTTAAGCAGACATTTAGTTCAATAAGATTCCTCATTTCT	360
Db	662	TGGCATTTGGGCTGTGGCCCTTAAGCAGACATTTAGTTCAATAAGATTCCTCATTTCT	721
OY	361	TCGGAAAGAGAAAGAGGGCTTGGTATGCTCTGTGGATNGGCTCTCTCTTCTTCCGCTCC	420
Db	722	TCGGAAAGAGAAAGAGGGCTTGGTATGCTCTGTGGATNGGCTCTCTCTTCTTCCGCTCC	781
OY	421	AAGAAGCCCATAGTAGGGGTCATTGGGCTGTGGCTCAGTTCTTTAGSCAATTGAGGTCAG	480
Db	782	AAGAAGCCCATAGTAGGGGTCATTGGGCTGTGGCTCAGTTCTTTAGSCAATTGAGGTCAG	841
OY	481	AATTTGCTCCAGCTTTTCAACATACCTCAGATTGCTTATCTCAGCAACCATCATGATCTG	540
Db	842	AATTTGCTCCAGCTTTTCAACATACCTCAGATTGCTTATCTCAGCAACCATCATGATCTG	901
OY	541	AGTGCAGACCTCTGTTCAAAATTTTCATGAGGGTTGTGCTTTCAGATGCTCAGACGCA	600
Db	902	AGTGCAGACCTCTGTTCAAAATTTTCATGAGGGTTGTGCTTTCAGATGCTCAGACGCA	961
OY	601	AGGTCATGTTGGAATAGTGAAGAGGTACAACTGACCTATGTATACGCGGTACACACA	660
Db	962	AGGTCATGTTGGAATAGTGAAGAGGTACAACTGACCTATGTATACGCGGTACACACA	1021
OY	661	GA-----	662
Db	1022	GAAAGCAGAGCTAATTGTGAGGAAGATTGGCTACAAAGTGAGCAGAAACTGATCTAATAC	1081
OY	663	-----	662
Db	1082	AAATGAAATGCGCAGTTTTCTATATGATACCCATAAAGTAGATGATATACTTAAGAT	1141
OY	663	-----	662
Db	1142	ATATPAGCAGAAATGCTGATGAAAAAGGCATTGTGATGCCAAATPACATTCATCTCAAT	1201
OY	663	-----	662
Db	1202	TGTCTAATAGCAGACAGAAATTTTGAGTTCAAGCTATTCTCATATGCTCAGCCTCCAGAG	1261
OY	663	-----	662
Db	1262	AGCTAGGCTGTCTTCAACTCTTGGCTCAAGTGATCTGCTGTGGCTTTCCAATTT	1321
OY	663	-----	662
Db	1322	GCTGGGATTTATGGGANTAGCCACACAGCACCCGGCCAGTGCCGCATCTTAGAACATCTC	1381
OY	663	-----	701
Db	1382	TTGAGGTGCTTCTTGATTTTATAGGCACTATGAGAAAGTGGGATGAGAGCCTTCANAGA	1441
OY	702	TATGTCAAGCAGAAAGGATTTTGATCGCCCACTTTACAAATCTTACAGTAATGACAG	761
Db	1442	TATGTCAAGCAGAAAGGATTTTGATCGCCCACTTTACAAATCTTACAGTAATGACAG	1501
OY	762	GGAGCAGAGCTTTGATTAAGCTGTGCTGAAGAGCTCAAGTCACTTGTCCCAAGGCCGGGT	821
Db	1502	GGAGCAGAGCTTTGATTAAGCTGTGCTGAAGAGCTCAAGTCACTTGTCCCAAGGCCGGGT	1561
OY	822	GGTGGCCCTACTTCTGTGAGGCGATGACGGGTGAGAGGTCTGCTGATNGGCAATGAGCGCT	881
Db	1562	GGTGGCCCTACTTCTGTGAGGCGATGACGGGTGAGAGGTCTGCTGATNGGCAATGAGCGCT	1621

QY	882	GGGCTGAGTGGAGAAATTTCTGCTTCTGGGACAGGAACCAATGCACTTTATTTAGAT	941
Db	1632	GGGCTGAGTGGAGAAATTTCTGCTTCTGGGACAGGAACCAATGCACTTTATTTAGAT	1688
QY	942	CTCAAGAACGACATCTTATGGGAAGACAGAGAAAATGCCAGGTGGCTTCTTACAGG	1001
Db	1682	CTCAAGAACGACATCTTATGGGAAGACAGAGAAAATGCCAGGTGGCTTCTTACAGG	1741
QY	1002	TTTTGGAGACATATTAACAGAAATGATGCCGTCTGTGACATGCCGCCAGCCTCTGAA	1066
Db	1742	TTTTGGAGACATATTAACAGAAATGATGCCGTCTGTGACATGCCGCCAGCCTCTGAA	1801
QY	1062	TCTAGAGCTCAGTTCAAGGAGCCATCACTGACCTAGGGACAGGGCTCATCTAATCTGAGT	1121
Db	1802	TCTAGAGCTCAGTTCAAGGAGCCATCACTGACCTAGGGACAGGGCTCATCTAATCTGAGT	1861
QY	1122	GGATATTACTCTGCATTATATAAGAACCAACAGTCATATCTTCTGATGTGGAGATTGAG	1181
Db	1862	GGATATTACTCTGCATTATATAAGAACCAACAGTCATATCTTCTGATGTGGAGATTGAG	1921
QY	1182	AAGCATTTGATTTGGAATGTGACCTCAAAATGGCCCCCATATCACTGCAACACTTACAG	1241
Db	1922	AAGCATTTGATTTGGAATGTGACCTCAAAATGGCCCCCATATCACTGCAACACTTACAG	1981
QY	1242	TTTTCTTGCAATGGGGTGTCTGAGCTTTCACCTCTGGCAAGATTAATCTGGAGGTCCATGT	1301
Db	1982	TTTTCTTGCAATGGGGTGTCTGAGCTTTCACCTCTGGCAAGATTAATCTGGAGGTCCATGT	2041
QY	1302	GGGGGACTCTTGGAAATTTGGGCTTCCGTGTTTGTATTAAGTACTGAAAGGGAAGATCA	1361
Db	2042	GGGGGACTCTTGGAAATTTGGGCTTCCGTGTTTGTATTAAGTACTGAAAGGGAAGATCA	2101
QY	1362	GAATGGCAATATATATGGAAGAGAGGGAATCTTTAAGTCTTGGATTGTGAAGACGACAT	1421
Db	2102	GAATGGCAATATATATGGAAGAGAGGGAATCTTTAAGTCTTGGATTGTGAAGACGACAT	2161
QY	1422	TCAGTGCAAGTCTCTTTACCAACCTCCAGATTACACTGCAAGTATGCCAAGACTTACAA	1481
Db	2162	TCAGTGCAAGTCTCTTTACCAACCTCCAGATTACACTGCAAGTATGCCAAGACTTACAA	2221
QY	1482	CCATGTAGGATTTATCTCTGGAATGTGTGAAGCTAGAACTGTGAGCTTCGTTGATTTATCA	1541
Db	2222	CCATGTAGGATTTATCTCTGGAATGTGTGAAGCTAGAACTGTGAGCTTCGTTGATTTATCA	2281
QY	1542	AAGTCCCCCTATATATACCAATCCCTTAATTTGCTCTTTCACCTCTCTCAGGCTTATCTT	1601
Db	2282	AAGTCCCCCTATATATACCAATCCCTTAATTTGCTCTTTCACCTCTCTCAGGCTTATCTT	2341
QY	1602	TTGCTGATTTCACTCTGACACAGAGCAAAATGCAAAATGTTTATCTGCTGTGGGAAC	1661
Db	2342	TTGCTGATTTCACTCTGACACAGAGCAAAATGCAAAATGTTTATCTGCTGTGGGAAC	2401
QY	1662	CCTTTATCCCATTAAGGCCCTCTTCTCTGTGACCTTATCAACAGACAAATAGGTTCTGTT	1721
Db	2402	CCTTTATCCCATTAAGGCCCTCTTCTCTGTGACCTTATCAACAGACAAATAGGTTCTGTT	2461
QY	1722	TTATGTCTTGAATTCGATCTTAATGTTATTTAAATCTCATTTATTTGTGTTACTATTAATG	1781
Db	2462	TTATGTCTTGAATTCGATCTTAATGTTATTTAAATCTCATTTATTTGTGTTACTATTAATG	2521
QY	1782	TTGGTAAAMCAGCAAAAAAAAAAAAAAAAAAAAAA 1811	
Db	2522	TTGGTAAAMCAGCTTAAAAAAAAAAAAAAAAAAAAA 2551	

AAFP29992	standard; DNA; 2241 BP
DT	06-APR-2001 (first entry)
XX	
XX	
XX	
XX	
XX	

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QY 663 -----A 663
DB 1142 ACCACAGCACCCGCGCAGTGCCTTGAACAACCTTTGAGTGTCTTCAATTTTA 1201
QY 664 GGGCACTATGAGAAAGTGGATGGAAGCTTCAAAAGATATGTCAAGGAAGAGGAT 723
DB 1202 GGGCACTATGAGAAAGTGGATGGAAGCTTCAAAAGATATGTCAAGGAAGAGGAT 1261
QY 724 TGCATGCCCCACTCTTACAAAATCTACATATGACAGGAGGAGCAAGCTTGAATAGCTG 783
DB 1262 TGCATGCCCCACTCTTACAAAATCTACATATGACAGGAGGAGCAAGCTTGAATAGCTG 1321
QY 784 CTGAAGAAGCTCAACAAGTCACTTGCCCAAGGCCGGGTGTGGCTCACTCTGTAGAGGC 843
DB 1322 CTGAAGAAGCTCAACAAGTCACTTGCCCAAGGCCGGGTGTGGCTCACTCTGTAGAGGC 1381
QY 844 ATGACGGTGAAGAGTCTGCTGATGAGCCATGAGCGCGCTGGGTCTAGTGGAGAAATTTCTG 903
DB 1382 ATGACGGTGAAGAGTCTGCTGATGAGCCATGAGCGCGCTGGGTCTAGTGGAGAAATTTCTG 1441
QY 904 CTTCTGGGGGAGGAAACCAAGTGCATCTTATTTGAATCTCAAAAGACAGATCTTATG 963
DB 1442 CTTCTGGGGGAGGAAACCAAGTGCATCTTATTTGAATCTCAAAAGACAGATCTTATG 1501
QY 964 GAAGACAGAAAGAAATGCGCAAGGTGCTCTCAGGGTTTGGAGACATATTAACAGAGA 1023
DB 1502 GAAGACAGAAAGAAATGCGCAAGGTGCTCTCAGGGTTTGGAGACATATTAACAGAGA 1538
QY 1024 AGTGAATCCGTGTGCTGCAATGCCCCAGCCTTGAATCTAGAGCTCACTTGAAGGCC 1083
DB 1539 AGTGAATCCGTGTGCTGCAATGCCCCAGCCTTGAATCTAGAGCTCACTTGAAGGCC 1598
QY 1084 ATCACTGAGATGAGGAGCAAGGCTCATTAATTTGAGTGAATATTAATCTGCACTTATTAAT 1143
DB 1599 ATCACTGAGATGAGGAGCAAGGCTCATTAATTTGAGTGAATATTAATCTGCACTTATTAAT 1658
QY 1144 GAAGCCAAAGTATATCTCTGATGAGATTTGAGAGCAATTTGATTTGAGATGAG 1203
DB 1659 GAAGCCAAAGTATATCTCTGATGAGATTTGAGAGCAATTTGATTTGAGATGAG 1718
QY 1204 CGTCAAAATGCGCCCATATCACTGCAACAAGCTTCAAGTTTCTTGAGTGGGTGCTCAG 1263
DB 1719 CGTCAAAATGCGCCCATATCACTGCAACAAGCTTCAAGTTTCTTGAGTGGGTGCTCAG 1778
QY 1264 ACTTTACCTCTGAGCAATTAATGAGAGTCCATGTGGGGAGCTTTGGAATGGGCT 1323
DB 1779 ACTTTACCTCTGAGCAATTAATGAGAGTCCATGTGGGGAGCTTTGGAATGGGCT 1838
QY 1324 TTGGGTGTTTGTATATAGTACGTGAAGAGGAAAGATCAGATGAGCATATATATGAGAG 1383
DB 1839 TTGGGTGTTTGTATATAGTACGTGAAGAGGAAAGATCAGATGAGCATATATATGAGAG 1898
QY 1384 GAGGAGCTCTTAATGCTTTGGGATTTGTAAGACAGCAATTCAGTCACTCTTTACCAACC 1443
DB 1899 GAGGAGCTCTTAATGCTTTGGGATTTGTAAGACAGCAATTCAGTCACTCTTTACCAACC 1958
QY 1444 TCCCCAGTTACATGCAATGATGTCCTCAAGACCTACCAACCATGATGATTTCTTGAT 1503
DB 1959 TCCCCAGTTACATGCAATGATGTCCTCAAGACCTACCAACCATGATGATTTCTTGAT 2018
QY 1504 TGTGAAGCTGAGAGTGTGAGCTTGTGATGTTTATCAAAAGCTCCCTATATACACCATC 1563
DB 2019 TGTGAAGCTGAGAGTGTGAGCTTGTGATGTTTATCAAAAGCTCCCTATATACACCATC 2078
QY 1564 CTTAATTTGCTCTTCACTCTCTCAGGCTTATCTTTTGTGCTATATCACTTGAACA 1623
DB 2079 CTTAATTTGCTCTTCACTCTCTCAGGCTTATCTTTTGTGCTATATCACTTGAACA 2138
QY 1624 GAGACAAATAGAAATGTGTTTATCTGCTGTGGGAAACCCCTTTATCCCATAAAGCCCTCT 1683
DB 2139 GAGACAAATAGAAATGTGTTTATCTGCTGTGGGAAACCCCTTTATCCCATAAAGCCCTCT 2198
QY 1684 TCCCTGTGCTTATCAAAAGAGACAAATAGGTTCTGTTTATGCTTGAATGATCTTA 1743

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DB 2199 TCCCTATGCTTATACAAACAGACAAATAGTCTGCTTTATGCTTGAATGCAATCTTA 2258
QY 1744 ATGTTATTAATACTCACTTTATTTGTTACTATTAATGATGATTAAMCAGCAAAAAA 1803
DB 2259 ATGTTATTAATACTCACTTTATTTGTTACTATTAATGATGATTAAMCAGCTAAAAA 2318
QY 1804 AAAAAAA 1811
DB 2319 AAAAAAA 2326

RESULT 8
AAF29989
ID AAF29989 standard; DNA; 2551 BP.
XX
AC AAF29989;
XX
DT 06-APR-2001 (first entry)
XX
DE Human GRMx-1a DNA.
XX
KW Human; metabotropic glutamate receptor; schizophrenia; GRMx;
KW Alzheimer's; Parkinson's; stroke; depression; anxiety; pain; ds.
XX
OS Homo sapiens.
XX
PN WO200102566-A1.
XX
PD 11-JAN-2001.
XX
PE 27-JUN-2000; 2000MO-US17798.
XX
PR 02-JUL-1999; 99US-0346326.
XX
PA (NEUR-) NEUROCRINE BIOSCIENCES INC.
XX
PI Schwarz DA, Maki RA;
XX
DR WPI, 2001-123112/13.
XX
PT Novel metabotropic glutamate receptor for prevention, treatment of
PT conditions associated with undesirable glutamate levels, e.g.
PT Alzheimer's, Parkinson's disease, stroke, depression, anxiety, pain and
PT schizophrenia -
XX
PS Claim 2; Fig 1; 59pp; English.
XX
CC The present invention relates to human metabotropic glutamate
CC receptor. An agent that decreases expression or activity of the
CC metabotropic glutamate receptor is useful for treating schizophrenia.
CC Metabotropic glutamate receptor polynucleotides, polypeptides
CC are useful for treating diseases associated with undesirable
CC levels of glutamate, such as Alzheimer's disease, Parkinson's
CC disease, stroke, depression, anxiety, pain and schizophrenia.
XX
SQ Sequence 2551 BP; 666 A; 566 C; 630 G; 689 T; 0 other;

Query Match 77.5%; Score 1413.6; DB 22; Length 2551;
Best Local Similarity 82.4%; Pred. No. 0;
Matches 1805; Conservative 1; Mismatches 5; Indels 379; Gaps 1;
QY 1 AAAAAAGTCTTCTGTTGATTCCTGATCTTCACTTTTGAAGAAAGATGCGGTGGAGT 60
DB 362 AAAAAAGTCTTCTGTTGATTCCTGATCTTCACTTTTGAAGAAAGATGCGGTGGAGT 421
QY 61 GCACAGTCAGTGAAGAGAGGTGTGCTCAATGCTGGGTGACATATTTAGAGCT 120
DB 422 GCACAGTCAGTGAAGAGAGGTGTGCTCAATGCTGGGTGACATATTTAGAGCT 481
QY 121 CTTCTTTCTGTTTCATCAGCAAGCTTACTGTGAGCAAGATTTCATGAGAGAGTGTGGGCA 180
DB 482 CTTCTTTCTGTTTCATCAGCAAGCTTACTGTGAGCAAGATTTCATGAGAGAGTGTGGGCA 541

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Db 1454 GACCGTCAAAATGCGCCCATATCACTGCAACACTCAAGTTTCTTGATGGGGTCT 1513
Qy 1261 CAACTTTCACCTCTGCGCAAGTATTAATGCGAGGTCCATGTGGGGACTCTTGAATGG 1320
Db 1514 CAACTTTCACCTCTGCGCAAGTATTAATGCGAGGTCCATGTGGGGACTCTTGAATGG 1573
Qy 1321 GCTTTGGGTGTTTGAATTAAGTACTGGAAGGAAGAAATGAGATGAGCAATATATATGA 1380
Db 1574 GCTTTGGGTGTTTGAATTAAGTACTGGAAGGAAGAAATGAGATGAGCAATATATATGA 1533
Qy 1381 GAGAGAGGACTCTTGAATGCTTGGAGTGTAGAACGACATTCAGTCACTCTTACC 1440
Db 1634 GAGAGAGGACTCTTGAATGCTTGGAGTGTAGAACGACATTCAGTCACTCTTACC 1693
Qy 1441 ACCTCCCACTTACATGCGAGTATGTCCCAAGACTTACCAACATGATGATATCTTG 1500
Db 1694 ACCTCCCACTTACATGCGAGTATGTCCCAAGACTTACCAACATGATGATATCTTG 1753
Qy 1501 GATTGTAAGCTAGAACTGAGCTTGATGATGTTAATGAAGCTCCCTATATACACC 1560
Db 1754 GATTGTAAGCTAGAACTGAGCTTGATGATGTTAATGAAGCTCCCTATATACACC 1813
Qy 1561 ATCCCTAATGCTCTCTTCACTCTCTCAGGCTATCTTTGCTGATATCACTCTGA 1620
Db 1814 ATCCCTAATGCTCTCTTCACTCTCTCAGGCTATCTTTGCTGATATCACTCTGA 1873
Qy 1621 CCAGAGCAAAATGAGAAATGTGTTATCTGCTGTGGAAACCCCTTATCCATAAGCCC 1680
Db 1874 CCAGAGCAAAATGAGAAATGTGTTATCTGCTGTGGAAACCCCTTATCCATAAGCCC 1933
Qy 1681 TCTTCTGTCCTTATCAACAGAGCAAAATGAGTCTGTTTATGCTGTAATGCAAT 1740
Db 1934 TCTTCTGTCCTTATCAACAGAGCAAAATGAGTCTGTTTATGCTGTAATGCAAT 1993
Qy 1741 CTATGTTATTAATAACTCATTTATGTGTACTATTAAATGTGTAAACACAAATAAA 1800
Db 1994 CTATGTTATTAATAACTCATTTATGTGTACTATTAAATGTGTAAACACATTAATA 2053
Qy 1801 AAAAAAAAAA 1811
Db 2054 AAAAAAAAAA 2064

RESULT 7
AAF29991 standard; DNA; 2326 BP.
XX AAF29991;
AC
XX 06-APR-2001 (first entry)
DT
XX Human GRMX-1c DNA.
DE
XX Human; metabotropic glutamate receptor; schizophrenia; GRMX;
KM Alzheimer's; Parkinson's; stroke; depression; anxiety; pain; ds.
XX
OS Homo sapiens.
XX
XX WO200102566-A1.
XX
XX 11-JAN-2001.
PD
XX 27-JUN-2000; 2000MO-US17798.
PF
XX 02-JUL-1999; 99US-0346326.
PR
XX (NEUR-) NEUROCRINE BIOSCIENCES INC.
PA
XX Schwarz DA, Maki RA;
PI
XX WPI; 2001-123112/13.
XX

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PT Novel metabotropic glutamate receptor for prevention, treatment of
PT conditions associated with undesirable glutamate levels, e.g.
PT Alzheimer's, Parkinson's disease, stroke, depression, anxiety, pain and
PT schizophrenia -
XX
XX Claim 2; Fig 5; 59p; English.
XX
CC The present invention relates to human metabotropic glutamate
CC receptor. An agent that decreases expression or activity of the
CC metabotropic glutamate receptor is useful for treating schizophrenia.
CC Metabotropic glutamate receptor polynucleotides, polypeptides
CC are useful for treating diseases associated with undesirable
CC levels of glutamate, such as Alzheimer's disease, Parkinson's
CC disease, stroke, depression, anxiety, pain and schizophrenia.
XX
SQ Sequence 2326 BP; 581 A; 535 C; 580 G; 630 T; 0 other;
Query Match 85.6%; Score 1559.6; DB 22; Length 2326;
Best Local Similarity 89.6%; Pred. No. 0;
Matches 1782; Conservative 1; Mismatches 5; Indels 200; Gaps 2;
Qy 1 AAAAAAAAAAATGCTTGTGATCTCTGATCTTCACTTATCTTTGAAAGAAATGCTCGGAGT 60
Db 362 AAAAAAAAAAATGCTTGTGATCTCTGATCTTCACTTATCTTTGAAAGAAATGCTCGGAGT 421
Qy 61 GCAAGTCCAGTGAAGAGAGAGGAGTGGCTCCAGTGGGAGTCAATTAATGAGCT 120
Db 422 GCAAGTCCAGTGAAGAGAGAGGAGTGGCTCCAGTGGGAGTCAATTAATGAGCT 481
Qy 121 CTCTTTTCTGTTCAATCAGAGCTTACTGTGAGCAAGATTCAATGAGAGAGTGGGCA 180
Db 482 CTCTTTTCTGTTCAATCAGAGCTTACTGTGAGCAAGATTCAATGAGAGAGTGGGCA 541
Qy 181 GTCCGGAACAGTATGAGCAATTCAGAGAGTGAAGGCCATGCTGATACCTTGAAAGATC 240
Db 542 GTCCGGAACAGTATGAGCAATTCAGAGAGTGAAGGCCATGCTGATACCTTGAAAGATC 601
Qy 241 AATTGAGACCCCACTCTTGGCCCAATCACTGAGGCTGAGATTAAGGATTCCTGC 300
Db 602 AATTGAGACCCCACTCTTGGCCCAATCACTGAGGCTGAGATTAAGGATTCCTGC 661
Qy 301 TGGCATTCGGCTGTGCGCCCTAGAGCAGACATTAAGTCAATTAAGATTCCTCATTTCT 360
Db 662 TGGCATTCGGCTGTGCGCCCTAGAGCAGACATTAAGTCAATTAAGATTCCTCATTTCT 721
Qy 361 TGGAAAGAGAGAGGCTTGTGATGCTGTGATGCTCTCTCTCTCTCTCTCTCTCTCTC 420
Db 722 TGGAAAGAGAGAGGCTTGTGATGCTGTGATGCTCTCTCTCTCTCTCTCTCTCTCTC 781
Qy 421 AAGAACCCCATGATGAGGCTCAATGGGCTGTGCTCAGTCTTTAGCAATTAAGTCAAG 480
Db 782 AAGAACCCCATGATGAGGCTCAATGGGCTGTGCTCAGTCTTTAGCAATTAAGTCAAG 841
Qy 481 AATTGCTCAGCTTTTCAATCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 540
Db 842 AATTGCTCAGCTTTTCAATCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 901
Qy 541 AGTGAACAAGCTCTGTTCAATATTTCAATGAGGCTTGTGCTTCACTCACTCACTCACT 600
Db 902 AGTGAACAAGCTCTGTTCAATATTTCAATGAGGCTTGTGCTTCACTCACTCACTCACT 961
Qy 601 AGTGCATGATGAGCACTAGTGAAGAGTCACTGAGCACTATGATACAGCCGTACACCA 660
Db 962 AGTGCATGATGAGCACTAGTGAAGAGTCACTGAGCACTATGATACAGCCGTACACCA 1021
Qy 661 GA-----
Db 1022 GAAGTTCAAGCTATTTCTATGCTCAGCTCCAGAGAGTGAAGCTGATCTTCAACTCT 1081
Qy 663 -----
Db 1082 TGGCTCAAGTATGCTGCTTGGCTTCCAAATGCTGGGATTAATGGCATGAGCC 1141

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Db 2162 GAGACAAATCAGAAATGCTTTATCTGCTGTGGAAACCCCTTATCCCATTAAGCCCTCT 2221  
Qy 1684 TCCTTGTGCTTATCAACAGAGCAAAATAGTTCTGTTTATGCTTGAATTCATTCTA 1743  
Db 2222 TCCTTATGCTTATCAACAGAGCAAAATAGTTCTGTTTATGCTTGAATTCATTCTA 2281  
Qy 1744 ATGTTATTAATACTCTTATTTGTCTTACTATTAATATGCTTAAMCAAAATTAATA 1803  
Db 2282 ATGTTATTAATACTCTTATTTGTCTTACTATTAATATGCTTAAMCAAAATTAATA 2341  
Qy 1804 AAAAAAAAA 1811  
Db 2342 AAAAAAAAA 2349

RESULT 6  
AAF29995  
ID AAF29995 standard; DNA; 2064 BP.  
XX  
XX AAF29995;  
AC  
XX  
XX 06-APR-2001 (first entry)  
DT  
XX  
XX Human GRMX-Ig DNA.

DE Human GRMX-Ig DNA.  
KW Human; metabotropic glutamate receptor; schizophrenia; GRMX;  
KW Alzheimer's; Parkinson's; stroke; depression; anxiety; pain; ds.  
XX  
XX Homo sapiens.  
OS  
XX  
XX W0200102566-A1.  
PN  
XX  
XX 11-JAN-2001.  
PD  
XX  
XX 27-JUN-2000; 2000WC-US17798.  
PF  
XX  
XX 02-JUL-1999; 99US-0346326.  
PR  
XX  
XX (NEUR-) NEUROCRINE BIOSCIENCES INC.

PA Schwarz DA, Maki RA;  
PI  
XX  
XX WPI; 2001-123112/13.  
DR  
XX  
XX Novel metabotropic glutamate receptor for prevention, treatment of  
PT conditions associated with undesirable glutamate levels, e.g.  
PT Alzheimer's; Parkinson's disease, stroke, depression, anxiety, pain and  
PT schizophrenia -  
PS  
XX  
XX Claim 2; Fig 11; 59pp; English.

XX  
XX The present invention relates to human metabotropic glutamate  
CC receptor. An agent that decreases expression or activity of the  
CC metabotropic glutamate receptor is useful for treating schizophrenia.  
CC Metabotropic glutamate receptor polynucleotides, polypeptides  
CC are useful for treating diseases associated with undesirable  
CC levels of glutamate, such as Alzheimer's disease, Parkinson's  
CC disease, stroke, depression, anxiety, pain and schizophrenia.  
XX  
XX

SQ Sequence 2064 BP; 518 A; 466 C; 519 G; 561 T; 0 other;  
Query Match 86.5%; Score 1576.6; DB 22; Length 2064;  
Best Local Similarity 93.7%; Pred. No. 0;  
Matches 1697; Conservative 1; Mismatches 5; Indels 108; Gaps 1;

Qy 1 AAAAAAAAACTCTTCTGTTGATCTCTGACGCTTACTTTTGAAGAAGATCCGCGGAGT 60  
Db 362 AAAAAAAAACTCTTCTGTTGATCTCTGACGCTTACTTTTGAAGAAGATCCGCGGAGT 421  
Qy 61 GCACAGTCAGTGAAGAGGAGGTGTGCTCACAATGCTGAGTGAATCATTTATTTGAGCT 120  
Db 422 GCACAGTCAGTGAAGAGGAGGTGTGCTCACAATGCTGAGTGAATCATTTATTTGAGCT 481

Qy 121 CTCTTTCTGTTTCAACAGCCTTACTGTGAGCAAGATTTCATGAGAGAGTGTGGGCA 180  
Db 482 CTCTTTCTGTTTCAACAGCCTTACTGTGAGCAAGATTTCATGAGAGAGTGTGGGCA 541  
Qy 181 GTCCGTGAACAGTATGAGATTTCAGAGAGTGAAGGCCATGCTGCATATCCCTGAAAGATC 240  
Db 542 GTCCGTGAACAGTATGAGATTTCAGAGAGTGAAGGCCATGCTGCATATCCCTGAAAGATC 601  
Qy 241 AATTGACACCCCACTCTTGTCCCAACATCACTGGGTGTGAGATTAAGGATTCCTGCG 300  
Db 602 AATTGACACCCCACTCTTGTCCCAACATCACTGGGTGTGAGATTAAGGATTCCTGCG 661  
Qy 301 TGGCATTTGGGTGTGGCCCTTAGAGCAGAGCATTGATTCATTAAGATTCCTCATTTCT 360  
Db 662 TGGCATTTGGGTGTGGCCCTTAGAGCAGAGCATTGATTCATTAAGATTCCTCATTTCT 721  
Qy 361 TCGAAGAGAGAGAGGCTTGTGATGCTCTGTGATGCTCTCTCTCTCTCTCTCTCTCC 420  
Db 722 TCGAAGAGAGAGAGGCTTGTGATGCTCTGTGATGCTCTCTCTCTCTCTCTCTCTCC 781  
Qy 421 AAGAGCCCATATGATGAGGCTCATTTGGGCTGTGATTCATTTAGCCATTCAAGTCCAG 480  
Db 782 AAGAGCCCATATGATGAGGCTCATTTGGGCTGTGATTCATTTAGCCATTCAAGTCCAG 841  
Qy 481 AATTGCTCAGCTTTTCAACATPACTCAGATTGCTTACTAGCAACCATCATGATCTG 540  
Db 842 AATTGCTCAGCTTTTCAACATPACTCAGATTGCTTACTAGCAACCATCATGATCTG 901  
Qy 541 AGTGAACAAGCTCTGTTCAAAATATTTCAATGAGGGTGTGCTTCAGATGCTCAGACGCA 600  
Db 902 AGTGAACAAGCTCTGTTCAAAATATTTCAATGAGGGTGTGCTTCAGATGCTCAGACGCA 961  
Qy 601 AGGTCCATGATGATCAATGATGAAGGTCAACTGGAACCTATATGATCAACCTGACACA 660  
Db 962 AGGTCCATGATGATCAATGATGAAGGTCAACTGGAACCTATATGATCAACCTGACACA 1021  
Qy 661 GAAGGCACTATGAGAGAGAGTGAAGTGAAGGCTTCAAAAGATATGTCAGGAGAGAGG 720  
Db 1022 GAAGGCACTATGAGAGAGAGTGAAGTGAAGGCTTCAAAAGATATGTCAGGAGAGAGG 1081  
Qy 721 AATTGATGCGCCCACTCTTACAAATCTACATATGATGAGGGAGAGGAGCTTTGATTAAG 780  
Db 1082 AATTGATGCGCCCACTCTTACAAATCTACATATGATGAGGGAGAGGAGCTTTGATTAAG 1141  
Qy 781 CTCTGTAAGAAGTCAACAGTCACTTGTCCCAAGGCCGCGGTGTGCTTCTGTGAG 840  
Db 1142 CTCTGTAAGAAGTCAACAGTCACTTGTCCCAAGGCCGCGGTGTGCTTCTGTGAG 1201  
Qy 841 GGCATGACGGTGAAGAGTGTGCTGATGGCCATGAGGCGCTGGGTCTAGTGGAGAAATT 900  
Db 1202 GGCATGACGGTGAAGAGTGTGCTGATGGCCATGAGGCGCTGGGTCTAGTGGAGAAATT 1261  
Qy 901 CTCTCTTGTGGGCAAGGAGCAAGATGCCATCTTTATGAGATCTCAAGAGCATCTTA 960  
Db 1262 CTCTCTTGTGG----- 1272  
Qy 961 TGGAGAGACAGAGAGAAATGCCAAGTCCCTTCAAGGTTTGGAGCATATTAAC 1020  
Db 1273 -----C 1273  
Qy 1021 AGAAGTATGTCGGTGTGCTGCAATGCCAGCTCTGAATCTAGAGTCAAGTTCAGAGG 1080  
Db 1274 AGAAGTATGTCGGTGTGCTGCAATGCCAGCTCTGAATCTAGAGTCAAGTTCAGAGG 1333  
Qy 1081 CCCATCACTGATGAGGAGCAGGCTCATTTAATTTGAGTGAATTAATTAATCTGCAATTAT 1393  
Db 1334 CCCATCACTGATGAGGAGCAGGCTCATTTAATTTGAGTGAATTAATTAATCTGCAATTAT 1453  
Qy 1141 AATGAAGCAACAGTCAATATCTTGTGATGAGATTTGAGAGCATTTGTATTTGATGT 1200  
Db 1394 AATGAAGCAACAGTCAATATCTTGTGATGAGATTTGAGAGCATTTGTATTTGATGT 1453  
Qy 1201 GACCGTCAAAATGCGCCCATATCACTGCAACACTCAAGTATTCTTGCATGGGAGTCT 1260

XX MPI; 2001-123112/13.  
DR Novel metabotropic glutamate receptor for prevention, treatment of  
XX PT conditions associated with undesirable glutamate levels, e.g.  
PT Alzheimer's, Parkinson's disease, stroke, depression, anxiety, pain and  
PT schizophrenia -  
XX Claim 2; Fig 3; 59pp; English.  
XX  
XX The present invention relates to human metabotropic glutamate  
CC receptor. An agent that decreases expression or activity of the  
CC metabotropic glutamate receptor is useful for treating schizophrenia.  
CC Metabotropic glutamate receptor polymucleotides, polypeptides  
CC are useful for treating diseases associated with undesirable  
CC levels of glutamate, such as Alzheimer's disease, Parkinson's  
CC disease, stroke, depression, anxiety, pain and schizophrenia.  
XX  
XX Sequence 2349 BP; 588 A; 538 C; 586 G; 637 T; 0 other;  
SQ  
Query Match 88.6%; Score 1615.6; DB 22; Length 2349;  
Best Local Similarity 90.8%; Pred. No. 0;  
Matches 1805; Conservative 1; Mismatches 5; Indels 177; Gaps 1;  
QY 1 AAAATGCTCTTCTGTGATCTGTGATCTTGAAGAAGATGCTGGAGT 60  
DB AAAATGCTCTTCTGTGATCTGTGATCTTGAAGAAGATGCTGGAGT 421  
QY GCACATGTCAGTGAAGAGAGGCTGTGCTCAATGCTGGTGAATCATTTAGACT 120  
DB GCACATGTCAGTGAAGAGAGGCTGTGCTCAATGCTGGTGAATCATTTAGAGCT 481  
QY CTCCTTTCTGTTGATCAGCAGCTTCTGTTGAGGAGATGAGGAGGAGTGGGGA 180  
DB CTCCTTTCTGTTGATCAGCAGCTTCTGTTGAGGAGATGAGGAGGAGTGGGGA 482  
QY CTCCTTTCTGTTGATCAGCAGCTTCTGTTGAGGAGATGAGGAGGAGTGGGGA 541  
QY 181 GTCCGTGAACAGTATGAGATTCAGAGTGAAGCCATGCTGATACCTGGAAGATC 240  
DB 542 GTCCGTGAACAGTATGAGATTCAGAGTGAAGCCATGCTGATACCTGGAAGATC 601  
QY 241 AATTGAGACCCCACTCTTGGCCAAATCACTGAGGCTGTGAGATTAAGGATTCCTGC 300  
DB 602 AATTGAGACCCCACTCTTGGCCAAATCACTGAGGCTGTGAGATTAAGGATTCCTGC 661  
QY 301 TGGCATTGGGCTGTGGCCCTGAGAGAGATGATTAAGATTCCTCATTTCT 360  
DB 662 TGGCATTGGGCTGTGGCCCTGAGAGAGATGATTAAGATTCCTCATTTCT 721  
QY 361 TCGGAAGAGAGAGGCTGTGATCTGTGATGAGTCTCTCTTCCGCTCC 420  
DB 722 TCGGAAGAGAGAGGCTGTGATCTGTGATGAGTCTCTCTTCCGCTCC 781  
QY 421 AAGAAGCCATATGAGGCTCATTTGGCTGTTCAGATTCCTTACCATTCAGTCCAG 480  
DB 782 AAGAAGCCATATGAGGCTCATTTGGCTGTTCAGATTCCTTACCATTCAGTCCAG 841  
QY 481 AATTGCTCAGCTTTCAACATCTCAATGATTCCTTACAGCAACCATATGATTCG 540  
DB 842 AATTGCTCAGCTTTCAACATCTCAATGATTCCTTACAGCAACCATATGATTCG 901  
QY 541 AGTGAAGAGACTCTGTTCAATATTTCAAGAGGTTGCTCTCAATGCTCAGAGGCA 600  
DB 902 AGTGAAGAGACTCTGTTCAATATTTCAAGAGGTTGCTCTCAATGCTCAGAGGCA 961  
QY 601 AGTTCATGATGAGATCAATGAGGTAACAATGAGCTATATATCAGCCGTACACACA 660  
DB 962 AGTTCATGATGAGATCAATGAGGTAACAATGAGCTATATATCAGCCGTACACACA 1021  
QY 661 GA----- 662  
DB 1022 GAAGTTCAAGCTATTTCTATGCTCAGCTCCAGAGAGATGAGTGTGTTCAATCT 1081  
QY 663 ----- 662

DB 1082 TGGCTCAAGTATCTGCTGCTTTGGCTTCCAAATGCTGGATTTATGGCATGAGCC 1141  
QY 663 ----- A 663  
DB 1142 ACCACAGACCCCGGCGAGTGGCGCATTTAGAACATCTTGAAGTCTTTCTGATTTTGA 1201  
QY 664 GGCACATATGAGAAAGTGGATGGAAGCTTCAAGATATATCAGCGAAGAGAGGATTT 723  
DB 1202 GGCACATATGAGAAAGTGGATGGAAGCTTCAAGATATATCAGCGAAGAGAGGATTT 1261  
QY 724 TGCATGCGCACTCTTACAAAATCTACATTAATGCAAGGAGACAGCTTTGATTAAGCTG 783  
DB 1262 TGCATGCGCACTCTTACAAAATCTACATTAATGCAAGGAGACAGCTTTGATTAAGCTG 1321  
QY 784 CTGAANAACCTCAAGATCACTTGGCCAAAGGCTGGTGTGCTTATCTGTGAGGCT 843  
DB 1322 CTGAANAACCTCAAGATCACTTGGCCAAAGGCTGGTGTGCTTATCTGTGAGGCT 1381  
QY 844 ATGACGATGAGAGTCTGCTGATGAGCATGAGGCTGGTCTGATGAGAGAAATTTCTG 903  
DB 1382 ATGACGATGAGAGTCTGCTGATGAGCATGAGGCTGGTCTGATGAGAGAAATTTCTG 1441  
QY 904 CTTCGGGAGGGAACAGATGCAATCTTATTAAGATCTCAAGAACAGATCTATGG 963  
DB 1442 CTTCGGGAGGGAACAGATGCAATCTTATTAAGATCTCAAGAACAGATCTATGG 1501  
QY 964 GAAGACAGAAAGAAATGCAAGTGGCTTCTTCAAGGCTTTTGGAGACATATTAACACA 1023  
DB 1502 GAAGACAGAAAGAAATGCAAGTGGCTTCTTCAAGGCTTTTGGAGACATATTAACACA 1561  
QY 1024 AGTGAATCCGCTGTGTCAGATGAGCCGCTGATCTGATGAGTCTGAGTCTGAGGCTCC 1083  
DB 1562 AGTGAATCCGCTGTGTCAGATGAGCCGCTGATCTGATGAGTCTGAGTCTGAGGCTCC 1621  
QY 1084 ATCACTGAGCTGAGGAGACAGGCTCATTAATCTGAGTGAATTAATCTGATTAAT 1143  
DB 1622 ATCACTGAGCTGAGGAGACAGGCTCATTAATCTGAGTGAATTAATCTGATTAAT 1681  
QY 1144 GAAGCCACAGTCATATCTTGAATGAGATTTGAGAGACATTTGATGAGTGAAC 1203  
DB 1682 GAAGCCACAGTCATATCTTGAATGAGATTTGAGAGACATTTGATGAGTGAAC 1741  
QY 1204 GGTCAAAATGGGCCCCATATCACTGCAACACCTTCAAGTTTCTGCAATGGGCTGAG 1263  
DB 1742 GGTCAAAATGGGCCCCATATCACTGCAACACCTTCAAGTTTCTGCAATGGGCTGAG 1801  
QY 1264 ACTTTCACCTTGGAGATTAATCTGAGAGTCAATGAGGAGCTCTTGAATTTGGCT 1323  
DB 1802 ACTTTCACCTTGGAGATTAATCTGAGAGTCAATGAGGAGCTCTTGAATTTGGCT 1861  
QY 1324 TTGCGGTTTGAATTAATGATCTGGAAGAGGAATTCAGATGCAATTAATGAGAG 1383  
DB 1862 TTGCGGTTTGAATTAATGATCTGGAAGAGGAATTCAGATGCAATTAATGAGAG 1921  
QY 1384 GAGGACCTTTAGCTTGGAGTTGTTAAGAACGATTCAGTGAAGTCTTTTCAACC 1443  
DB 1922 GAGGACCTTTAGCTTGGAGTTGTTAAGAACGATTCAGTGAAGTCTTTTCAACC 1981  
QY 1444 TCCCAAGTTACATGCAATGATTCCTCAAGACCTTACCAACATGATGATTAATCTCTGAT 1503  
DB 1982 TCCCAAGTTACATGCAATGATTCCTCAAGACCTTACCAACATGATGATTAATCTCTGAT 2041  
QY 1504 TGTGAAGCTAAGACTGTGATGATTTCAAGTCCCTATATACCATC 1563  
DB 2042 TGTGAAGCTAAGACTGTGATGATTTCAAGTCCCTATATACCATC 2101  
QY 1564 CCTAATTTCTCTTCTCACTCTCTGAGGCTAATCTTGTGATTAATCATCTGAGACA 1623  
DB 2102 CCTAATTTCTCTTCTCACTCTCTGAGGCTAATCTTGTGATTAATCATCTGAGACA 2161  
QY 1624 GAGACAAATCAGAAATGATTAATCTGCTGAGGAAACCTTTATCCCATTAAGCCCTCT 1683

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Db      422 GCACAGTCCAGTGAAGAGGGGTGGTGCACATGTGGGTGACATATTTGAGCT 481
Qy      121 CTTCTTTCTGTTATCAACAGCTACTGTGAGAGAGTTATTAAGAGAAAGTGGGGCA 180
Db      482 CTCCTTTCTGTTATCAACAGCTACTGTGAGAGAGTTATTAAGAGAAAGTGGGGCA 541
Qy      181 GTCGGAACAGTATGGCATTTAGAGAGTGAAGGCCATGCTGATACCTCGAAAGGATC 240
Db      542 GTCCGTGAACAGTATGGCATTTAGAGAGTGAAGGCCATGCTGATACCTCGAAAGGATC 601
Qy      241 AATTGAGACCCCACTCTTGGCCCAATCACTGGGCTGTGAGATTAAGGATTCCTGC 300
Db      602 AATTGAGACCCCACTCTTGGCCCAATCACTGGGCTGTGAGATTAAGGATTCCTGC 661
Qy      301 TGGCATTGCGCTGTGGCTTGAAGAGAGCATTTGATTAAGAGATTCCTCATTTCT 360
Db      662 TGGCATTGCGCTGTGGCTTGAAGAGAGCATTTGATTAAGAGATTCCTCATTTCT 721
Qy      361 TGGGAAGAGAGAGGGCTGGTATGCTGTGGAATGGCTCTCTCTCCGCTCC 420
Db      722 TCGGAAGAGAGAGGGCTGGTATGCTGTGGAATGGCTCTCTCTCCGCTCC 781
Qy      421 AAGAAGCCATAGTAGGGGTCAATTGGGCTGTGCTCAGTCTTTAGCCATTCAAGTCCAG 480
Db      782 AAGAAGCCATAGTAGGGGTCAATTGGGCTGTGCTCAGTCTTTAGCCATTCAAGTCCAG 841
Qy      481 AATTGCTCAGCTTTCAACATACCTCAATGCTTATCTCAAGAACCATATGATCTG 540
Db      842 AATTGCTCAGCTTTCAACATACCTCAATGCTTATCTCAAGAACCATATGATCTG 901
Qy      541 AGTGAAGAAGCTGTGTTCAAAATTTTCAATAGGGTGTGGCTTCAGATGCTCAAGAGCA 600
Db      902 AGTGAAGAAGCTGTGTTCAAAATTTTCAATAGGGTGTGGCTTCAGATGCTCAAGAGCA 961
Qy      601 AGGTCCATGTGACATATGAGAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 660
Db      962 AGGTCCATGTGACATATGAGAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 1021
Qy      661 GAAGGCACTATGAGAGAGAGTGGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 720
Db      1022 GAAGGCACTATGAGAGAGAGTGGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 1081
Qy      721 AATTGATGGCCCACTTTCAAAATTTTCAATAGTGAAGAGTGAAGAGTGAAGAGTGAAG 780
Db      1082 AATTGATGGCCCACTTTCAAAATTTTCAATAGTGAAGAGTGAAGAGTGAAGAGTGAAG 1141
Qy      781 CTGCTGAAGAAGCTCACAAGTCACTTGCCTCAAGGCCCGGGTGTGCTTCTCTGAG 840
Db      1142 CTGCTGAAGAAGCTCACAAGTCACTTGCCTCAAGGCCCGGGTGTGCTTCTCTGAG 1201
Qy      841 GGCATGACGGTGAAGAGTCTGTGATGGCCATGAGGGCTGTGATGAGAGAAATTT 900
Db      1202 GGCATGACGGTGAAGAGTCTGTGATGGCCATGAGGGCTGTGATGAGAGAAATTT 1261
Qy      901 CTGCTTCTGGGAGGGGAAACAAGATGCATCTTTATTAAGATCTCAAGAACAGATCTTA 960
Db      1262 CTGCTTCTGGGAGGGGAAACAAGATGCATCTTTATTAAGATCTCAAGAACAGATCTTA 1321
Qy      961 TGGGAAGACAGAAAGAAATGCAAGTGTGCTTCTTCAAGGGTTTGGAGACATATTAAC 1020
Db      1322 TGGGAAGACAGAAAGAAATGCAAGTGTGCTTCTTCAAGGGTTTGGAGACATATTAAC 1358
Qy      1021 AGAAGTAGTCCGTGCTGTGACATGCCAGCTTGTGAATTAAGACTCAAGTCAAGG 1080
Db      1359 AGAAGTAGTCCGTGCTGTGACATGCCAGCTTGTGAATTAAGACTCAAGTCAAGG 1418
Qy      1081 CCATCATCTGGAAGAGGAGCAGGCTCATTAATTTGAGTGAATTAAGTCAAGTCAAT 1140
Db      1419 CCATCATCTGGAAGAGGAGCAGGCTCATTAATTTGAGTGAATTAAGTCAAGTCAAT 1478
Qy      1141 AATGAAGCCAACTCATATCTTCTGATGTGAGATTTGAAGACATTTGATGATGT 1200

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Db      1479 AATGAAGCCAAAGTCAATCTTCTGATGTGAGATTTGAGAGCATTTGATGATGT 1538
Qy      1201 GACCGTCAAAATGCGGCCCATATATCTGCAACACCTACAAGTTTCTTGATAGGGTGTCT 1260
Db      1539 GACCGTCAAAATGCGGCCCATATATCTGCAACACCTACAAGTTTCTTGATAGGGTGTCT 1598
Qy      1261 CAGACTTTCAACCTCTGGAAGATTAATCTGAGAGTCCATGTGGGGAGCTTTGAAATTTGG 1320
Db      1599 CAGACTTTCAACCTCTGGAAGATTAATCTGAGAGTCCATGTGGGGAGCTTTGAAATTTGG 1658
Qy      1321 GCTTTCGTTGTTTGAATAAGTACTGAAAGAGAGAAATCAAGATGCAATATATATGA 1380
Db      1659 GCTTTCGTTGTTTGAATAAGTACTGAAAGAGAGAAATCAAGATGCAATATATATGA 1718
Qy      1381 GAGAGAGGACTCTTATAGTCTGGGATTTGTAAGACGATTCAGTCAAGTCTTACC 1440
Db      1719 GAGAGAGGACTCTTATAGTCTGGGATTTGTAAGACGATTCAGTCAAGTCTTACC 1778
Qy      1441 ACCTCCCAAGTTACATGAGATATGTCACCAAGACTACCAACCATATGAGATTAATCTG 1500
Db      1779 ACCTCCCAAGTTACATGAGATATGTCACCAAGACTACCAACCATATGAGATTAATCTG 1838
Qy      1501 GATTGTAAGCTAAGAACTGTAGCTTGTGATGTTAATCAAGTCCCTATATACACC 1560
Db      1839 GATTGTAAGCTAAGAACTGTAGCTTGTGATGTTAATCAAGTCCCTATATACACC 1898
Qy      1561 ATCCCTAATGCTCTTCTCAACCTCCTCAGGCTTATCTTGTGATTAATCTCTGA 1620
Db      1899 ATCCCTAATGCTCTTCTCAACCTCCTCAGGCTTATCTTGTGATTAATCTCTGA 1958
Qy      1621 CCAGAGCAAAATGAGAAATGTGTTATCTGCTGTGGAAGCCCTTTATCCATTAAGCCC 1680
Db      1959 CCAGAGCAAAATGAGAAATGTGTTATCTGCTGTGGAAGCCCTTTATCCATTAAGCCC 2018
Qy      1681 TCTTCTGTGCTTATCAAAAGAGAAATAGCTTGTGTTATGCTTGAATTCAT 1740
Db      2019 TCTTCTGTGCTTATCAAAAGAGAAATAGCTTGTGTTATGCTTGAATTCAT 2078
Qy      1741 CTATGTTTATTAATCAATCTTATGTTTATCTTAAATGCTTAATCAAAAGAA 1800
Db      2079 CTATGTTTATTAATCAATCTTATGTTTATCTTAAATGCTTAATCAAAAGAA 2138
Qy      1801 AAAAAAAAAA 1811
Db      2139 AAAAAAAAAA 2149

RESULT 5
AAF2990
ID AAF2990 standard; DNA; 2349 BP.
XX
AC AAF2990;
XX
DT 06-APR-2001 (first entry)
XX
DE Human GRMX-1b DNA.
XX
KW Human; metabotropic glutamate receptor; schizophrenia; GRMX;
XX Alzheimer's; Parkinson's; stroke; depression; anxiety; pain; ds.
XX Homo sapiens.
XX OS
XX NO200102566-A1.
XX PN
XX 11-JAN-2001.
XX PD
XX 27-JUN-2000; 2000MO-US17798.
XX PF
XX 02-JUL-1999; 99US-0346326.
XX PR
XX (NEUR-) NEUROCRINE BIOSCIENCES INC.
XX PA
XX Schwarz DA; Maki RA;
XX PI

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D	b		421	GCCCATAGAGGGGTCATTGGGCGCTGGTTCCAGTTCCTTAGGCATTCAGGCTCGAAGATT	480
Q	y		486	GCTCAGCTTTTCAACATACCTCAGATTGCTTACTCAGCAACCATCAGATCTGAGTGA	545
D	b		481	GCTCAGGCTTTTCAACATACCTCAGATTGCTTACTCAGCAACCATCAGATCTGAGTGA	540
Q	y		546	CAAGACTCTGTTCAATATATTTATGAGGGGTATGGCTTCAGATGGCTCAGCAGAGGTC	605
D	b		541	CAGACTCTGTTCAATATATTTATGAGGGGTATGGCTTCAGATGGCTCAGCAGAGGTC	600
Q	y		606	CATGTGTGACATAGTGAAGAGGTACAACCTGAGCCTATGATCAGCCGTACACAGAAAG	665
D	b		601	CATGTGTGACATAGTGAAGAGGTACAACCTGAGCCTATGATCAGCCGTACACAGAAAG	660
Q	y		666	CAACTATGAGAAAGTGGAGTGAAGACCTTCAAGATATGTCAAGCAAGAAAGGATTTG	725
D	b		661	CAACTATGAGAAAGTGGAGTGAAGACCTTCAAGATATGTCAAGCAAGAAAGGATTTG	720
Q	y		726	CATGCCCACTCTTTCAAATTTACAGTAAATGCAAGGAGGACGAGCTTGAATAACTGCT	785
D	b		721	CATGCCCACTCTTTCAAATTTACAGTAAATGCAAGGAGGACGAGCTTGAATAACTGCT	780
Q	y		786	GAAGAAGCTCAACAAGTCACTTGGCCCAAGGCCGGGGTGGGCGCTACTTCGTGAGAGGAT	845
D	b		781	GAAGAAGCTCAACAAGTCACTTGGCCCAAGGCCGGGGTGGGCGCTACTTCGTGAGAGGAT	840
Q	y		846	GACGGTGAAGGTCGTGCTGATGAGCAGTAAAGCGCCTCGGCTCTAGTGGAGAAATTTCTGCT	905
D	b		841	GACGGTGAAGGTCGTGCTGATGAGCAGTAAAGCGCCTCGGCTCTAGTGGAGAAATTTCTGCT	900
Q	y		906	TCTGGGCAAGGAAACAGATGCCATCTTTAATTGAGATCTCAAGAACAGCATCTCTATGGGA	965
D	b		901	TCTGGGCAAGGAAACAGATGCCATCTTTAATTGAGATCTCAAGAACAGCATCTCTATGGGA	960
Q	y		966	AGACAGAAGAAATATCCAAAGTCGCTTCCTTCAGGGTATTTGGAGACATATTACACAGAAG	1025
D	b		961	AGACAGAAGAAATATCCAAAGTCGCTTCCTTCAGGGTATTTGGAGACATATTACACAGAAG	1022
Q	y		1026	TGAGTCGCTGCTGCTGACATATGCCCAAGCCTCTGAATCTAAGACTCAGTTCAGGGCCAT	1085
D	b		1021	TGAGTCGCTGCTGCTGACATATGCCCAAGCCTCTGAATCTAAGACTCAGTTCAGGGCCAT	1080
Q	y		1086	CACGTGATGAGGGAACAGGCTCATCTAATTCGAGTGCATATTACTCTGCATTATTAATGA	1145
D	b		1081	CACGTGATGAGGGAACAGGCTCATCTAATTCGAGTGCATATTACTCTGCATTATTAATGA	1140
Q	y		1146	AGCCAAACGTATATCTTCTGATGTGGAGATTTGGAAGACATTTGATTTGATGTGACCG	1205
D	b		1141	AGCCAAACGTATATCTTCTGATGTGGAGATTTGGAAGACATTTGATTTGATGTGACCG	1200
Q	y		1206	TCAAAATATGCGCCCATATCACTGCAACAACCTACAGATTTCTTCGATGGGTCACAGC	1265
D	b		1201	TCAAAATATGCGCCCATATCACTGCAACAACCTACAGATTTCTTCGATGGGTCACAGC	1260
Q	y		1266	TTTCACTCTGCGCAAGTATTACTGGGAGGTCCATGTGGGGGACCTTGGAAATTTGGGCTTT	1325
D	b		1261	TTTCACTCTCTGCGCAAGTATTACTGGGAGGTCCATGTGGGGGACCTTGGAAATTTGGGCTTT	1320
Q	y		1326	CGGTGTTTGTAAATAGTACTGGAAGAGGAAGATACAGAAATGGCAATATATATGAGAGGA	1385
D	b		1321	CGGTGTTTGTAAATAGTACTGGAAGAGGAAGATACAGAAATGGCAATATATATGAGAGGA	1380
Q	y		1386	GGGACTCTTTAGTCTTGGGATTTGTAAAGACACTTACAGTGCAGTCTCTTACCACTGC	1445
D	b		1381	GGGACTCTTTAGTCTTGGGATTTGTAAAGACACTTACAGTGCAGTCTCTTACCACTGC	1440
Q	y		1446	CCCAAGTTACACTGACGATATGTCCCAAGACTTACCAACATGATAGGATTAATCTGTGATTG	1505
D	b		1441	CCCAAGTTACACTGACGATATGTCCCAAGACTTACCAACATGATAGGATTAATCTGTGATTG	1500
Q	y		1506	TGAAGCTAAGACTGTGAGACTCGTTGATGTTAATCAAGGCTCCCTAATATACACATCCC	1565
D	b		1501	TGAAGCTAAGACTGTGAGACTCGTTGATGTTAATCAAGGCTCCCTAATATACACATCCC	1560

QY	1566	TAATGCTCCCTTCACCTCCCTCGAGGCTATCTTTGGGTATTTCAATCTGACACAGA	166
Db	1561	TAAATGCTCTTCCTACCTCCCTCTCGAGGCTATCTTTGGGTATTTCAATCTGACACAGA	162
QY	1626	GACAAATCAGAAATGTGTATTTATCTGCTGTGGAAACCCCTTATATCCCATTAAGCCCTCTTC	168
Db	1621	GACAAATCAGAAATGTGTATTTATCTGCTGTGGAAACCCCTTATATCCCATTAAGCCCTCTTC	168
QY	1686	CTTGCGCTTATCAAAACGACGACAAATAGATTCGTGTTTATATGCTTGAAATGCATTTCTAAT	174
Db	1681	CTTGCGCTTATCAAAACGACGACAAATAGATTCGTGTTTATATGCTTGAAATGCATTTCTAAT	174
QY	1746	GTTATTAATAACCTATTATATGTTGTTACTATTAAATATGTTGTTAAATGCAAT	1793
Db	1741	GTTATTAATAACCTATTATATGTTGTTACTATTAAATATGTTGTTAAATGCAAT	1788
RESULT 4			
AAFP29994			
ID	AAFP29994	standard; DNA; 2149 BP.	
XX	AAFP29994;		
AC			
XX	06-APR-2001	(first entry)	
DT			
XX	Human GRMx-1f DNA.		
DE			
XX	Human; metabotropic glutamate receptor; schizophrenia; GRMx;		
KM	Alzheimer's; Parkinson's; stroke; depression; anxiety; pain; ds.		
KW			
XX	Homo sapiens.		
OS			
PN	WO200102566-A1.		
XX			
PD	11-JAN-2001.		
XX			
PF	27-JUN-2000; 2000WO-US17798.		
XX			
PR	02-JUL-1999; 99US-0346326.		
XX			
PA	(NEUR-) NEUROCRINE BIOSCIENCES INC.		
XX			
PI	Schwarz DA, Maki RA;		
XX			
DR	WPI; 2001-123112/13.		
XX			
PT	Novel metabotropic glutamate receptor for prevention, treatment of		
PT	conditions associated with undesirable glutamate levels, e.g.		
PT	Alzheimer's, Parkinson's disease, stroke, depression, anxiety, pain and		
PT	schizophrenia -		
XX			
PS	Claim 2; Fig 9; 59pp; English.		
XX			
CC	The present invention relates to human metabotropic glutamate		
CC	receptor. An agent that decreases expression or activity of the		
CC	metabotropic glutamate receptor is useful for treating schizophrenia.		
CC	Metabotropic glutamate receptor polynucleotides, polypeptides		
CC	are useful for treating diseases associated with undesirable		
CC	levels of glutamate, such as Alzheimer's disease, Parkinson's		
CC	disease, stroke, depression, anxiety, pain and schizophrenia.		
XX			
XX			
SQ	Sequence 2149 BP; 547 A; 485 C; 538 G; 579 T; 0 other;		
Query Match 95.8%; Score 1746.6; DB 22; Length 2149;			
Best Local Similarity 98.4%; Pred. No. 0;			
Matches 1782; Conservative 1; Mismatches 5; Indels 23; Gaps 1;			
QY	1	AAATGCGCTTCCTGTTGATCCCTGACGCTTACTTTTGAAGAAGATGTCGCGGAGT	60
Db	362	AAATGCGCTTCCTGTTGATCCCTGACGCTTACTTTTGAAGAAGATGTCGCGGAGT	421
QY	61	GCAACGTCAGATGAGAGAGGGTGTGAGCTCACAAGCTGGGTGACATCATTTATGGAGCT	120

Db 1382 AGAAGAGAGCCCTGCTGCTGCACATGCCCAAGCTCTGATCTAGAGCTCAAGTCAAGG 1441  
Qy 1081 CCCATCACTGAGTGAAGGAGCAGGCTCATTAATCTGAGTGAATTAATCTGCAATTAT 1140  
Db 1442 CCCATCACTGAGTGAAGGAGCAGGCTCATTAATCTGAGTGAATTAATCTGCAATTAT 1501  
Qy 1141 AATGAAGCCCAAGTCAATCTGATGAGTGAATTTGAAGCAATTTGATGATGAT 1200  
Db 1502 AATGAAGCCCAAGTCAATCTGATGAGTGAATTTGAAGCAATTTGATGATGAT 1561  
Qy 1201 GACCGTCAAAATGCGCCCATATCACTGACAACTCAAGTTCTTTCGATGAGGCT 1260  
Db 1562 GACCGTCAAAATGCGCCCATATCACTGACAACTCAAGTTCTTTCGATGAGGCT 1621  
Qy 1261 CAGACTTCACTCTGAGAGATTAATCTGAGAGGTCATGAGGAGCTCTTGAATTTG 1320  
Db 1622 CAGACTTCACTCTGAGAGATTAATCTGAGAGGTCATGAGGAGCTCTTGAATTTG 1681  
Qy 1321 GCTTTGGGCTTTGTAATAGTCTGGAAGGAGAAATGGAATGCAATTAATTAATGA 1380  
Db 1682 GCTTTGGGCTTTGTAATAGTCTGGAAGGAGAAATGGAATGCAATTAATTAATGA 1741  
Qy 1381 GAGAGGAGACTTTTATGCTTGGGATGTTAAGAACAGCAATTCAGTCACTCTTACC 1440  
Db 1742 GAGAGGAGACTTTTATGCTTGGGATGTTAAGAACAGCAATTCAGTCACTCTTACC 1801  
Qy 1441 ACCTCCCAAGTCACTGAGATATGTCACAAAGCTTACCAACCAATGAGATTAATTC 1500  
Db 1802 ACCTCCCAAGTCACTGAGATATGTCACAAAGCTTACCAACCAATGAGATTAATTC 1861  
Qy 1501 GATTGGAAGTGAAGTGAAGTGTGAGTGTGATTAATCAAGCTCCCTTAATTAATACC 1560  
Db 1862 GATTGGAAGTGAAGTGAAGTGTGAGTGTGATTAATCAAGCTCCCTTAATTAATACC 1921  
Qy 1561 ATCCCTAATGCTCTCTCACTCTCTGAGGCTTATCTTTGCTGATTAATCACTCTGA 1620  
Db 1922 ATCCCTAATGCTCTCTCTCACTCTCTGAGGCTTATCTTTGCTGATTAATCACTCTGA 1981  
Qy 1621 CCAAGACAAATGAGAAATGTTTATCTGCTGAGAACCCCTTAATCCCAATTAAGCCC 1680  
Db 1982 CCAAGACAAATGAGAAATGTTTATCTGCTGAGAACCCCTTAATCCCAATTAAGCCC 2041  
Qy 1681 TCTTCTTGCTGCTTATCAACAGAGCAAAATAGTTCTGTTTATGCTTGAATTCAT 1740  
Db 2042 TCTTCTTGCTGCTTATCAACAGAGCAAAATAGTTCTGTTTATGCTTGAATTCAT 2101  
Qy 1741 CTATGTTATTAATACTCATTTATGTTACTATTAATGTTGTTAAACACAAATAAAA 1800  
Db 2102 CTATGTTATTAATACTCATTTATGTTACTATTAATGTTGTTAAACACCTTAATA 2161  
Qy 1801 AAAAAAAAAA 1811  
Db 2162 AAAAAAAAAA 2172

RESULT 3  
ID AAS62274 standard; cDNA; 1788 BP.  
XX AAS62274;  
XX  
XX  
XX 14-FEB-2002 (first entry)  
XX  
XX cDNA sequence #61 encoding novel human secreted protein.  
DE  
XX Human secreted protein; hyperproliferative disorder; autoimmune disorder;  
KM immune deficiency disorder; blood disorder; inflammatory disorder;  
KM infectious disorder; gene therapy; antimicrobial; hepatotropic;  
KM immunosuppressive; antirheumatic; ss.  
XX  
XX Homo sapiens.  
OS  
XX

PN WO200177291-A2.  
XX  
XX 18-OCT-2001.  
XX  
XX 29-MAR-2001; 2001WO-US10485.  
XX  
XX 06-APR-2000; 2000US-195604P.  
XX  
XX (GEMT) GENETICS INST INC.  
XX  
XX Wong GG, Clark HF, Fecthel K, Agostino MJ, Howes SH, Resnick RJ,  
PI Gulukota K, Graham JR;  
XX  
XX WPI; 2002-010900/01.  
XX  
XX  
XX New polynucleotides encoding secreted proteins useful for treating e.g.  
PT asthma, HIV and Crohn's disease -  
XX  
XX  
XX Claim 1; Page 106-107; 391pp; English.  
XX  
XX The present invention relates to the isolation of novel cDNA sequences  
CC which encode human secreted proteins. The cDNA sequences have been  
CC derived from a variety of human tissues. The invention also provides  
CC a method for producing proteins from these polynucleotide sequences.  
CC The proteins are useful for identifying compounds that modulate their  
CC activity and production, and the cell is also useful for identifying  
CC compounds that modulate expression of the polynucleotide sequences  
CC encoding the secreted proteins. The sequences of the invention are  
CC useful for treating diseases such as hyperproliferative disorders  
CC (e.g. cancer), immune deficiency disorders (e.g. severe combined  
CC immunodeficiency (SCID)), autoimmune disorders (e.g. multiple  
CC sclerosis), blood disorders (e.g. thrombocytopaenia), inflammatory  
CC disorders (e.g. arthritis) and infectious disorders (e.g. hepatitis).  
CC The polynucleotide sequences of the invention are also useful in gene  
CC therapy. AAS62214-AAS62838 represent the cDNA sequences of the  
CC invention that encode for novel human secreted proteins.  
XX  
XX  
SQ Sequence 1788 BP; 454 A; 398 C; 444 G; 492 T; 0 other;  
Query Match 98.1%; Score 1787.6; DB 24; Length 1788;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1787; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 6 GGTCTTCTGTTGATCTCTGCTCACTCTTACTTTGAAGAAGATCCGTGGAGTGACA 65  
Db 1 GGTCTTCTGTTGATCTCTGCTCACTCTTACTTTGAAGAAGATCCGTGGAGTGACA 60  
Qy 66 GTCCAGTGAAGAGGAGGTGGTGGCTCAATGCTGGTGAATCATTAATGAGACTCTT 125  
Db 61 GTCCAGTGAAGAGGAGGTGGTGGCTCAATGCTGGTGAATCATTAATGAGACTCTT 120  
Qy 126 TTCTGTTCAATCAACAGCTTACTGTGAGCAAGTTCTGAGAGAGATGTGGGCACTCC 185  
Db 121 TTCTGTTCAATCAACAGCTTACTGTGAGCAAGTTCTGAGAGAGATGTGGGCACTCC 180  
Qy 186 TGAACAGTATGAGATTCAGAGAGTGAAGGCTCATGCTGCAATCCCTGGAAGATTCAT 245  
Db 181 TGAACAGTATGAGATTCAGAGAGTGAAGGCTCATGCTGCAATCCCTGGAAGATTCAT 240  
Qy 246 AGACCCCACTCTTCCCAATCACTGAGCTGTGAGATTAAGGATTCCTGCTGGCA 305  
Db 241 AGACCCCACTCTTCCCAATCACTGAGCTGTGAGATTAAGGATTCCTGCTGGCA 300  
Qy 306 TTGAGCTGTGGCCCTTGAAGAGAGATTAAGTTCAATAGAGATTCCTCATTTCTTGGGA 365  
Db 301 TTGAGCTGTGGCCCTTGAAGAGAGATTAAGTTCAATAGAGATTCCTCATTTCTTGGGA 360  
Qy 366 AGAGGAAGAGGCTTGTATGCTGTGAGATGCTCTCTCTTCTTCCGCTCCAGAA 425  
Db 361 AGAGGAAGAGGCTTGTATGCTGTGAGATGCTCTCTCTCTTCCGCTCCAGAA 420  
Qy 426 GCCCATAGTAGGGGTGATTTGGGCTGCTCAAGTTCTTTAGCAATTCAGGTCAGAAATT 485

Db	1441	ACCTCCCAAGTTACACTGCAATATATGTCCCAAGACCTACCAACATATGATGATTTATTCCTG	1500
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Db	1501	GATTGTGAAGCTAGAACTGTAAGCTTCGTTGATGTATTAATCAAAGCTCCCTATATACACC	1560
Qy	1561	ATCCCTAATTCCTCTCTCTCAACCTCCCTCAGGCGTATCTTTTGCTGATTCATCTCTGA	1620
Db	1561	ATCCCTAATTCCTCTCTCTCAACCTCCCTCAGGCGTATCTTTTGCTGATTCATCTCTGA	1620
Qy	1621	CCAGAGACAAATCAGAAAATGTGTTATCTGCTGTGGGAACCCCTTTATCCCATAAAGCC	1680
Db	1621	CCAGAGACAAATCAGAAAATGTGTTATCTGCTGTGGGAACCCCTTTATCCCATAAAGCCC	1680
Qy	1681	TCTTCCTGTGSCCTTATCAAA CAGGACAAATAGGTTCTGTTTATGCTCTGAAATGGCATTT	1740
Db	1681	TCTTCCTGTGSCCTTATCAAA CAGGACAAATAGGTTCTGTTTATGCTCTGAAATGGCATTT	1740
Qy	1741	CTAATGTTATTAACCTCATTTATTTGTTACTATTAATGTGTAAMCACAAAAAA	1800
Db	1741	CTAATGTTATTAACCTCATTTATTTGTTACTATTAATGTGTAAMCACAAAAAA	1800
Qy	1801	AAAAAAAAAAAAAAAAAAAAA	1823
Db	1801	AAAAAAAAAAAAAAAAAAAAA	1823

XX	SEQUENCE 2172 BP; 554 A; 488 C; 544 G; 586 T; 0 OTHER;
CC	DISEASE, STROKE, DEPRESSION, ANXIETY, PAIN AND SCHIZOPHRENIA.
CC	LEVELS OF GLUTAMATE, SUCH AS ALZHEIMER'S DISEASE, PARKINSON'S
CC	ARE USEFUL FOR TREATING DISEASES ASSOCIATED WITH UNDESIRABLE
CC	METABOTROPIC GLUTAMATE RECEPTOR POLYNUCLEOTIDES, POLYPEPTIDES
CC	RECEPTOR. AN AGENT THAT DECREASES EXPRESSION OR ACTIVITY OF THE
CC	THE PRESENT INVENTION RELATES TO HUMAN METABOTROPIC GLUTAMATE
PS	CLAIM 2; FIG 7; 59PP; ENGLISH.
XX	
PT	NOVEL METABOTROPIC GLUTAMATE RECEPTOR FOR PREVENTION, TREATMENT OF
PT	CONDITIONS ASSOCIATED WITH UNDESIRABLE GLUTAMATE LEVELS, E.G.
PT	ALZHEIMER'S, PARKINSON'S DISEASE, STROKE, DEPRESSION, ANXIETY, PAIN AND
XX	SCHIZOPHRENIA -
XX	
PI	SCHWARZ DA, MAKI RA;
DR	WPI; 2001-123112/13.
XX	
XX	(NEUR.-) NEUROCRINE BIOSCIENCES INC.
PA	
XX	
XX	02-JUL-1999; 99US-0346326.
PR	
PF	27-JUN-2000; 2000WO-US17798.
XX	
PD	11-JAN-2001.
PN	WO200102566-A1.
XX	
OS	HOMO SAPIENS.
XX	
KM	Alzheimer's; Parkinson's; stroke; depression; anxiety; pain; de.
XX	
XX	Human GRMX-Ie DNA.
DE	
DT	06-APR-2001 (first entry)
AC	AAE29993;
XX	
ID	AAF29993 standard; DNA; 2172 BP.
RESULT 2	

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			Indels	0
			Gaps	0
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DB	362	AAAATGGTCTCTTGTTGATCTCTGACGTCTTACTTTTGAAGAAGATGTCGGTGGAGT	421	
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DB	422	GCACAGTCCAGTAGAGAGAGGGGTGTGGCTCACTGCTGGGTGACATCTATTGAGACT	481	
OY	121	CTCTTTTCTGTTCATCAACAGCCCTTACGTGTGACACAACTTCAATGAGAAATGTGGGCA	180	
DB	482	CTCTTTTCTGTTCATCAACAGCCCTTACGTGTGACACAACTTCAATGAGAAATGTGGGCA	541	
OY	181	GTCCGTGAACAGTAGAGATTCAGAGATGAGAGCCATGCTGCATACCCCTGGAAGATC	240	
DB	542	GTCCGTGAACAGTAGAGATTCAGAGATGAGAGCCATGCTGCATACCCCTGGAAGATC	601	
OY	241	AATTCAAGCCCACTCTTTCGCCCAATCACTGCGGCTGTGTGATPAAGGATTCCTGC	300	
DB	602	AATTCAAGCCCACTCTTTCGCCCAATCACTGCGGCTGTGTGATPAAGGATTCCTGC	661	
OY	301	TGGCATTCGGGTGTGGCCCTTAGAGACAGATTTAGTTCAATPAAGATTCCTCATTTCT	360	
DB	662	TGGCATTCGGGTGTGGCCCTTAGAGACAGATTTAGTTCAATPAAGATTCCTCATTTCT	721	
OY	361	TCCGAAGAGAAAGGGCTTGTATGCTCTGTGTGATGGACTCTCTCTTCCCTCCGCTCC	420	
DB	722	TCCGAAGAGAAAGGGCTTGTATGCTCTGTGTGATGGACTCTCTCTTCCCTCCGCTCC	781	
OY	421	AAGAAGCCCATAGTAGAGGGGTCAATTGGGCTGTGTCAAGTTCTTTAGCCATTCAAGSTCCAG	480	
DB	782	AAGAAGCCCATAGTAGAGGGGTCAATTGGGCTGTGTCAAGTTCTTTAGCCATTCAAGSTCCAG	841	
OY	481	AATTTGCTCCAGCTTTTCAACATCTCAATGTGCTTACTCAGCAACCTTCATGTGATCTG	540	
DB	842	AATTTGCTCCAGCTTTTCAACATCTCAATGTGCTTACTCAGCAACCTTCATGTGATCTG	901	
OY	541	AGTAGCAAGACTCTGTTCAAAATATTTATGATGAGGGTTGTGCTTCAGATGTCTCAGAGCA	600	
DB	902	AGTAGCAAGACTCTGTTCAAAATATTTATGATGAGGGTTGTGCTTCAGATGTCTCAGAGCA	961	
OY	601	AGGTCCATGTGTGACATATGTAGAGAGGTACAATGTGACTATGTATCAGCCGTACACACA	660	
DB	962	AGGTCCATGTGTGACATATGTAGAGAGGTACAATGTGACTATGTATCAGCCGTACACACA	1021	
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DB	1022	GAAGGCAACTATGAGAAATGTGGATGGAAGCTTCAAAAGTATGTACGGAAGAAAGGG	1081	
OY	721	ATTTCATTCGCCCACTCTTCAAAATATTAACAGTAAATCAAGGAGGACAGCTTTGATAG	780	
DB	1082	ATTTCATTCGCCCACTCTTCAAAATATTAACAGTAAATCAAGGAGGACAGCTTTGATAG	1141	
OY	781	CTGCTGAAGAAGCTCAACAATCTTTCAGAGGCCCGGGTGTGTGACTTCTCTGTAG	840	
DB	1142	CTGCTGAAGAAGCTCAACAATCTTTCAGAGGCCCGGGTGTGTGACTTCTCTGTAG	1201	
OY	841	GGCATGACGGTAGAGGTCTGTGTATGGCCATGAGGCGCTGGGGTCTTAGTGTGGAAATTT	900	
DB	1202	GGCATGACGGTAGAGGTCTGTGTATGGCCATGAGGCGCTGGGGTCTTAGTGTGGAAATTT	1261	
OY	901	CTGCTTCGTGGCAGGGAAACAAGATGCCATCTTTATTAAGATCTCAAGAAACAGATCTTA	960	
DB	1262	CTGCTTCGTGGCAGGGAAACAAGATGCCATCTTTATTAAGATCTCAAGAAACAGATCTTA	1321	
OY	961	TGGGAACAAGAAATAATGCCAAGTCTGCTTCTTCAAGGGTTTTGGAGCATTTACAC	1020	
DB	1322	TGGGAACAAGAAATAATGCCAAGTCTGCTTCTTCAAGGGTTTTGGAGCATTTACAC	1381	
OY	1021	AGAAATGATGTCCTGCTGTCTGTGCACATGCCCAAGCTCTGAAATCTTAGACTTACAGG	1080	

PD 12-SEP-2002.  
 XX  
 PF 21-DEC-2001; 2001MO-US49817.  
 XX  
 PR 22-DEC-2000; 2000US-257589P.  
 XX  
 PA (AMHP) WYETH.  
 XX  
 PI Bates BG, Xie Y, Gulukota K, Paulsen JR,  
 XX  
 DR P-PSDB; ABP54921.  
 XX  
 PT New mglur5m nucleic acid molecules and proteins, useful for treating  
 PT neurological or psychiatric disorders such as schizophrenia,  
 PT schizoaffective disorder, bipolar or unipolar affective disorder, or  
 PT adolescent conduct disorder -  
 XX  
 PS Claim 11, Fig 1A; 99p; English.  
 CC The present sequence is that of cDNA clone y1176 (deposited as  
 CC ATCC PTA-21715) encoding a novel human metabotropic glutamate  
 CC receptor subtype modulatory protein (mglur5m). The cDNA was  
 CC isolated from a human brain cDNA library. Expression of mglur5m  
 CC is predominant in cells and tissues of the central nervous system.  
 CC The gene maps to a region of chromosome 11 associated with  
 CC schizophrenia and related psychiatric disorders. The invention  
 CC provides mglur5m polypeptides and nucleic acids, and methods for  
 CC their detection, as well as methods for using them to identify  
 CC compounds that modulate metabotropic receptor (mglur) activity.  
 CC Such modulators include a mglur5m nucleic acid, a mglur5m antibody,  
 CC a ribozyme, an antisense oligonucleotide, a small molecule  
 CC modulator, a peptide and a peptidomimetic. They can be used in a  
 CC claimed method for treating a subject having a neurological  
 CC disorder, especially a psychiatric disorder selected from  
 CC schizophrenia, schizoaffective disorder, bipolar affective disorder,  
 CC unipolar affective disorder or adolescent conduct disorder (all  
 CC claimed). mglur5m polypeptides, nucleic acids and antibodies are  
 CC also useful for screening assays, and in predictive medicine, e.g.  
 CC diagnostic assays (e.g. chromosome mapping and tissue typing),  
 CC prognostic assays, monitoring clinical trials, and pharmacogenomics.  
 CC  
 XX  
 SO Sequence 1823 BP; 488 A; 397 C; 444 G; 493 T; 1 other;  
 Query Match 100.0%; Score 1822.6; DB 24; Length 1823;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1823; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 DB 1 AAAATGCTCTTCTGTTGATCTGTCAGTCTTACTTTTGAAGAAGATGCCGAGAGT 60  
 QY 61 GCACAGTCCAGTGAAGAGAGGGTGGTGCACATGCTGGGTGACATCATTTATGAGCT 120  
 DB 61 GCACAGTCCAGTGAAGAGAGGGTGGTGCACATGCTGGGTGACATCATTTATGAGCT 120  
 QY 121 CTCCTTTCTGTTCACTACACAGCTACTGTGAGCAGAGTTCAATGAGAGAGTGGGCA 180  
 DB 121 CTCCTTTCTGTTCACTACACAGCTACTGTGAGCAGAGTTCAATGAGAGAGTGGGCA 180  
 QY 121 CTCCTTTCTGTTCACTACACAGCTACTGTGAGCAGAGTTCAATGAGAGAGTGGGCA 180  
 DB 121 CTCCTTTCTGTTCACTACACAGCTACTGTGAGCAGAGTTCAATGAGAGAGTGGGCA 180  
 QY 181 GTCCTGGAACAGTATGAGTTCAGAGAGTGAAGGCGCATGTGCTACCTCGAGAAAGATC 240  
 DB 181 GTCCTGGAACAGTATGAGTTCAGAGAGTGAAGGCGCATGTGCTACCTCGAGAAAGATC 240  
 QY 241 AATTGACAGCCCACTCTTGCCCAATCACTGGGCTGTGAGATAAGGAGTTCTGTC 300  
 DB 241 AATTGACAGCCCACTCTTGCCCAATCACTGGGCTGTGAGATAAGGAGTTCTGTC 300  
 QY 301 TGGCATTCGGCTGGGCGCTTAGAGCAGAGCATTTGATTAAGAGATTCCCTCATTTCT 360  
 DB 301 TGGCATTCGGCTGGGCGCTTAGAGCAGAGCATTTGATTAAGAGATTCCCTCATTTCT 360  
 QY 361 TCGGAAGAGAGAGGCGCTTGATGCTGTGTGATGAGTGCCTCTTCCCTCCGCTCC 420

DB 361 TCGGAAGAGAGAGGCGCTTGATGCTGTGTGATGAGTGCCTCTTCCCTCCGCTCC 420  
 QY 421 AAGAGCCCAATGATAGAGGGTCAATTGGGCTGGTTCAGATTCTTTAGCCATTCAGTCCAG 480  
 DB 421 AAGAGCCCAATGATAGAGGGTCAATTGGGCTGGTTCAGATTCTTTAGCCATTCAGTCCAG 480  
 QY 481 AATTGCTCAGATTTTCAACATPACTCAGATTGCTTACTCAGCAACCATATGATATCG 540  
 DB 481 AATTGCTCAGATTTTCAACATPACTCAGATTGCTTACTCAGCAACCATATGATATCG 540  
 QY 541 AGTGAACAAGCTCTGTTCAAAATATTTATGAGAGGTGTGCTTCAGATGCTCAGAGGCA 600  
 DB 541 AGTGAACAAGCTCTGTTCAAAATATTTATGAGAGGTGTGCTTCAGATGCTCAGAGGCA 600  
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 DB 601 AGGTCCATGATGAGCACTATGTAAGAGGTCAACTGACCTATATGATCAGCCGTACACA 660  
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 QY 721 AATTGATGCGCCCACTCTTACAAATCTACATATGATGAGAGGAGAGGAGCTTTGATAG 780  
 DB 721 AATTGATGCGCCCACTCTTACAAATCTACATATGATGAGAGGAGAGGAGCTTTGATAG 780  
 QY 781 CTGCTGAAGAGTCAAGAGTCACTTCCCAAGGCCCGGAGTGTGCTTACTCTGTAG 840  
 DB 781 CTGCTGAAGAGTCAAGAGTCACTTCCCAAGGCCCGGAGTGTGCTTACTCTGTAG 840  
 QY 841 GGCATGACGTTGAGAGTCTGCTGATGAGCCATGAGGCGCTGGGTATGAGGAAGATT 900  
 DB 841 GGCATGACGTTGAGAGTCTGCTGATGAGCCATGAGGCGCTGGGTATGAGGAAGATT 900  
 QY 901 CTGCTTCTGGGCGAGGAAACAGATGCACTTTATTTAGATCTCAAGAACACATCTCTA 960  
 DB 901 CTGCTTCTGGGCGAGGAAACAGATGCACTTTATTTAGATCTCAAGAACACATCTCTA 960  
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 QY 1141 AATGAAGCAACAGTATATCTTCTGATGAGATTTGAGAAAGATTGATTTGAGATGT 1200  
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 DB 1201 GACCTGCAAAATGCGCCCATATCATCTGCAACACCTCAAGTTTCTTGATAGGGTGTCT 1260  
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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(Without alignments)  
9369.765 Million cell updates/sec

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Scoring table: IDENTITY\_NIC  
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1822.6	100.0	1823	24	ABV73899 Human glutamate re
2	1802.6	98.9	2172	22	AAE29993 Human GRM4-1e DNA.
3	1787.6	98.1	1788	24	AAE29993 Human GRM4-1e DNA.
4	1746.6	95.8	2149	22	AAE29994 Human GRM4-1f DNA.
5	1615.6	88.6	2349	22	AAE29990 Human GRM4-1b DNA.
6	1576.6	86.5	2064	22	AAE29995 Human GRM4-1c DNA.
7	1559.6	85.6	2336	22	AAE29991 Human GRM4-1c DNA.
8	1413.6	77.5	2551	22	AAE29989 Human GRM4-1a DNA.

9	1389.6	76.2	2241	22	AAE29992
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11	891.4	48.9	4207	22	AAE04990
12	891.4	48.9	4207	22	AAE05029
13	891.4	48.9	4207	22	AAE05030
14	891.4	48.9	4207	22	AAE05033
15	891.4	48.9	4303	22	AAE04991
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22	888.2	48.7	4085	16	AAE080421
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24	754.4	41.4	3591	20	AAE210801
25	739.4	40.6	3918	20	AAE210803
26	715.6	39.3	2163	23	AAE21449
27	715.6	39.3	2163	23	AAE21449
28	458.2	25.1	2634	23	AAE27267
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30	458.2	25.1	3321	16	AAE080416
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33	458.2	25.1	6619	25	AAE242689
34	449.2	24.6	3219	18	AAE242689
35	449.2	24.6	3384	18	AAE242689
36	449.2	24.6	4300	13	AAE25812
37	449.2	24.6	5236	13	AAE25815
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#### ALIGNMENTS

RESULT 1	ABV73899	standard; cDNA, 1823 BP.
ID	ABV73899	
XX	ABV73899;	
AC	ABV73899;	
XX	08-JAN-2003 (first entry)	
DT	08-JAN-2003 (first entry)	
XX		
DE	Human glutamate receptor modulatory protein mglur5m cDNA.	
XX		
KW	Metabotropic glutamate receptor subtype 5 modulatory protein;	
KW	mglur5m; human; G-protein coupled receptor; receptor; schizophrenia;	
KW	schizophrenia; bipolar affective disorder; adolescent conduct disorder;	
KW	unipolar affective disorder; neuroleptic; neuroleptic; chromosome 11;	
KW	neuroleptic; neuroleptic; neuroleptic; chromosome 11;	
KW	gene therapy; gene; ss.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
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FT		/tag= c
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PN	MO200270708-A2.	
XX		



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Db 448 TGGCATTCGGCTGAGCCCTAGACAGACATGATTGATTAAGATTCCTCATTTCT 507
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Db 508 TCAGAAAGAGAGAGAGGCTTGATAGCTGTGTGTGATGAGGCTCTCTCTCCGCTCC 567
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QY 421 AAGAAGCCCATAGAGGGGCTATGGGCTGTCCAGTTCTTAAGCCATTCAAGTCCAG 480
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Db 568 AAGAAGCCCATAGAGGGGCTATGGGCTGTCCAGTTCTTAAGCCATTCAAGTCCAG 627
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QY 481 AATTGCTCCAGCTTTCAACATACCTCAAGTTGCTTACTACAGCAACCATCATGATCTG 540
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Db 628 AATTGCTCCAGCTTTCAACATACCTCAAGTTGCTTACTACAGCAACCATCATGATCTG 687
   |||||
QY 541 AGTGACAAGACTCTGTTCAAAATATTTGATGAGGGTTGTGCTTCAGATGCTCAGCAGCA 600
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Db 688 AGTGACAAGACTCTGTTCAAAATATTTGATGAGGGTTGTGCTTCAGATGCTCAGCAGCA 747
   |||||
QY 601 AGGTCCATGTGTGACATAGTGAAGAGGTACACCTGACCTATGTATCAGCCGTACACACA 660
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Db 748 AGGCCCATGTGTGACATAGTGAAGAGGTACACCTGACCTATGTATCAGCCGTGACACA 807
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QY 661 GAAGGCAACTATGGAAGAAAGTGGATGAAAGCCTTCAAGATATGTCAGGGAAGGAAGG 720
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Db 808 GAAGGCAACTATGGAAGAAAGTGGATGAAAGCCTTCAAGATATGTCAGGGAAGGAAGG 867
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QY 721 AATTGATGCCCCACTCTTTAATAAATCTACATATGACAGGGAGACAGAGCTTTGATTAAG 780
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Db 868 AATTGATGCCCCACTCTTTAATAAATCTACATATGACAGGGAGACAGAGCTTTGATTAAG 927
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QY 781 CTGCTGAAGAAGCTCAAAAGTCACTTGTCCCAAGGCCCGGGTGTGGCTTACTTCTGTAG 840
   |||||
Db 928 CTGCTGAAGAAGCTCAAAAGTCACTTGTCCCAAGGCCCGGGTGTGGCTTACTTCTGTAG 987
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QY 841 GGCATGACGGGTGAGAGGCTGTGATGAGCCATGAGGGGCTGGGCTTAAGTGGAGAAATTT 900
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Db 988 GGCATGACGGGTGAGAGGCTGTGATGAGCCATGAGGGGCTGGGCTTAAGTGGAGAAATTT 1047
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Search completed: December 14, 2003, 13:24:23  
Job time : 6914.99 secs

Db 1297 GGCATGACGGGTGAGAGTCTGCTGATGGCCATGAGGCGCTGGTCTAGCGGAGAAATTT 1356  
QY 901 CTGCTTCTGGGACAGGA 917  
Db 1357 CTGCTTCTGGGACAGTA 1373

RESULT 14  
ARI45367  
LOCUS ARI45367 4303 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 6 from patent US 6211353.  
ACCESSION ARI45367  
VERSION ARI45367.1 GI:15107234  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 4303)  
AUTHORS Burnette,J.Paul, Jr., Mayne,N.Gall., Sharp,R.Leon. and Snyder,Y.Marie.  
TITLE Isolated nucleic acid encoding a human mgluR5  
JOURNAL Patent: US 6211353-A 6 03-APR-2001;  
FEATURES Location/Qualifiers  
source 1..4303  
BASE COUNT 1043 a 1139 c 1144 g 977 t

Query Match 48.9%; Score 891.4; DB 6; Length 4303;  
Best Local Similarity 98.3%; Pred. No. 2.6e-226;  
Matches 901; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1 AAAATGCTCTTCTGTTGATCTGTCACTCTTACTTTTGAAGAAGATGTCCTGGAGT 60  
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QY 61 GCACAGTCAGTGAAGAGAGGTGGTGCACATGCTGGGTGACATCATTTATTTGAGCT 120  
Db 517 GCACAGTCAGTGAAGAGAGGTGGTGCACATGCTGGGTGACATCATTTATTTGAGCT 576  
QY 121 CTCTTTCTGTTGATCAACAGCCTACTGTGAGCAGAACTTATGATGAGAGAGTGGGCA 180  
Db 577 CTCTTTCTGTTGATCAACAGCCTACTGTGAGCAGAACTTATGATGAGAGAGTGGGCG 636  
QY 181 GTCCGTGAACATGATGAGATTCAGAGAGTGAAGGCCATGCTGCTTACCTCTGAAAGATC 240  
Db 637 GTCCGTGAACATGATGAGATTCAGAGAGTGAAGGCCATGCTGCTTACCTCTGAAAGATC 696  
QY 241 AATTGAGCCCACTCTTGCCCAATCACTGGGCTGTGATTAAGGAGATTCCCTGC 300  
Db 697 AATTGAGCCCACTCTTGCCCAATCACTGGGCTGTGATTAAGGAGATTCCCTGC 756  
QY 301 TGGCATTCGGCTGTGGCCTTAGACAGACAGATTGAGTTCAATAGAGATTCCTCATTTCT 360  
Db 757 TGGCATTCGGCTGTGGCCTTAGACAGACAGATTGAGTTCAATAGAGATTCCTCATTTCT 816  
QY 361 TCGAAGAGAGAGAGGCTTGGTATGCTGTGAGATGCTCTCTCTTCTCCGCTCC 420  
Db 817 TCGAAGAGAGAGAGGCTTGGTATGCTGTGAGATGCTCTCTCTTCTCCGCTCC 876  
QY 421 AAGAAGCCCATGATAGAGGGGTCAATTGGGCTGGTCCAGTTCTTAGCCATTCAAGTCCAG 480  
Db 877 AAGAAGCCCATGATAGAGGGGTCAATTGGGCTGGTCCAGTTCTTAGCCATTCAAGTCCAG 936  
QY 481 AATTGCTCCAGCTTTTCAACATACCTCAGATTGCTTACTCAGAACCATCATGATCTG 540  
Db 937 AATTGCTCCAGCTTTTCAACATACCTCAGATTGCTTACTCAGAACCATCATGATCTG 996  
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Db 997 AGTGAACAAGACTCTGTCTCAAAATATTTCATGAGGGTGTGCTTCAAGTCTCAGAGCA 1056  
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Db 1057 AGGGCCATGTGTGACATATGTGAAGGTATCAATGTGACCTTAGTATCACCGGTGACACACA 1116  
QY 661 GAAGGCACTATGAGAGAAAGTGGATGAAAGCTTTCAAAAGATATGTACAGGAAAGAGG 720  
Db 1117 GAAGGCACTATGAGAGAAAGTGGATGAAAGCTTTCAAAAGATATGTACAGGAAAGAGG 1176  
QY 721 AATTGATGCGCCCACTTACAAAATCTACAGTAATGACGGGAGCAGAGCTTGTATAG 780  
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QY 781 CTGCTGAAGAGCTCAACAGTCACTTGCCCAAGCCCGGGTGTGCTTACTTCTGTAG 840  
Db 1237 CTGCTGAAGAGCTCAACAGTCACTTGCCCAAGCCCGGGTGTGCTTACTTCTGTAG 1296  
QY 841 GGCATGACGGTGAAGAGTCTGCTGATGGCCATGAGAGCGCTCGGCTTACTGAGAAATTT 900  
Db 1297 GGCATGACGGTGAAGAGTCTGCTGATGGCCATGAGAGCGCTCGGCTTACTGAGAAATTT 1356  
QY 901 CTGCTTCTGGGACAGGA 917  
Db 1357 CTGCTTCTGGGACAGTA 1373

RESULT 15  
AX548892  
LOCUS AX548892 4518 bp DNA linear PAT 26-NOV-2002  
DEFINITION Sequence 177 from Patent W002061087.  
ACCESSION AX548892  
VERSION AX548892.1 GI:25813755  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Burner,G.C., Roush,C.L. and Brown,J.P.  
TITLE Antigenic peptides, such as for G protein-coupled receptors (GPCRs), antibodies thereto, and systems for identifying such antigenic peptides  
JOURNAL Patent: WO 02061087-A 177 08-AUG-2002;  
FEATURES Location/Qualifiers  
source 1..4518  
BASE COUNT 1114 a 1170 c 1145 g 1089 t

Query Match 48.9%; Score 891.4; DB 6; Length 4518;  
Best Local Similarity 98.3%; Pred. No. 2.6e-226;  
Matches 901; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1 AAAATGCTCTTCTGTTGATCTGTCACTTACTTTTGAAGAAGATGTCCTGGAGT 60  
Db 148 AAAATGCTCTTCTGTTGATCTGTCACTTACTTTTGAAGAAGATGTCCTGGAGT 207  
QY 61 GCACAGTCAGTGAAGAGAGGTGGTGCACATGCTGGGTGACATCATTTATTTGAGCT 120  
Db 208 GCACAGTCAGTGAAGAGAGGTGGTGCACATGCTGGGTGACATCATTTATTTGAGCT 267  
QY 121 CTCTTTCTGTTGATCAACAGCCTACTGTGAGAGAACTTATGAGAGAAAGTGGGCA 180  
Db 268 CTCTTTCTGTTGATCAACAGCCTACTGTGAGAGAACTTATGAGAGAAAGTGGGCG 327  
QY 181 GTCCGTGAACATGATGAGATTCAGAGAGTGAAGGCCATGCTGATACCTCTGAAAGATC 240  
Db 328 GTCCGTGAACATGATGAGATTCAGAGAGTGAAGGCCATGCTGATACCTCTGAAAGATC 387  
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Db 61 GCACAGTCCAGTGAAGAGAGGAGTGTGCTCACTGCTGGGTGACATCATTAATTGAGCT 516  
QY GCACAGTCCAGTGAAGAGAGGAGTGTGCTCACTGCTGGGTGACATCATTAATTGAGCT 516  
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QY CTCTTTTCTGTTCAATCAAGCCTTCTGTGACGAAAGTTGATGAGAGAAAGTGTGGGCA 180  
Db 577 CTCTTTTCTGTTCAATCAAGCCTTCTGTGACGAAAGTTGATGAGAGAAAGTGTGGGCG 636  
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Db 181 GTCCGGAACAGTATGAGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATC 240  
QY GTCCGGAACAGTATGAGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATC 696  
Db 637 GTCCGGAACAGTATGAGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATC 696  
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Db 757 TGGCATTCGGCTGTGAGCCTTAAGAGAGAGAGATTAAGATTCCTGATTCCTCATTTCT 816  
QY TCGGAAG 420  
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QY TCGGAAG 421  
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Db 877 AAGAAAGCCCACTAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 936  
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Db 481 AATTGCTCCAGCTTTTCAACATACCTCAGATTGCTTACTGACCAACAGCATGATCTG 937  
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Db 997 AAGTGAACAAGCTGTGTTCAAAATTTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1057  
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RESULT 13  
LOCUS ARI45366 4303 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 4 from Patent US 6211353.  
ACCESSION ARI45366  
VERSION ARI45366.1 GI:15107233  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.

Db 457 AAAATGCTCTTCTGTTGATCTGTGACGTCTTAATTGAAAGAAATGTCGGTGGAGT 516  
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QY GCACAGTCCAGTGAAGAGAGGAGTGTGCTCACTGCTGGGTGACATCATTAATTGAGCT 516  
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Db 361 TCGGAAG 817  
QY TCGGAAG 421  
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REFERENCE 1 (bases 1 to 4303)  
AUTHORS Burnett,J.Paul., Jr., Mayne,N.Gail., Sharp,R.Leon. and Snyder Y.Marie.  
TITLE Isolated nucleic acid encoding a human mGLURS  
JOURNAL Patent: US 6211353-A 4 03-APR-2001;  
FEATURES  
Source Location/Qualifiers  
1. 4303  
BASE COUNT 1044 a 1138 c 1144 g 977 t  
ORIGIN

Query Match 48.9%; Score 891.4; DB 6; Length 4303;  
Best Local Similarity 98.3%; Pred. No. 2.6e-226;  
Matches 901; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1 AAAATGCTCTTCTGTTGATCTGTGACGTCTTAATTGAAAGAAATGTCGGTGGAGT 60  
Db 457 AAAATGCTCTTCTGTTGATCTGTGACGTCTTAATTGAAAGAAATGTCGGTGGAGT 516  
QY GCACAGTCCAGTGAAGAGAGGAGTGTGCTCACTGCTGGGTGACATCATTAATTGAGCT 120  
Db 61 GCACAGTCCAGTGAAGAGAGGAGTGTGCTCACTGCTGGGTGACATCATTAATTGAGCT 516  
QY GCACAGTCCAGTGAAGAGAGGAGTGTGCTCACTGCTGGGTGACATCATTAATTGAGCT 516  
Db 121 CTCTTTTCTGTTCAATCAAGCCTTCTGTGACGAAAGTTGATGAGAGAAAGTGTGGGCA 180  
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Db 577 CTCTTTTCTGTTCAATCAAGCCTTCTGTGACGAAAGTTGATGAGAGAAAGTGTGGGCG 636  
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QY 841 GGCATACCGGTGAGAGGTCTGCTGATGAGCCATGAGAGGCTTGGGTCTAGTGGAGAAATT 900
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QY 901 CTGCTTCTGGGACAGGA 917
Db 1048 CTGCTTCTGGGACAGTGA 1064
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RESULT 11
ARI45364 4207 bp DNA linear PAT 08-AUG-2001
LOCUS Sequence 1 from patent US 6211353.
DEFINITION ARI45364
ACCESSION ARI45364
VERSION ARI45364.1 GI:15107231
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4207)
AUTHORS Burnette,J.Paul, Jr., Mayne,N.Gail., Sharp,R.Leon. and
Snyder,Y.Marie.
TITLE Isolated nucleic acid encoding a human mglur5
JOURNAL Patent: US 6211353-A 1 03-APR-2001;
FEATURES
Source 1. .4207
Location/Qualifiers
/organism="unknown"
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BASE COUNT 1011 a 1120 c 1112 g 964 t
ORIGIN
Query Match 48.9%; Score 891.4; DB 6; Length 4207;
Best Local Similarity 98.3%; Pred. No. 2.5e-226;
Matches 901; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
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QY 1 AAAATGGTCTTCTGTTGATCTGTGATCTGTGATCTTACTTTTGAAGAAGATGCCGTGGAGT 60
Db 457 AAAATGGTCTTCTGTTGATCTGTGATCTTACTTTTGAAGAAGATGCCGTGGAGT 516
QY 61 GCACAGTCCAGTGAAGAGAGGGTGGTGCACATGCTGGGTGACATCATTTATTTGAGCT 120
Db 517 GCACAGTCCAGTGAAGAGAGGGTGGTGCACATGCTGGGTGACATCATTTATTTGAGCT 576
QY 121 CTCTTTTCTGTTTATCATCCAGCCCTACTGTGAGCAAAATTTCATGAGAGAAAGTGTGGGCA 180
Db 577 CTCTTTTCTGTTTATCATCCAGCCCTACTGTGAGCAAAATTTCATGAGAGAAAGTGTGGGCA 636
QY 181 GTCGCTGAACAGTATGAGCATTTACAGAGTGAAGGCAATGCTGACATCCCTGAAAAGATC 240
Db 637 GTCGCTGAACAGTATGAGCATTTACAGAGTGAAGGCAATGCTGACATCCCTGAAAAGATC 696
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Db 1177 ATTTGATGCGCCACTCTTCAAAATCTACATATGACAGGAGCAGACCTTTGATAG 1236
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Db 1237 CTGCTGAAGAAGTCAACAAGTCACTTGCCCAAGGCCCGGGTGGTGTGCTTCTGTAG 1296
QY 841 GGCATACCGGTGAGAGGTCTGCTGATGAGCCATGAGAGGCTTGGGTCTAGTGGAGAAATT 900
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ARI45365 4207 bp DNA linear PAT 08-AUG-2001
LOCUS Sequence 3 from patent US 6211353.
DEFINITION ARI45365
ACCESSION ARI45365
VERSION ARI45365.1 GI:15107232
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4207)
AUTHORS Burnette,J.Paul, Jr., Mayne,N.Gail., Sharp,R.Leon. and
Snyder,Y.Marie.
TITLE Isolated nucleic acid encoding a human mglur5
JOURNAL Patent: US 6211353-A 3 03-APR-2001;
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Location/Qualifiers
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 ACCESSION AR270570  
 VERSION AR270570.1 GI:29701804  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 4078)  
 AUTHORS Au-Young,J. and Sellhammer,J.J.  
 TITLE Composition for the detection of signaling pathway gene expression  
 JOURNAL Patent: US 6500938-A 1133 31-DEC-2002;  
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 Best Local Similarity 98.3%; Pred. No. 2.5e-226;  
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 QY 181 GTCCGGAACAGATGAG 240  
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 QY 361 TCGGAAG 420  
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 LOCUS AX068371  
 DEFINITION Sequence 6 from Patent WO0102566.  
 ACCESSION AX068371  
 VERSION AX068371.1 GI:12578536  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE  
 AUTHORS Schwarz, D.A. and Maki, R.A.  
 TITLES Metabotropic glutamate receptors and methods of use therefor  
 JOURNAL Patent: WO 0102566-A 6 11-JAN-2001;  
 Neurocrine Biosciences, Inc. (US)  
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 Best Local Similarity 85.4%; Pred. No. 0;  
 Matches 1697; Conservative 1; Mismatches 5; Indels 285; Gaps 2;  
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DEFINITION	Sequence 1 from Patent WO010256.
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VERSION	AX068366.1
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KEYWORDS	.
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DNA	linear
PAT	25-JAN-2001

REFERENCE	Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
AUTHORS	1
TITLE	Schwarz, D.A. and Makl, R.A.
JOURNAL	Metabotropic glutamate receptors and methods of use therefor
FEATURES	Patent: WO 0102566-A 1 11-JUN-2001; Neurocrine Biosciences, Inc. (US)
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121 CTCCTTCTGTCATCACGACCTACTGTGACGAAGTTCATGACAGGAAGTGTGGGGCA 180

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 REFERENCE 1  
 AUTHORS Schwarz, D.A. and Maki, R.A.  
 TITLES Weledotopic glutamate receptors and methods of use therefor  
 JOURNAL Patent: WO 0102566-A 5 11-JAN-2001;  
 Neurocrine Biosciences, Inc. (US)  
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QY 1324 TTCCGTTTGTAAATAGTACGAAAGGAGATCAGATGGAATATATATGAGAG 1383  
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QY 1384 GAGGACCTTTTATAGTCTTGAGATTTTAAAGCAATTCAGTCACTTTTACACC 1443  
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DB 2342 AAAAAA 2349

RESULT 5  
AX068376  
LOCUS AX068376 2064 bp DNA linear PAT 25-JAN-2001  
DEFINITION Sequence 11 from Patent WO01025566.  
ACCESSION AX068376  
VERSION AX068376.1 GI:12578539  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1  
AUTHORS Schwarz,D.A. and Maki,R.A.  
TITLE Metabotropic glutamate receptors and methods of use therefor  
JOURNAL Patent: WO 0102556-A 11 11-JAN-2001;  
Neurocrine Biosciences, Inc. (US)  
FEATURES  
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BASE COUNT 518 a 466 c 519 g 561 t  
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Matches 1697; Conservative 1; Mismatches 5; Indels 108; Gaps 1;

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QY 181 GTCCGTGAACAGTATGAGCTTCAAGAGTGAAGGCCATCTGCTATCCCTGAAAGATC 240  
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DB 662 TGGCATTTGGCTGTGGCCCTTGAAGCAGAGCATTTGATTAAGATTCCTCATTTCT 721  
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DB 962 AGTCAATGATGACATGATGAAGAGTCACTGCACTTATCTACAGCCGATCAACACA 1021  
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RESULT 4  
LOCUS AX068368 2349 bp DNA linear PAT 25-JAN-2001  
DEFINITION Sequence 3 from Patent WO0102566.  
ACCESSION AX068368  
VERSION AX068368.1 GI:12578534  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1  
AUTHORS Schwarz, D.A. and Maki, R.A.  
TITLE Metabotropic glutamate receptors and methods of use therefor  
JOURNAL Patent: WO 0102566-A 3 11-JAN-2001;  
Neurocrine Biosciences, Inc. (US)  
FEATURES  
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BASE COUNT 588 a 538 c 586 g 637 t  
ORIGIN

Query Match 88.6%; Score 1615.6; DB 6; Length 2349;  
Best Local Similarity 90.8%; Pred. No. 0;  
Matches 1805; Conservative 1; Mismatches 5; Indels 177; Gaps 1;

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RESULT 3  
AX068374 2149 bp DNA linear PAT 25-JAN-2001  
LOCUS AX068374 Sequence 9 from Patent WO0102566.  
ACCESSION AX068374  
VERSION AX068374.1 GI:12578538  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
  
REFERENCE 1  
AUTHORS Schwarz, D.A. and Maki, R.A.  
TITLE Metabotropic glutamate receptors and methods of use therefor  
JOURNAL Patent: WO 0102566-A 9 11-JAN-2001;  
Neurocrine Biosciences, Inc. (US)  
FEATURES  
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Matches 1782; Conservative 1; Mismatches 5; Indels 23; Gaps 1;  
  
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Db 362 AAAATGCTCTTCTGTTGATCTGTCACTCTTACTTTTGAAGAAAGTCCGAGAGT 421  
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RESULT 2  
AX068372 2172 bp DNA linear PAT 25-JAN-2001  
LOCUS AX068372  
DEFINITION Sequence 7 from Patent WO0102566.  
ACCESSION AX068372  
VERSION AX068372.1 GI:12578537  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS Schwarz, D.A. and Maki, R.A.  
TITLE Metabotropic glutamate receptors and methods of use therefor  
JOURNAL Patent: WO 0102566-A 7 11-JAN-2001;  
Neuroscience Biociences, Inc. (US)  
FEATURES  
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ORIGIN

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GenCore version 5.1.6  
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## OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues  
Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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DEFINITION Sequence 1 from Patent WO02070708.  
ACCESSION AX709347  
VERSION AX709347.1 GI:29564889  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Bukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS Bates,B.G., Xie,Y., Gulukota,K. and Paulsen,J.B.  
TITLE Glutamate receptor modulatory proteins and nucleic acids encoding them



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 1 (bases 1 to 268)  
 AUTHORS Alfrey, C., Behar, G., Bois, F., Bouchier, C., da Silva, C., Devignes, M.D., Duprat, S., Hougatte, R., Dumau, M.N., Lam, B., Lorenzo, F., Mitchell, H., Mariage-Samson, R., Pletu, G., Pouliot, Y., Sebasteian-Kabackich, C. and Tessier, A.  
 TITLE IMAGE: molecular integration of the analysis of the human genome and its expression  
 JOURNAL C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)  
 MEDLINE 95277534  
 PUBMED 7757816  
 COMMENT Contact: Genethon  
 Genexpress-Genethon  
 Genethon Centre de recherche sur le Genome Humain  
 1 rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE  
 Tel: 33169472800  
 Fax: 33160778698  
 Email: genexpress@genethon.fr  
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 VERSION BX282658  
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 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 516)  
 AUTHORS Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M., Radetof, U., Schneider, D. and Korn, B.  
 TITLE Human Unigeneset - RZPD3

JOURNAL Unpublished  
 COMMENT Contact: Ina Rolfs  
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
 Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany  
 RZPD; IMAGp9860711417.  
 RZPDLIB; I.M.A.G.B. CDNA Clone Collection;  
 Human Unigeneset - RZPD3 (RZPDLIB No.972)  
 http://www.rzpd.de/CloneCards/cgi-bin/showlib.pl/cgi/response?libNo=972 Contact: Ina Rolfs  
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
 Heubnerweg 6, D-14059 Berlin, Germany  
 Tel: +49 30 32639 101  
 Fax: +49 30 32639 111  
 www.rzpd.de  
 This clone is available royalty-free from RZPD;  
 contact RZPD (clone@rzpd.de) for further information. Seq primer:  
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 Job time: 4166.78 secs

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ACCESSION AF55261.1 GI:4739240

VERSION AF55261.1

KEYWORDS EST.

SOURCE Homo sapiens

ORGANISM Homo sapiens (human)

REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 455)

AUTHORS Ebert, L., Hell, O., Hennig, S., Neubert, P., Paruch, E., Peters, M., Radelof, U., Schneider, D. and Korn, B.

TITLE Human UnigeneSet - RZPD3

JOURNAL Unpublished

COMMENT Contact: Ina Rolfs  
RZPD Deutsches Reassoizenzentrum fuer Genomforschung GmbH  
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany  
RZPD; IMAGP998A225727.  
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;  
http://www.rzpd.de/CloneCards/cgi-bin/shwLib.pl.cgi/responseLibNo=972 Contact: Ina Rolfs  
RZPD Deutsches Reassoizenzentrum fuer Genomforschung GmbH  
Heubnerweg 6, D-14059 Berlin, Germany  
Tel: +49 30 32639 101  
Fax: +49 30 32639 111  
www.rzpd.de  
This clone is available royalty-free from RZPD; contact RZPD (clone@rzpd.de) for further information. Seq primer: M13r. Primer sequence: TTTCACACAGGAAACGCTATGAC.

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BASE COUNT 138 a 82 c 111 g 124 t

ORIGIN

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DEFINITION BX116917 NCI CGAP GC6 Homo sapiens cDNA clone IMAGE:2310813, mRNA sequence.  
ACCESSION BX116917  
VERSION BX116917.1 GI:27840301

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 494)

AUTHORS Ebert, L., Hell, O., Hennig, S., Neubert, P., Paruch, E., Peters, M., Radelof, U., Schneider, D. and Korn, B.

TITLE Human UnigeneSet - RZPD3

JOURNAL Unpublished

COMMENT Contact: Ina Rolfs  
RZPD Deutsches Reassoizenzentrum fuer Genomforschung GmbH  
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany  
RZPD; IMAGP998A225727.  
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;  
http://www.rzpd.de/CloneCards/cgi-bin/shwLib.pl.cgi/responseLibNo=972 Contact: Ina Rolfs  
RZPD Deutsches Reassoizenzentrum fuer Genomforschung GmbH  
Heubnerweg 6, D-14059 Berlin, Germany  
Tel: +49 30 32639 101  
Fax: +49 30 32639 111  
www.rzpd.de  
This clone is available royalty-free from RZPD; contact RZPD (clone@rzpd.de) for further information. Seq primer: M13r. Primer sequence: TTTCACACAGGAAACGCTATGAC.

FEATURES  
source  
1.494  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/clone="IMAGP998A225727 ; IMAGE:2310813"  
/tissue\_type="pooled germ cell tumors"  
/lab\_host="DH10B"  
/note="Vector: pTRT3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA from the normalized library NCI CGAP GC6 was prepared, and 86 clones were made in vitro. Following HAP purification, this DNA was used as tracer in a subtracive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clones 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 118 a 118 c 105 g 153 t

ORIGIN

Query Match 5.9%; Score 107; DB 13; Length 494;  
Best Local Similarity 99.4%; Pred. No. 0;  
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1451 TTACACTGCAAGTATGTCCTCAAGACCTACCAACATGATGATTAATTCCTGATTTGAAG 1510  
DB 210 TTACACTGCAAGTATGTCCTCAAGACCTACCAACATGATGATTAATTCCTGATTTGAAG 269

QY 1511 CTGAACCTGAGAGCTTGTGATGATTAATCAAGCTCCCTATATACCAATCCCTAATT 1570  
DB 270 CTGAACCTGAGAGCTTGTGATGATTAATCAAGCTCCCTATATACCAATCCCTAATT 329

QY 1571 GCTCCTTTCACCTCTCTCAGGACCTATCTTTGCTGT 1608  
DB 330 GCTCCTTTCACCTCTCTCAGGACCTATCTTTGCTGT 367

RESULT 14  
LOCUS F05449 268 bp mRNA linear EST 19-FEB-1995  
DEFINITION HSC08C11 normalized infant brain cDNA Homo sapiens cDNA clone c-0bc11, mRNA sequence.  
ACCESSION F05449  
VERSION F05449.1 GI:669265  
KEYWORDS EST.  
SOURCE Homo sapiens (human)

QY 241 AATTGAGACCCACACTCTTGGCCCAATGACACTGGGCTGTGTGATGATTAAGGATTCCTGC 300  
 DB 608 AATTGAGACCCACACTCTTGGCCCAATGACACTGGGCTGTGTGATGATTAAGGATTCCTGC 667  
 QY 301 TGGCATTGGCTGTGGCCCTTGAAGACAGCATTTGATTCATTAAGATTTCCCTCATTTCT 360  
 DB 668 TGGCATTGGCTGTGGCCCTTGAAGACAGCATTTGATTCATTAAGATTTCCCTCATTTCT 727  
 QY 361 TC 362  
 DB 728 TC 729

RESULT 10  
 BI826234 664 bp mRNA linear EST 04-OCT-2001  
 LOCUS 603075928F1 NIH\_MGC\_119 Homo sapiens cDNA clone IMAGE:5167902 5',  
 DEFINITION mRNA sequence.

ACCESSION BI826234 GI:15937784  
 VERSION BI826234  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 1 (bases 1 to 664)  
 NIH-MGC http://mgs.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgabs-r@mail.nih.gov  
 Tissue Procurement: Life Technologies, Inc.  
 CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.lnl.gov  
 plate: LLAM1417 row: 9 column: 07  
 High quality sequence stop: 662.  
 Location/Qualifiers

## FEATURES

source

1. 664  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
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 /clone="IMAGE:5167902"  
 /tissue\_type="medulla"  
 /lab\_host="DH10B"  
 /clone\_1ib="NIH MGC 119"  
 /note="Organ: brain; Vector: PCWV-SPORT6; Site 1: NotI;  
 site\_2: EcoRV (destroyed); RNA source normal medulla from  
 anonymous male age 27. Library is oligo-dT primed and  
 directionally cloned (EcoRV site is destroyed upon  
 cloning). Average insert size 1.3 kb, insert size range  
 0.9-3 kb. Library is normalized and enriched for  
 full-length clones and was constructed by C. Gruber  
 (Invitrogen). Research Genetics tracking code 013. Note:  
 this is a NIH MGC library."  
 BASE COUNT 151 a 177 c 179 g 157 t  
 ORIGIN

Query Match 6.2%; Score 113; DB 12; Length 664;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 181 GTCCGTGAACAGATGATGATTCAGAGATGAGAGCCATGCTGATACCTGTGAAGATC 240  
 DB 547 GTCCGTGAACAGATGATGATTCAGAGATGAGAGCCATGCTGATACCTGTGAAGATC 606  
 QY 241 AATTGAGACCCACACTCTTGGCCCAATGACACTGGGCTGTGTGATGATTAAGGGA 293  
 DB 607 AATTGAGACCCACACTCTTGGCCCAATGACACTGGGCTGTGTGATGATTAAGGGA 659

RESULT 11  
 AI950429/c 452 bp mRNA linear EST 08-MAR-2000  
 LOCUS wq35601.x1 NCI CGAP GC6 Homo sapiens cDNA clone IMAGE:2473249 3',  
 DEFINITION similar to SW-BUTY\_HUMAN Q13410 BUTYROPHILIN PRECURSOR, mRNA  
 sequence.

ACCESSION AI950429 GI:5742739  
 VERSION AI950429  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 1 (bases 1 to 452)  
 NCI-CGAP http://www.nci.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgabs-r@mail.nih.gov  
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael  
 R. Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
 Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 www.bio.lnl.gov/btrp/image/image.html  
 Insert Length: 607 Std Error: 0.00  
 Seg primer: -40UP from Gibco.  
 Location/Qualifiers

## FEATURES

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 /clone="IMAGE:2473249"  
 /tissue\_type="pooled germ cell tumors"  
 /lab\_host="DH10B"  
 /clone\_1ib="NCI CGAP GC6"  
 /note="Vector: p773D-Pac (Pharmacia) with a modified  
 polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA  
 from the normalized library NCI CGAP GC4 was prepared, and  
 ss circles were made in vitro. Following HAP purification,  
 this DNA was used as tracer in a subtractive hybridization  
 reaction. The driver was PCR-amplified cDNAs from a pool  
 of 5,000 clones made from the same library (cloneids  
 1257096-1258631, 1469064-1470983, and 1475592-1476743).  
 Subtraction by Bento Soares and M. Fatima Bonaldo."  
 BASE COUNT 139 a 81 c 109 g 122 t 1 others  
 ORIGIN

Query Match 5.9%; Score 107; DB 9; Length 452;  
 Best Local Similarity 99.4%; Pred. No. 0;  
 Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1451 TTAACTGAGATGATGTCGAGAACCTTACCAACATGATGATTAATTCGTGATGTGAAG 1510  
 DB 349 TTAACTGAGATGATGTCGAGAACCTTACCAACATGATGATTAATTCGTGATGTGAAG 290  
 QY 1511 CTAGAACTGTGAGCTTCGTGATGATTAATCAAGCTCCCTTATATACACATCCCTAAT 1570  
 DB 289 CTAGAACTGTGAGCTTCGTGATGATTAATCAAGCTCCCTTATATACACATCCCTAAT 230  
 QY 1571 GCTCCTTCACTCCTCTCAGGCTATCTTTTGCTGT 1608  
 DB 229 GCTCCTTCACTCCTCTCAGGCTATCTTTTGCTGT 192

RESULT 12  
 AI655261/c 455 bp mRNA linear EST 17-DEC-1999  
 LOCUS AI655261



CB153433 449 bp mRNA linear EST 29-JAN-2003  
 LOCUS K-EST0210877 B1T694954 Homo sapiens cDNA clone B1T694954-28-C09 5',  
 DEFINITION mRNA sequence.  
 ACCESSION CB153433  
 VERSION CB153433.1 GI:28138427  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 449)  
 Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,  
 Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and  
 Kim, Y.S.  
 21C Frontier Korean EST Project 2001  
 TITLE Unpublished  
 JOURNAL Contact: Kim YS  
 COMMENT Genome Research Center  
 Korea Research Institute of Bioscience & Biotechnology  
 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea  
 Tel: +82-42-860-4470  
 Fax: +82-42-860-4409  
 Email: yonggun@kribb.re.kr  
 Plate: 28 row: C column: 09  
 High quality sequence stop: 449.  
 Location/Qualifiers  
 1..449  
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 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="B1T694954-28-C09"  
 /sex="M"  
 /lab\_host="Top10F"  
 /clone\_1b="B1T694954"  
 /note="Organ: Brain; Vector: PCNS-D2; Site: 1: EcoRI;  
 Site 2: NotI; The poly (A)+ RNA was dephosphorylated with  
 bacterial alkaline phosphatase (BAP) and then deacapped  
 with tobacco acid pyrophosphatase (TAP). The decapped  
 intact mRNA was ligated with RNA-RNA linker including  
 EcoRI site by treatment of T4 DNA ligase and the first  
 strand cDNA was synthesized from oligo dT-selected mRNA by  
 priming with dT-tailed vector. The dT-tailed vector was  
 adjusted to have about 60nt. The cDNA after digestion of  
 circularized with R. coli DNA ligase after digestion of  
 EcoRI which site is also included in vector. An RNA strand  
 converted to a DNA strand by Okayama-Berg method. The  
 obtained cDNA vectors were used for transfection of  
 competent cells R. coli Top10F by electroporation method.  
 The cDNA libraries constructed by this method are  
 full-length enriched cDNA library."  
 full-length enriched cDNA library."
 BASE COUNT 106 a 112 c 112 g 119 t  
 ORIGIN  
 Query Match 19.0%; Score 347; DB 14; Length 449;  
 Best Local Similarity 99.6%; Pred. No. 0;  
 Matches 447; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 123 CTTTCTGTCATCAGCAGCTCTGTCGACGATTCATGAGAGAGTGTGGGCACT 182  
 1 CTTTCTGTCATCAGCAGCTCTGTCGACGATTCATGAGAGAGTGTGGGCACT 60  
 183 CCGTGAACAGTATGAGCATTGAGAGAGAGGCGATGCTGCTGCTGCTGCTGCT 242  
 61 CCGTGAACAGTATGAGCATTGAGAGAGAGGCGATGCTGCTGCTGCTGCTGCT 120  
 243 TTGAGACCCACAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 302  
 121 TTGAGACCCACAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180  
 303 GCATTGGCTGTGGCCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 362  
 181 GCATTGGCTGTGGCCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240

363 GGAG 422  
 241 GGAG 300  
 423 GAAGCCATAGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 482  
 301 GAAGCCATAGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360  
 483 TTGCTCAGCTTTTCAACATACCTCAGATGCTTCTGAGCAACATCATGATGAG 542  
 361 TTGCTCAGCTTTTCAACATACCTCAGATGCTTCTGAGCAACATCATGATGAG 420  
 543 TGACAAAGCTCTGTTCAATATATTCATGA 571  
 421 TGACAAAGCTCTGTTCAATATATTCATGA 449

RESULT 7.  
 LOCUS AO313970/c 625 bp DNA linear GSS 04-MAY-1999  
 DEFINITION RPI11-103J21.TV RPI1-11 Homo sapiens genomic clone RPI1-11-103J21,  
 genomic survey sequence.  
 ACCESSION AO313970  
 VERSION AO313970.1 GI:4045433  
 KEYWORDS GSS.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 625)  
 Adams, M.D., Rounsley, S.D., Zhao, S., Baas, S., Linher, K., Golden, K.,  
 Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C.  
 Use of human BAC End Sequences for Sequence-Ready Map Building  
 Other GSSes: RPI11-103J21.T1  
 Contact: Shaying Zhao, William Nierman, Mark Adams  
 Department of Eukaryotic Genomics  
 The Institute for Genomic Research  
 9712 Medical Center Dr., Rockville, MD 20850  
 Tel: 301 838 0208  
 Fax: 301 838 0208  
 Email: hbe@tigr.org  
 Clones are derived from the human BAC library RPI1-11. For BAC  
 library availability, please contact Pieter de Jong  
 (pieter@dejong.med.buffalo.edu). Clones may be purchased from  
 BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from  
 Research Genetics (<http://inforesgen.com>). BAC end search page:  
[http://www.tigr.org/cdb/humgen/bac\\_end\\_search/bac\\_end\\_search.html](http://www.tigr.org/cdb/humgen/bac_end_search/bac_end_search.html)  
 Seq primer: T7  
 Class: BAC ends.  
 Location/Qualifiers  
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 /sex="Male"  
 /cell\_type="Lymphocytes"  
 /note="Vector: pBAC3.6; Site 1: EcoRI; Site 2: EcoRI;  
 RPI11 Human Male BAC Library"  
 RPI11 Human Male BAC Library"  
 98 c 115 g 177 t

BASE COUNT 235 a 98 c 115 g 177 t  
 ORIGIN  
 Query Match 12.0%; Score 219; DB 28; Length 625;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 219; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1571 GCTCTTCTACCTCTCTCTGAGGCTATCTTTGCGTATTCATCTGACCAAGACA 1630  
 524 GCTCTTCTACCTCTCTCTGAGGCTATCTTTGCGTATTCATCTGACCAAGACA 465

This clone is available royalty-free from RZPD;  
 contact RZPD (clone@rzpd.de) for further information. Seq primer:  
 M13r. Primer sequence: TTTCACACAGGAAAGCTATATAC.  
 Location/Qualifiers

## FEATURES

source

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1. 515
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/lab_host="DH10B"
/clone_11b="NCI CGAP Lu24"
/note="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Plasmid DNA from the normalized
library NCI CGAP Lu24 was prepared, and 88 circles were
made in vitro. Following HAP purification, this DNA was
used as tracer in a subtractive hybridization reaction.
The driver was PCR-amplified cDNAs from a pool of 5,000
clones made from the same library (clonoids
1414920-1417991 and 1520904-1522439). Subtraction by Bento
Soares and M. Fatima Bonaldo."
Soares and M. Fatima Bonaldo. " 2 others
137 a 138 c 105 g 133 t

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BASE COUNT 137 a 138 c 105 g 133 t 2 others

## ORIGIN

Query Match 22.6%; Score 412; DB 13; Length 515;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 462; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 905 TTCTGGGCGAGGAAACAGATGCTCTTATATGATCTCAAGAAACAGATCTATGG 964
Db 466 TTCTGGGCGAGGAAACAGATGCTCTTATATGATCTCAAGAAACAGATCTATGG 407
QY 965 AAGACAGAGAAATGCGAAAGTCTCTTCAAGGTTTGGAGACATATACAGAA 1024
Db 406 AAGACAGAGAAATGCGAAAGTCTCTTCAAGGTTTGGAGACATATACAGAA 347
QY 1025 GTAGTCCGCTGCTGCGACATGCGCCAGCTCTGATCTAGAGCTCAAGTCCAGGCCCA 1084
Db 346 GTAGTCCGCTGCTGCGACATGCGCCAGCTCTGATCTAGAGCTCAAGTCCAGGCCCA 287
QY 1085 TCACTGAGCTGAGGAGCAGGCTCATCTAATTTGAGTGAATTAATCTGCAATTAATG 1144
Db 286 TCACTGAGCTGAGGAGCAGGCTCATCTAATTTGAGTGAATTAATCTGCAATTAATG 227
QY 1145 AAGCCAAAGCTATATCTTGTATGAGATTTGAGAGCATTTGTATGATGACC 1204
Db 226 AAGCCAAAGCTATATCTTGTATGAGATTTGAGAGCATTTGTATGATGATGACC 167
QY 1205 GTCAAAATGGGCCCCATATCACTGCAACACCTTAAGTTTCTTGCAATGGGCTCAGA 1264
Db 166 GTCAAAATGGGCCCCATATCACTGCAACACCTTAAGTTTCTTGCAATGGGCTCAGA 107
QY 1265 CTTTCACTCTGAGCAATTAATCTGAGAGGTCATGTCAGGAGAACTCTTGGAATGGGCTT 1324
Db 106 CTTTCACTCTGAGCAATTAATCTGAGAGGTCATGTCAGGAGAACTCTTGGAATGGGCTT 47
QY 1325 TCGGCTTTGTATTAAGTACTGGAAGGAGAAATGCAAGTGG 1367
Db 46 TCGGCTTTGTATTAAGTACTGGAAGGAGAAATGCAAGTGG 4

```

## RESULT 5

BG150163

LOCUS 414 bp mRNA linear EST 05-FEB-2001  
 DEFINITION nrad4603.x1 NCI CGAP Lu24 Homo sapiens cDNA IMAGE:3368404 3'

similar to SW:MG85 HUMAN P41594 METABOTROPIC GLUTAMATE RECEPTOR 5  
 PRECURSOR. [1] ;, mRNA sequence.

ACCESSION BG150163  
 VERSION BG150163.1 GI:12662193

KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

## REFERENCE

1 (bases 1 to 414)  
 NCI CGAP <http://www.ncbi.nlm.nih.gov/ncigap>.  
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgaaps-remail.nih.gov  
 Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: M. Bento Soares, Ph.D.  
 DNA Sequencing by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLN, send email to:  
 info@image.llnl.gov  
 Seq primer: -40UP from G1bco  
 High quality sequence stop: 354.

## FEATURES

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1. 414
/organism="Homo sapiens"
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/tissue_type="carcinoid"
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/clone_11b="NCI CGAP Lu24"
/note="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Plasmid DNA from the normalized
library NCI CGAP Lu24 was prepared, and 88 circles were
made in vitro. Following HAP purification, this DNA was
used as tracer in a subtractive hybridization reaction.
The driver was PCR-amplified cDNAs from a pool of 5,000
clones made from the same library (clonoids
1414920-1417991 and 1520904-1522439). Subtraction by Bento
Soares and M. Fatima Bonaldo."
Soares and M. Fatima Bonaldo. " 95 t
110 a 91 c 118 g

```

BASE COUNT 110 a 91 c 118 g 95 t

## ORIGIN

Query Match 21.1%; Score 384; DB 10; Length 414;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 505 CCTCAAGTTCCTTACTCAGCAACATCATGATCTGAGTGAAGCAAGCTCTGTTCAATAT 564
Db 25 CCTCAAGTTCCTTACTCAGCAACATCATGATCTGAGTGAAGCAAGCTCTGTTCAATAT 84
QY 565 TTTATAGAGGTTTGCTTCAAGTGTCTCAGACGAGGATGTCATGGTGAATGGAAG 624
Db 85 TTTATAGAGGTTTGCTTCAAGTGTCTCAGACGAGGATGTCATGGTGAATGGAAG 144
QY 625 AGGTACAAGTGAAGCTATGATGATGAGCCGTACACAGAAAGCAATATGAGAAAGTGG 664
Db 145 AGGTACAAGTGAAGCTATGATGATGAGCCGTACACAGAAAGCAATATGAGAAAGTGG 204
QY 685 ATGGAAGCTTCAAAATATGTACAGGAGAAAGGATTTGCAATGCCCACTTTACAA 744
Db 205 ATGGAAGCTTCAAAATATGTACAGGAGAAAGGATTTGCAATGCCCACTTTACAA 264
QY 745 ATCTACAGTAAAGCAGAGGAGCAGAGCTTTGATTAAGCTGTGAAGAGCTCAAGTCAAC 804
Db 265 ATCTACAGTAAAGCAGAGGAGCAGAGCTTTGATTAAGCTGTGAAGAGCTCAAGTCAAC 324
QY 805 TTGCCCAAGGCCCGGGTGTGGCTTCTCTGTGAGGGCATGACGGTGAAGAGTCTGCTG 864
Db 325 TTGCCCAAGGCCCGGGTGTGGCTTCTCTGTGAGGGCATGACGGTGAAGAGTCTGCTG 384
QY 865 ATGGCCATGAGGCGCTGGGCTTCA 888
Db 385 ATGGCCATGAGGCGCTGGGCTTCA 408

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RESULT 6

Db 391 ATGAGCGCTGGGTCTAGTGGAGAAATTTCTGCTTCTGGGCAAGGAGCAAGCCATC 450

Qy 931 TTATTGAGATCTCAAGAACAGCATCTTATGGAGAGAGAAATGCAAGGTGCG 990

Db 451 TTTATTGAGATCTCAAGAACAGCATCTTATGGAGAGAGAAATGCAAGGTGCG 510

Qy 991 TTCCTTCAG 999

Db 511 TTCCTTCAG 519

RESULT 3  
AM015382  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AM015382 442 bp mRNA linear EST 10-SEP-1999  
UT-H-BIO-aat-d-06-0-UI-s1 NCI CGAP\_Sub1 Homo sapiens cDNA clone  
IMAGE:2710331.3', mRNA sequence.

AM015382  
AM015382.1 GI:5864139  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 442)  
NCI CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished  
Contact: Robert Straubeberg, Ph.D.  
Email: cgaaps-f@mail.nih.gov  
Oligo-dt track not found, Not 1 site shown in beginning of sequence  
is likely internal to the message. CDNA Library Preparation: M.B.  
Soares Lab clone distribution: NCI-CGAP clone distribution  
Information can be found through the I.M.A.G.E. Consortium/LLNL at:  
www.bio.llnl.gov/bdrip/image/image.html  
Seq primer: M13 forward  
POLYA=No.

FEATURES  
source

1..442 Location/Qualifiers  
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/db\_xref="taxon:9606"  
/clone="IMAGE:2710331"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_1b="NCI CGAP Sub1"  
/note="Vector: pT773D-Pac (Pharmacia) with a modified  
polylinker. Site 1: Not 1; Site 2: Eco RI; The  
NCI CGAP Sub1 library is a subcloned library derived from  
BI. BI constitutes a mixture of 21 normalized or  
subcloned NCI CGAP libraries: NCI CGAP C04,  
NCI CGAP Pr22, NCI CGAP Pr28, NCI CGAP C010, NCI CGAP C016,  
NCI CGAP Kid5, NCI CGAP Kid12, NCI CGAP Kid3,  
NCI CGAP Kid11, NCI CGAP Lym2, NCI CGAP Br2, NCI CGAP C08,  
NCI CGAP CL11, NCI CGAP Le12, NCI CGAP Brn3, NCI CGAP Lu5,  
NCI CGAP Lu24, NCI CGAP Lu19, NCI CGAP GC4, NCI CGAP GC6,  
NCI CGAP Brn25. These 21 libraries were pooled and a  
single-stranded DNA preparation of the resulting mixture  
was used as a tracer in a subtractive hybridization with a  
driver whose composition is detailed below: NCI CGAP Kid3  
pool 1 L1AM 3334-3337, 3682-3683, 3798-3803 (IMAGE  
Cloneids 1322376-1323911, 1456008-1456755, 1500552-1502855  
) NCI CGAP Kid5 pool 1 L1AM 3338-3342, 3722-3725,  
3776-3778 (IMAGE Cloneids 1323912-1325831,  
1471368-1472903, 1492104-1493255) NCI CGAP Lu5 pool 1 L1AM  
3575-3582, 3851-3854 (IMAGE Cloneids 141920-141991,  
1520904-1522439) NCI CGAP GC4 pool 1 L1AM 3164-3167,  
3716-3720, 3733-3735 (IMAGE Cloneids 1257096-1258631,  
1469064-1470983, 1475592-1476743) NCI CGAP Pr22 pool 1  
L1AM 2457-2459, 2758-2759, 3062-3068 (IMAGE Cloneids  
98508-986759, 1101192-1101959, 1217928-1220615)  
NCI CGAP C010 pool 1 L1AM 2644-2653, 2871-2872 (IMAGE  
Cloneids 1057416-1061255, 114584-1145351) The resulting  
subcloned library contained 530,000 recombinants.

Subtraction was performed as previously described [Bonaldo  
, Lennon & Soares (1996): Normalization and Subtraction:  
Two Approaches To Facilitate Gene Discovery. Genome  
Research 6, 791-806.  
TAG\_LIB=NCI CGAP\_Lel12  
TAG\_TISSUE=Leiomyosarcoma  
TAG\_SEQ=AATCG"

BASE COUNT 118 a 97 c 127 g 100 t

ORIGIN

Query Match 22.6%; Score 412; DB 9; Length 442;  
Best Local Similarity 100.0%; Pred.No. 0;  
Matches 412; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 7 CGAGCTTTCAACATACCTAGATGCTTACTAGACACCATATGATGATGACAA 66

Qy 549 GACTCTGTTCAATATTTTCATGAGGGTGTGCTTCAGATGCTCAGCAGCAAGTCCAT 608

Db 67 GACTCTGTTCAATATTTTCATGAGGGTGTGCTTCAGATGCTCAGCAGCAAGTCCAT 126

Qy 609 GGTGACATATGTGAAGAGGTACATGACCTATATGATACCCGTACACAGAGGCAA 668

Db 127 GGTGACATATGTGAAGAGGTACATGACCTATATGATACCCGTACACAGAGGCAA 186

Qy 669 CTATGAGAAAGTGGATGGAAGCCTTCAAGATATGTACGCAAGAGGATTTGCAT 728

Db 187 CTATGAGAAAGTGGATGGAAGCCTTCAAGATATGTACGCAAGAGGATTTGCAT 246

Qy 729 CGCCCACTCTTCAAAATCTACATATGATGAGGGAGCAGAGCTTGTATAGCTGTGAA 788

Db 247 CGCCCACTCTTCAAAATCTACATATGATGAGGGAGCAGAGCTTGTATAGCTGTGAA 306

Qy 789 GAAGCTCAAGTCACTGCTCCCAAGCCCGGGTGTGGCTTCTTGTAGGGCATGAC 848

Db 307 GAAGCTCAAGTCACTGCTCCCAAGCCCGGGTGTGGCTTCTTGTAGGGCATGAC 366

Qy 849 GGTGAGAGGTCTGCTGATGCGCATGAGGGCGCTGCTTGTAGGGCATGATTT 900

Db 367 GGTGAGAGGTCTGCTGATGCGCATGAGGGCGCTGCTTGTAGGGCATGATTT 418

RESULT 4  
BX280403/c  
LOCUS  
DEFINITION  
ACCESSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

BX280403 515 bp mRNA linear EST 04-MAR-2003  
BX280403 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE998A078034 ;  
IMAGE:3281166, mRNA sequence.

BX280403  
BX280403.1 GI:28612394  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 515)  
Radetof, U., Schneider, D. and Korn, B.  
Human Unigeneset - RZPD3  
Unpublished  
Contact: Ina Rolfs  
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
Im Neuenheimer Feld 580, D-69110 Heidelberg, Germany  
RZPD; IMAGE998A078034.  
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;  
Human Unigeneset - RZPD3 (RZPDLIB No.972)  
http://www.rzpd.de/cloncards/cgi-  
bin/showLib.pl.cgi?response=libNo-972 Contact: Ina Rolfs  
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
Heidelberg 6, D-14059 Berlin, Germany  
Tel: +49 30 32639 101  
Fax: +49 30 32639 111  
www.rzpd.de



infoimage.llnl.gov  
Seq primer: -40UP from Gibco  
High quality sequence stop: 493.  
Location/Qualifiers

# FEATURES

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/clone="IMAGE:3212943"  
/issue\_type="carcinoid"  
/lab\_host="DH10B"  
/note="Organ: lung; Vector: pRT3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI CGAP LUS was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneids 1414920-1417991 and 1520904-1522439). Subtraction by Bento Soares and M. Fatima Bernaldo."

## BASE COUNT

141 a 107 c 138 g 113 t

## ORIGIN

Query Match 27.4%; Score 499; DB 10; Length 499;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 499; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 ACATACCTCAGATTGCTTACTCAGCAACATCATGATCTGATGACAGACTCTGTCA  
560 AATATTCATGAGGGTGTGCTTCAAGTCTCAGACGAGGAGGTCATGCTGATGACATG  
61 AATATTCATGAGGGTGTGCTTCAAGTCTCAGACGAGGAGGTCATGCTGATGACATG  
620 TGAAGAGTCACTGACCTATGATCAGCCGACACAGAGGAGGTCATGCTGATGACATG  
121 TGAAGAGTCACTGACCTATGATCAGCCGACACAGAGGAGGTCATGCTGATGACATG  
680 GTGGGATGGAAGCCTTCAAGATATGTCAGCGAAGAGGATTTGATGCGCCACTTT  
181 GTGGGATGGAAGCCTTCAAGATATGTCAGCGAAGAGGATTTGATGCGCCACTTT  
740 ACAAAATCTCAAGTAATGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG  
241 ACAAAATCTCAAGTAATGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG  
800 GTCACTTGGCCAGAGCCGGGTGGTGGCTACTCTGTGAGGGGATGACGGTGAAGGTC  
301 GTCACTTGGCCAGAGCCGGGTGGTGGCTACTCTGTGAGGGGATGACGGTGAAGGTC  
860 TGCTGATGCGCATGAGCGCTGGGTCTAGTGGAGAAATTTCTGCTTGGGAGGAGAC  
361 TGCTGATGCGCATGAGCGCTGGGTCTAGTGGAGAAATTTCTGCTTGGGAGGAGAC  
920 CAGATGCGCATTTTATTGAGATCTCAAGAAACAGCATCTTATGGAAGAGAGAAAT  
421 CAGATGCGCATTTTATTGAGATCTCAAGAAACAGCATCTTATGGAAGAGAGAAAT  
980 GCCAAGGTCGCTTCTCA 998  
481 GCCAAGGTCGCTTCTCA 499

RESULT 2  
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LOCUS 7601804.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3281166 3.  
DEFINITION 8311804:1 to SW:WERS\_HUMAN\_P41594 METABOTROPIC GLUTAMATE RECEPTOR 5  
PBCURSORS: mRNA sequence.  
ACCESSION BE674422  
VERSION BE674422.1 GI:10034963

## KEYWORDS

SOURCE

ORGANISM

## REFERENCE

AUTHORS

TITLE

## JOURNAL

COMMENT

EST.  
Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 519)  
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: cgaaps-r@mail.nih.gov  
Tissue procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CCGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL, send email to:  
infoimage.llnl.gov  
Seq primer: -40UP from Gibco  
High quality sequence stop: 499.  
Location/Qualifiers

## FEATURES

Source

1. 519  
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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3281166"  
/issue\_type="carcinoid"  
/lab\_host="DH10B"  
/note="Organ: lung; Vector: pRT3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI CGAP LUS was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneids 1414920-1417991 and 1520904-1522439). Subtraction by Bento Soares and M. Fatima Bernaldo."

## BASE COUNT

143 a 114 c 143 g 119 t

## ORIGIN

Query Match 26.8%; Score 489; DB 10; Length 519;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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31 ATTGCTTACTCAGCAACATCATGATCTGATGACAGAGCTGTTCAATATTTCATG  
571 AGGGTGTGCTTCAAGTCTCAGACGAGGAGGTCATGCTGATGACATGAGAGGTAC  
91 AGGGTGTGCTTCAAGTCTCAGACGAGGAGGTCATGCTGATGACATGAGAGGTAC  
631 AACTGCACTATGATATGACGCTTACACACAGAGGAGGAGGAGGAGGAGGAGGAGGAG  
151 AACTGCACTATGATATGACGCTTACACACAGAGGAGGAGGAGGAGGAGGAGGAGGAG  
691 GCCTTCAAGATATGATGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG  
211 GCCTTCAAGATATGATGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG  
751 AGTATGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG  
271 AGTATGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG  
811 AAGGCGCGGTGGTGGCTACTCTGTGAGGGAGTACCGGTGAGAGGTCTGATGAGGCC  
331 AAGGCGCGGTGGTGGCTACTCTGTGAGGGAGTACCGGTGAGAGGTCTGATGAGGCC  
871 ATGAGCGCGGTGGTGGCTACTCTGTGAGGGAGTACCGGTGAGAGGTCTGATGAGGCC

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 14, 2003, 18:02:28 / Search time 4158.78 Seconds  
(without alignments)  
10653.866 Million cell updates/sec

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Perfect score: 1823  
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Scoring table: OLIGO\_NUC  
Gapop 60.0, Gapext 60.0

Searched: 22781392 seqs, 12152238056 residues

Word size : 0

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

EST:\*  
1: em\_estda:\*  
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3: em\_estin:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vit:\*  
21: em\_gss\_fun:\*  
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23: em\_gss\_mus:\*  
24: em\_gss\_piro:\*  
25: em\_gss\_rtd:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	412	22.6	515	13	BX280403 BX280403

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6	347	19.0	449	14	CB153433	CB153433 K-EST0210
7	219	12.0	625	28	AO313970	AO313970 RPT11-10
8	141	7.7	392	14	T78107	T78107 YC98A01.r1
9	131	7.2	1297	11	BC031602	BC031602 Homo sapi
10	113	6.2	664	12	BI826234	BI826234 603075928
11	107	5.9	452	9	A1950429	A1950429 wq35d01.x
12	107	5.9	455	9	A1655261	A1655261 wb68b11.x
13	107	5.9	494	13	BX116917	BX116917 BX116917
14	102	5.6	268	14	P05449	P05449 HSCORC11 n
15	97	5.3	516	13	BX282658	BX282658 BX282658
16	76	4.2	362	9	AM197327	AM197327 xm38e06.x
17	73	4.0	456	9	A1201184	A1201184 qf70d05.x
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19	67	3.7	888	13	BUL54755	BUL54755 AGENCOURT
20	66	3.6	667	29	AG046849	AG046849 Pan trogl
21	66	3.6	710	14	CA449274	CA449274 UT-H-E11-
22	63	3.5	378	28	B03872	B03872 GSRL-19D1-u
23	60	3.3	526	28	B16405	B16405 342C10.TVB
24	60	3.3	720	28	B65629	B65629 CIT-HSP-202
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26	59	3.2	682	10	BG695213	BG695213 NISC_iv13
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28	58	3.2	690	10	BG193349	BG193349 RST12477
29	58	3.2	729	10	BG199987	BG199987 RST19284
30	57	3.1	542	28	AO586224	AO586224 RPT1-11-4
31	56	3.1	435	28	AO443358	AO443358 HS_2231.B
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33	47	2.6	198	10	BE071193	BE071193 KCS-BT050
34	43	2.4	742	12	BI093942	BI093942 602857839
35	35	2.4	806	10	BF125311	BF125311 601762484
36	43	2.4	871	10	BE893553	BE893553 601438128
37	40	2.2	608	28	AO376196	AO376196 RPT11-15
38	40	2.2	647	10	BB625841	BB625841 BB625841
39	40	2.2	661	14	BY721282	BY721282 BY721282
40	40	2.2	1013	13	BQ070358	BQ070358 AGENCOURT
41	38	2.1	1201	13	BX421692	BX421692 BX421692
42	34	1.9	409	28	AO227301	AO227301 HS_2019.B
43	33	1.8	49	9	AA590547	AA590547 v16B04.F
44	33	1.8	58	14	CA336341	CA336341 NISC_lu11
45	33	1.8	63	12	BI491129	BI491129 d104C02.w

#### ALIGNMENTS

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LOCUS BE467477  
DEFINITION h266d08.x1 NCI CGAP Lu24 Homo sapiens CDNA clone IMAGE:3212943 3'  
similar to SW:MG95.HUMAN P41594 METABOTROPIC GLUTAMATE RECEPTOR 5  
PRECUSOR. ; mRNA sequence.

ACCESSION BE467477  
VERSION BE467477.1 GI:9513252

KEYWORDS Homo sapiens (human)

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished  
Contact: Robert Strauberg, Ph.D.  
Email: cgabs-remail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LINL, send email to:

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/072,574  
FILING DATE: 04-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen E.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: PP41 9772  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-546-4737  
TELEFAX: 619-546-9392  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4085 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 370..3912  
OTHER INFORMATION: /product= "HUMAN MGLUR5A"  
US-08-367-264-7

Query Match 9.4%; Score 171; DB 3; Length 4085;  
Best Local Similarity 98.8%; Pred. No. 1.4e-65;  
Matches 421; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
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DB 1250 GTCTAG 1255

Search completed: December 14, 2003, 15:19:12  
Job time: 123.716 secs

Db 890 CAACGACATGATCTGATGACAGACTCTGTTCAATAATTTCTGATGAGGTTGCTT 949  
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Db 1190 TGGCCTACTTCTGTGAGGGGATGACGGTGAAGAGTCTGTGATGAGCCATGAGCGCCTGG 1249  
QY 884 GTCTAG 889  
Db 1250 GTCTAG 1255

RESULT 14  
US-08-486-270-7  
; Sequence 7, Application US/08486270  
; Patent No. 5807689  
; GENERAL INFORMATION:  
; APPLICANT: Daggett, Lorrie  
; APPLICANT: Ellis, Steven B.  
; APPLICANT: Liaw, Chen  
; APPLICANT: Pontsler, Aaron  
; APPLICANT: Johnson, Edwin C.  
; APPLICANT: Hees, Stephen D.  
; TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS.  
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME AND USES THEREOF  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
; STREET: 444 South Flower Street, Suite 2000  
; CITY: Los Angeles  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/486,270  
; FILING DATE: 02-JUN-1994  
; CLASSIFICATION: 435  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: US 08/072,574  
; FILING DATE: 04-JUN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Reiter, Stephen E.  
; REGISTRATION NUMBER: 31,192  
; REFERENCE/DOCKET NUMBER: FP41 9772  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-546-4737  
; TELEFAX: 619-546-9392  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4085 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both

MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 370..3912  
OTHER INFORMATION: /product= "HUMAN MGUR5A"  
US-08-486-270-7

Query Match 9.4%; Score 171; DB 1; Length 4085;  
Best Local Similarity 98.8%; Pred. No. 1.4e-65;  
Matches 421; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 464 TACCATTCAGTTCAGAAATTTGCTCCAGCTTTTCAACATACCTGAGATTGTTACTAG 523  
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Db 890 CAACCATCATGATCTGAGTGAACAAGACTGTGTTCAAAATTTTCAATGAGGTTGTGCTT 949  
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QY 704 TGTCAAGGAGAGAGATTTGATGCTGCCCACTTTCAAAATTTACATGATGACAGGG 763  
Db 1070 TGTCAAGGAGAGAGATTTGATGCTGCCCACTTTCAAAATTTACATGATGACAGGG 1129  
QY 764 AGCAGAGCTTGTATGATGCTGTGAAGAGCTCAAGTCACTTGCCCAAGGCCCGGGTGG 823  
Db 1130 AGCAGAGCTTGTATGATGCTGTGAAGAGCTCAAGTCACTTGCCCAAGGCCCGGGTGG 1189  
QY 824 TGGCCTACTTCTGTGAGGGGATGACGGTGAAGAGTCTGTGATGAGCCATGAGCGCCTGG 883  
Db 1190 TGGCCTACTTCTGTGAGGGGATGACGGTGAAGAGTCTGTGATGAGCCATGAGCGCCTGG 1249  
QY 884 GTCTAG 889  
Db 1250 GTCTAG 1255

RESULT 15  
US-08-367-264-7  
; Sequence 7, Application US/08367264  
; Patent No. 6001581  
; GENERAL INFORMATION:  
; APPLICANT: Daggett, Lorrie  
; APPLICANT: Ellis, Steven B.  
; APPLICANT: Liaw, Chen  
; APPLICANT: Pontsler, Aaron  
; APPLICANT: Johnson, Edwin C.  
; APPLICANT: Hees, Stephen D.  
; TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS.  
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME AND USES THEREOF  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
; STREET: 444 South Flower Street, Suite 2000  
; CITY: Los Angeles  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/367,264  
; FILING DATE: 02-JUN-1994

GENERAL INFORMATION:  
APPLICANT: Daggett, Lorrie  
Ellis, Steven B.  
Llao, Chen  
Pontbier, Aaron  
Johnson, Edwin C.  
Hees, Stephen D.  
TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,  
NUCLEIC ACIDS ENCODING SAME AND USES THEREOF  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
STREET: 444 South Flower Street, Suite 2000  
CITY: Los Angeles  
STATE: CA  
COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/459,715  
FILING DATE: 13-Dec-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/367,264  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen E.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: P41 9772  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-546-4737  
TELEFAX: 619-546-9392  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3282 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 370..3003  
OTHER INFORMATION: /product= "HUMAN MGLUR5C"  
/note= "Variant of MGLUR5A with truncated 3' end."  
SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-09-459-715-11

Query Match 9.4%; Score 171; DB 4; Length 3282;  
Best Local Similarity 98.8%; Pred. No. 1.4e-65;  
Matches 421; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

464 TAGCATTGAGTCCAGATTGCTCCAGCTTTCAACATACCTCAGATTGTTACTCAG 523  
DB 830 TAGCATTGAGTCCAGATTGCTCCAGCTTTCAACATACCTCAGATTGTTACTCAG 889  
QY 524 CAACCATCATGATCTGAGTGAAGAAGCTGTTCAATATTTTCATGAGGGTTGTGCTT 583  
DB 890 CAACCATCATGATCTGAGTGAAGAAGCTGTTCAATATTTTCATGAGGGTTGTGCTT 949  
QY 584 CAGATGCTCAGCAGCAGAGTCCATGCTGATGACATGATGAGGATCACTGACCTATG 643  
DB 950 CAGATGCTCAGCAGCAGAGTCCATGCTGATGACATGATGAGGATCACTGACCTATG 1009  
QY 644 TATCAGCGGTACACACAGAGGCAACTATGAGAAAGTGAGTGAAGCCTTCAAGATA 703  
DB 1010 TATCAGCGGTACACACAGAGGCAACTATGAGAAAGTGAGTGAAGCCTTCAAGATA 1069  
QY 704 TGTGAGGAAGAGGATTTGATGCGCCACTCTTCAAAATCTACAGTAATGACAGGGG 763

DB 1070 TGTGAGGAAGAGGATTTGATGCGCCACTCTTCAAAATCTACAGTAATGACAGGGG 1129  
QY 764 AGCAGAGCTTTGATAGTCTGATGAGAGCTCAACAGTCACTTGCCCAAGCCCGGCTG 823  
DB 1130 AGCAGAGCTTTGATAGTCTGATGAGAGCTCAACAGTCACTTGCCCAAGCCCGGCTG 1189  
QY 824 TGCCCTCTCTGATGAGGAGCATGACGCTGATGAGAGTCTGATGAGCCTGAGCGCTG 883  
DB 1190 TGCCCTCTCTGATGAGGAGCATGACGCTGATGAGAGTCTGATGAGCCTGAGCGCTG 1249  
QY 884 GTCTAG 889  
DB 1250 GTCTAG 1255

RESULT 13  
US-08-072-574-7  
Sequence 7, Application US/08072574  
Patent No. 5521297  
GENERAL INFORMATION:  
APPLICANT: Daggett, Lorrie  
Ellis, Steven B.  
APPLICANT: Llao, Chen  
Pontbier, Aaron  
TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,  
NUCLEIC ACIDS ENCODING SAME AND USES THEREOF  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
STREET: 444 South Flower Street, Suite 2000.  
CITY: Los Angeles  
STATE: CA  
COUNTRY: USA  
ZIP: 00719  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/072,574  
FILING DATE: 19930604  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen E.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: P41 9383  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 213-622-7700  
TELEFAX: 213-489-4210  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4085 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 370..3912  
OTHER INFORMATION: /product= "HUMAN MGLUR5A"  
US-08-072-574-7

Query Match 9.4%; Score 171; DB 1; Length 4085;  
Best Local Similarity 98.8%; Pred. No. 1.4e-65;  
Matches 421; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

464 TAGCATTGAGTCCAGATTGCTCCAGCTTTCAACATACCTCAGATTGTTACTCAG 523  
DB 830 TAGCATTGAGTCCAGATTGCTCCAGCTTTCAACATACCTCAGATTGTTACTCAG 889  
QY 524 CAACCATCATGATCTGAGTGAAGAAGCTGTTCAATATTTTCATGAGGGTTGTGCTT 583

TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cdna  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 370..3003  
OTHER INFORMATION: /product= "HUMAN MGLUR5C"  
US-08-367-264-11  
OTHER INFORMATION: /note= "Variant of MGLUR5A with truncated 3' end."

Query Match  
Best Local Similarity 98.8%; Score 171; DB 3; Length 3282;  
Pred. No. 1,4e-65;  
Matches 421; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 464 TAGCCATTCAGGTCAGAAATTTGCTCCAGCTTTTCAACATACCTGATGCTTACTACAG 523  
DB 830 TAGCCATTCAGGTCAGAAATTTGCTCCAGCTTTTCAACATACCTGATGCTTACTACAG 889  
QY 524 CAACCATTCATGATCTGATGACAGACTCTGTTCAAAATATTTTCATGAGGGTTGCTT 583  
DB 890 CAACGACATGATCTGATGACAGACTCTGTTCAAAATATTTTCATGAGGGTTGCTT 949  
QY 584 CAGATCTCAGCAGGCAAGGTCATGATGACATAGTGAAGAGGTCACATGACCTATG 643  
DB 950 CAGATCTCAGCAGGCAAGGTCATGATGACATAGTGAAGAGGTCACATGACCTATG 1009  
QY 644 TATCAGCCGTCACAGAGGCACTATGAGAAAGTGGATGAGAAAGCTTCAAAAGTA 703  
DB 1010 TATCAGCCGTCACAGAGGCACTATGAGAAAGTGGATGAGAAAGCTTCAAAAGTA 1069  
QY 704 TGTACGCGAAGAGGATTTGATGCGCCACTCTTACAAATCTACATATGACAGGG 763  
DB 1070 TGTACGCGAAGAGGATTTGATGCGCCACTCTTACAAATCTACATATGACAGGG 1129  
QY 764 AGCAGAGCTTTGATAGTCTGTAAGAGCTCAAGATCACTTGCCCAAGGCCGGGTG 823  
DB 1130 AGCAGAGCTTTGATAGTCTGTAAGAGCTCAAGATCACTTGCCCAAGGCCGGGTG 1189  
QY 824 TGGCCATCTTCTGTAGGCGCATGACGCTGAGAGGTCTGCTGATGAGCGGCTT 883  
DB 1190 TGGCCATCTTCTGTAGGCGCATGACGCTGAGAGGTCTGCTGATGAGCGGCTT 1249  
QY 884 GTCTAG 889  
DB 1250 GTCTAG 1255

## RESULT 11

US-09-153-757-11  
Sequence 11, Application US/09153757  
Patent No. 6413764

## GENERAL INFORMATION:

APPLICANT: Daggett, Lorrie  
Ellis, Steven B.  
Liaw, Chen  
Pontsler, Aaron  
Johnson, Edwin C.  
Hees, Stephen D.

TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,  
NUCLEIC ACIDS ENCODING SAME AND USES THEREOF

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:  
ADDRESSER: Pretty, Schroeder, Brueggemann & Clark  
CITY: 444 South Flower Street, Suite 2000  
STATE: CA

COUNTRY: USA  
ZIP: 90071

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/153,757  
FILING DATE: 15-Sep-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,270  
FILING DATE: 02-JUN-1994  
APPLICATION NUMBER: US 08/072,574  
FILING DATE: 04-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen E.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: PP41 9772  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-546-4737  
TELEFAX: 619-546-9392  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3282 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cdna  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 370..3003  
OTHER INFORMATION: /product= "HUMAN MGLUR5C"  
/note= "Variant of MGLUR5A with truncated 3' end."  
SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-09-153-757-11

Query Match  
Best Local Similarity 98.8%; Score 171; DB 4; Length 3282;  
Pred. No. 1,4e-65;  
Matches 421; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 464 TAGCCATTCAGGTCAGAAATTTGCTCCAGCTTTTCAACATACCTGATGCTTACTACAG 523  
DB 830 TAGCCATTCAGGTCAGAAATTTGCTCCAGCTTTTCAACATACCTGATGCTTACTACAG 889  
QY 524 CAACCATTCATGATCTGATGACAGACTCTGTTCAAAATATTTTCATGAGGGTTGCTT 583  
DB 890 CAACGACATGATCTGATGACAGACTCTGTTCAAAATATTTTCATGAGGGTTGCTT 949  
QY 584 CAGATCTCAGCAGGCAAGGTCATGATGACATAGTGAAGAGGTCACATGACCTATG 643  
DB 950 CAGATCTCAGCAGGCAAGGTCATGATGACATAGTGAAGAGGTCACATGACCTATG 1009  
QY 644 TATCAGCCGTCACAGAGGCACTATGAGAAAGTGGATGAGAAAGCTTCAAAAGTA 703  
DB 1010 TATCAGCCGTCACAGAGGCACTATGAGAAAGTGGATGAGAAAGCTTCAAAAGTA 1069  
QY 704 TGTACGCGAAGAGGATTTGATGCGCCACTCTTACAAATCTACATATGACAGGG 763  
DB 1070 TGTACGCGAAGAGGATTTGATGCGCCACTCTTACAAATCTACATATGACAGGG 1129  
QY 764 AGCAGAGCTTTGATAGTCTGTAAGAGCTCAAGATCACTTGCCCAAGGCCGGGTG 823  
DB 1130 AGCAGAGCTTTGATAGTCTGTAAGAGCTCAAGATCACTTGCCCAAGGCCGGGTG 1189  
QY 824 TGGCCATCTTCTGTAGGCGCATGACGCTGAGAGGTCTGCTGATGAGCGGCTT 883  
DB 1190 TGGCCATCTTCTGTAGGCGCATGACGCTGAGAGGTCTGCTGATGAGCGGCTT 1249  
QY 884 GTCTAG 889  
DB 1250 GTCTAG 1255

## RESULT 12

US-09-459-715-11  
Sequence 11, Application US/09459715  
Patent No. 6485919

DB 1130 AGAGAGCTTTGTAAGCTGCTGAGAGCTCAAGAGTCACTTGCCCAAGGCCGGGTGG 1189  
QY 824 TGCGCTACTTCTGTGAGGCGATGACGGTGTGCTGATGCGCATGAGCGCGCTGG 883  
DB 1190 TGCGCTGCTTCTGTGAGGCGATGACGGTGTGCTGATGCGCATGAGCGCGCTGG 1249  
QY 884 GTCTAG 889  
DB 1250 GTCTAG 1255

RESULT 9  
US-08-486-270-11  
Sequence 11, Application US/08486270  
Patent No. 5807689  
GENERAL INFORMATION:  
APPLICANT: Daggett, Lorrie  
APPLICANT: Ellis, Steven B.  
APPLICANT: Liaw, Chen  
APPLICANT: Pontbier, Aaron  
APPLICANT: Johnson, Edwin C.  
TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,  
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME AND USES THEREOF  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
STREET: 444 South Flower Street, Suite 2000  
CITY: Los Angeles  
STATE: CA  
COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,270  
FILING DATE: 02-JUN-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/072,574  
FILING DATE: 04-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen B.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: FP41 9772  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-546-4737  
TELEFAX: 619-546-9392  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3282 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 370..3003  
OTHER INFORMATION: /product= "HUMAN MGLUR5C"  
OTHER INFORMATION: /note= "Variant of MGLUR5A with truncated 3' end."  
US-08-486-270-11

Query Match 9.4%; Score 171; DB 1; Length 3282;  
Best Local Similarity 98.8%; Pred. No. 1,4e-65;  
Matches 421; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 464 TAGCATTGAGTTCAGAGATTGCTTCAGCTTTTCAACATACCTCAGATTGCTTACTGAG 523  
DB 830 TAGCATTGAGTTCAGAGATTGCTTCAGCTTTTCAACATACCTCAGATTGCTTACTGAG 889

QY 524 CAACATCATGATCTGATGAGTGAACAAGCTCTGTCAATATTTCATGAGGTTGCTT 583  
DB 890 CAACCATGATGATCTGATGAGTGAACAAGCTCTGTCAATATTTCATGAGGTTGCTT 949  
QY 584 CAGATGCTCAGCAGGCAAGGTCATGCTGATGACATGATGAGAGTCAACATGAGCCTTAG 643  
DB 950 CAGATGCTCAGCAGGCAAGGTCATGCTGATGACATGATGAGAGTCAACATGAGCCTTAG 1009  
QY 644 TATCAGCCGTACACACAGAGGCAACTATGAGAGAAAGTGGATGAGAGCTTCAAGATA 703  
DB 1010 TATCAGCCGTACACACAGAGGCAACTATGAGAGAAAGTGGATGAGAGCTTCAAGATA 1069  
QY 704 TGTGAGCGAAGGAGGATTTGATGCGCCACTCTTACAAAATCTACAGTAATGAGGAG 763  
DB 1070 TGTGAGCGAAGGAGGATTTGATGCGCCACTCTTACAAAATCTACAGTAATGAGGAG 1129  
QY 764 AGCAGAGCTTTGTAAGTGTGTAAGAGTCAACAAGTCACTTGCCCAAGGCCGGGTGG 823  
DB 1130 AGAGAGCTTTGTAAGTGTGTAAGAGTCAACAAGTCACTTGCCCAAGGCCGGGTGG 1189  
QY 824 TGCGCTACTTCTGTGAGGCGATGACGGTGTGCTGATGCGCATGAGCGCGCTGG 883  
DB 1190 TGCGCTGCTTCTGTGAGGCGATGACGGTGTGCTGATGCGCATGAGCGCGCTGG 1249  
QY 884 GTCTAG 889  
DB 1250 GTCTAG 1255

RESULT 10  
US-08-367-264-11  
Sequence 11, Application US/08367264  
Patent No. 6001581  
GENERAL INFORMATION:  
APPLICANT: Daggett, Lorrie  
APPLICANT: Ellis, Steven B.  
APPLICANT: Liaw, Chen  
APPLICANT: Pontbier, Aaron  
APPLICANT: Johnson, Edwin C.  
TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,  
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME AND USES THEREOF  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
STREET: 444 South Flower Street, Suite 2000  
CITY: Los Angeles  
STATE: CA  
COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/367,264  
FILING DATE: 02-JUN-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/072,574  
FILING DATE: 04-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen B.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: FP41 9772  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-546-4737  
TELEFAX: 619-546-9392  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3282 base pairs





TELEFAX: (317) 276-3861  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4207 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: mRNA  
US-08-660-148-3

Query Match 12.2%; Score 222; DB 3; Length 4207;  
Best Local Similarity 76.3%; Pred. No. 6,9e-88;  
Matches 325; Conservative 97; Mismatches 4; Indels 0; Gaps 0;

QY 464 TAGCCATTGAGTTCAGATTTGCTGCTTCAACATACCTGAGATGCTTACTGAG 523  
DB 920 UAGCCAUUCAGGUCAGAAUUCUCUCCAGCUUUAACAUACCUAGUUGUCUACUAG 979  
QY 524 CAACCATCATGATCTGAGTGAAGAGAGCTGCTTCAAAATTTTCATGAGGGTTGTGCTT 583  
DB 980 CAACCAAGCAUAGUACUGAGUAGACACUCUCUCAAUUAUUCUAGAGGUGUGUCUU 1039  
QY 584 CAGATGCTCAGCAGGCAAGGTCCATGAGTGAAGAGTGAAGTGAAGTGAAGTGAAGTGA 643  
DB 1040 CAAUUGUCUACAGGCAAGGCGCAUGUGUGACAUAAGUAGAGGUGUACAUCUAGCUAUG 1099  
QY 644 TATCAGCCGTACACACAGAAAGCACTATGAGAAAGTGGATGGAAGCTTCAAGATA 703  
DB 1100 UAUACAGCGGUGACACAGAAAGCACTUAGAGAAUUGGAGUAGAGCCUCAAAGAU 1159  
QY 704 TGTCAAGGAAGAAAGGATTTGATGCGCCATCTTCAAAATCTAAGATGAAGAGGG 763  
DB 1160 UGUCAGGAAGAAAGGAAUUGCAUUGCCCAUCUCUUAUUAAGUAGUAGUAGUAGUAG 1219  
QY 764 AGCAGAGCTTGTAAAGCTGCTGAAGAGTCAAGTCACTTGCCCAAGGCGGCTGG 823  
DB 1220 AGCAGAGCTTGTAAAGCTGCTGAAGAGTCAAGTCACTTGCCCAAGGCGGCTGG 1279  
QY 824 TGGCCTACTTCTGTGAGGCGATGACGCTGAGAGGTCTGCTGATGCGCATGAGCGCTGG 883  
DB 1280 TGGCCTACTTCTGTGAGGCGATGACGCTGAGAGGTCTGCTGATGCGCATGAGCGCTGG 1339  
QY 884 GTCTAG 889  
DB 1340 GUCUAG 1345

## RESULT 6

US-08-660-148-4  
Sequence 4, Application US/08660148  
Patent No. 6211353  
GENERAL INFORMATION:  
APPLICANT: Burnett, J. P.  
APPLICANT: Mayne, Nancy G.  
APPLICANT: Sharp, Robert L.  
APPLICANT: Snyder, Yvonne M.  
TITLE OF INVENTION: EXCITATORY AMINO RECEPTOR PROTEIN AND  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Eli Lilly and Company  
STREET: Lilly Corporate Center  
CITY: Indianapolis  
STATE: Indiana  
COUNTRY: United States of America  
ZIP: 46285  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/660,148

FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/282,853  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Gaylo, Paul J.  
REGISTRATION NUMBER: 36,808  
REFERENCE/DOCKET NUMBER: X-9419  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (317) 276-0756  
TELEFAX: (317) 276-3861  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4303 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 460..4095  
US-08-660-148-4

Query Match 12.2%; Score 222; DB 3; Length 4303;  
Best Local Similarity 99.1%; Pred. No. 6,9e-88;  
Matches 422; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 464 TAGCCATTGAGTTCAGATTTGCTGCTTCAACATACCTGAGATGCTTACTGAG 523  
DB 920 TAGCCATTGAGTTCAGATTTGCTGCTTCAACATACCTGAGATGCTTACTGAG 979  
QY 524 CAACCATCATGATCTGAGTGAAGAGCTGCTTCAAAATTTTCATGAGGGTTGTGCTT 583  
DB 980 CAACCAAGCAUAGUACUGAGUAGACACUCUCUCAAUUAUUCUAGAGGUGUGUCUU 1039  
QY 584 CAGATGCTCAGCAGGCAAGGTCCATGAGTGAAGAGTGAAGTGAAGTGAAGTGAAGTGA 643  
DB 1040 CAAUUGUCUACAGGCAAGGCGCAUGUGUGACAUAAGUAGAGGUGUACAUCUAGCUAUG 1099  
QY 644 TATCAGCCGTACACACAGAAAGCACTATGAGAAAGTGGATGGAAGCTTCAAGATA 703  
DB 1100 TATCAGCCGTACACACAGAAAGCACTATGAGAAAGTGGATGGAAGCTTCAAGATA 1159  
QY 704 TGTCAAGGAAGAAAGGATTTGATGCGCCATCTTCAAAATCTAAGATGAAGAGGG 763  
DB 1160 TGTCAAGGAAGAAAGGATTTGATGCGCCATCTTCAAAATCTAAGATGAAGAGGG 1219  
QY 764 AGCAGAGCTTGTAAAGCTGCTGAAGAGTCAAGTCACTTGCCCAAGGCGGCTGG 823  
DB 1220 AGCAGAGCTTGTAAAGCTGCTGAAGAGTCAAGTCACTTGCCCAAGGCGGCTGG 1279  
QY 824 TGGCCTACTTCTGTGAGGCGATGACGCTGAGAGGTCTGCTGATGCGCATGAGCGCTGG 883  
DB 1280 TGGCCTACTTCTGTGAGGCGATGACGCTGAGAGGTCTGCTGATGCGCATGAGCGCTGG 1339  
QY 884 GTCTAG 889  
DB 1340 GTCTAG 1345

## RESULT 7

US-08-660-148-6  
Sequence 6, Application US/08660148  
Patent No. 6211353  
GENERAL INFORMATION:  
APPLICANT: Burnett, J. P.  
APPLICANT: Mayne, Nancy G.  
APPLICANT: Sharp, Robert L.  
APPLICANT: Snyder, Yvonne M.  
TITLE OF INVENTION: EXCITATORY AMINO RECEPTOR PROTEIN AND  
NUMBER OF SEQUENCES: 6

QY 644 TATCAGCCGTACACACAGAGGCACTATGAGAAAGTGGATGAGAGCCCTTCAAGATA 703  
DB 791 TATCAGCCGTACACACAGAGGCACTATGAGAAAGTGGATGAGAGCCCTTCAAGATA 850  
QY 704 TGTACGGAAGAGGAGATTGATGAGCCCACTTTACAAATCTACATATGACAGGG 763  
DB 851 TGTACGGAAGAGGAGATTGATGAGCCCACTTTACAAATCTACATATGACAGGG 910  
QY 764 AGAGAGCTTTGATTAAGCTGCTGAGAGAGCTCAAGTCACTTGGCCCAAGCCCGGTGG 823  
DB 911 AGAGAGCTTTGATTAAGCTGCTGAGAGAGCTCAAGTCACTTGGCCCAAGCCCGGTGG 970  
QY 824 TGGCCTACTTCTGTGAGGCGCATGACGCTGAGAGAGTCTGTATGAGCCATGAGGCGCTGG 883  
DB 971 TGGCCTACTTCTGTGAGGCGCATGACGCTGAGAGAGTCTGTATGAGCCATGAGGCGCTGG 1030  
QY 884 GTCTAG 889  
DB 1031 GTCTAG 1036

RESULT 4  
US-08-660-148-1  
Sequence 1, Application US/08660148  
Patent No. 6211353  
GENERAL INFORMATION:  
APPLICANT: Burnett, J. P.  
APPLICANT: Mayne, Nancy G.  
APPLICANT: Sharp, Robert L.  
APPLICANT: Snyder, Yvonne M.  
TITLE OF INVENTION: EXCITATORY AMINO RECEPTOR PROTEIN AND  
TITLE OF INVENTION: RELATED NUCLEIC ACID COMPOUNDS  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Eli Lilly and Company  
STREET: Lilly Corporate Center  
CITY: Indianapolis  
STATE: Indiana  
COUNTRY: United States of America  
ZIP: 46285  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/660,148  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/282,853  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Gaylo, Paul J.  
REGISTRATION NUMBER: 36,808  
REFERENCE/DOCKET NUMBER: X-9419  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (317) 276-0756  
TELEFAX: (317) 276-3861  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4207 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURES:  
NAME/KEY: CDS  
LOCATION: 460..3999  
US-08-660-148-1  
Query Match 12.2%; Score 222; DB 3; Length 4207;

Best Local Similarity 99.1%; Pred. No. 6,9e-88;  
Matches 422; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 464 TACCAATTACAGTCCCAAGATTTCCTCAGCTTTTCAACATACCTGATGCTTACTCAG 523  
DB 920 TACCAATTACAGTCCCAAGATTTCCTCAGCTTTTCAACATACCTGATGCTTACTCAG 979  
QY 524 CAACATCATGATCTGATGACAGACTGTTCAAATATTTTCATGAGGCTTGTGCTT 583  
DB 980 CAACATCATGATCTGATGACAGACTGTTCAAATATTTTCATGAGGCTTGTGCTT 1039  
QY 584 CAGATCTCAGCAGGAGGATTCATGATGACATGATGAGAGTCAAACTGACCTTATG 643  
DB 1040 CAGATCTCAGCAGGAGGATTCATGATGACATGATGAGAGTCAAACTGACCTTATG 1099  
QY 644 TATCAGCCGTACACACAGAGGCACTATGAGAAAGTGGATGAGAGCCCTTCAAGATA 703  
DB 1100 TATCAGCCGTACACACAGAGGCACTATGAGAAAGTGGATGAGAGCCCTTCAAGATA 1159  
QY 704 TGTACGGAAGAGGAGATTGATGAGCCCACTTTACAAATCTACATATGACAGGG 763  
DB 1160 TGTACGGAAGAGGAGATTGATGAGCCCACTTTACAAATCTACATATGACAGGG 1219  
QY 764 AGAGAGCTTTGATTAAGCTGCTGAGAGAGCTCAAGTCACTTGGCCCAAGCCCGGTGG 823  
DB 1220 AGAGAGCTTTGATTAAGCTGCTGAGAGAGCTCAAGTCACTTGGCCCAAGCCCGGTGG 1279  
QY 824 TGGCCTACTTCTGTGAGGCGCATGACGCTGAGAGAGTCTGTATGAGCCATGAGGCGCTGG 883  
DB 1280 TGGCCTACTTCTGTGAGGCGCATGACGCTGAGAGAGTCTGTATGAGCCATGAGGCGCTGG 1339  
QY 884 GTCTAG 889  
DB 1340 GTCTAG 1345

RESULT 5  
US-08-660-148-3  
Sequence 3, Application US/08660148  
Patent No. 6211353  
GENERAL INFORMATION:  
APPLICANT: Burnett, J. P.  
APPLICANT: Mayne, Nancy G.  
APPLICANT: Sharp, Robert L.  
APPLICANT: Snyder, Yvonne M.  
TITLE OF INVENTION: EXCITATORY AMINO RECEPTOR PROTEIN AND  
TITLE OF INVENTION: RELATED NUCLEIC ACID COMPOUNDS  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Eli Lilly and Company  
STREET: Lilly Corporate Center  
CITY: Indianapolis  
STATE: Indiana  
COUNTRY: United States of America  
ZIP: 46285  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/660,148  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/282,853  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Gaylo, Paul J.  
REGISTRATION NUMBER: 36,808  
REFERENCE/DOCKET NUMBER: X-9419  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (317) 276-0756

Db 701 TGTGAGGAGGAGGATTTGCATGCGCCACTTACAAATCTACAGTAATGACAGGG 760  
QY 764 AGCAGAGCTTTGATTAAGCTCTGTAAGAGCTCAACAAGTCACTTGCCCAAGGCCGGGTGG 823  
Db 761 AGCAGAGCTTTGATTAAGCTCTGTAAGAGCTCAACAAGTCACTTGCCCAAGGCCGGGTGG 820  
QY 824 TGGCCTACTCTGTGAGGGGATGACGGGTGAGAGGTCTGATAGAGGCCATGAGGGCCTGG 883  
Db 821 TGGCCTACTCTGTGAGGGGATGACGGGTGAGAGGTCTGATAGAGGCCATGAGGGCCTGG 880  
QY 884 GTCTAG 889  
Db 881 GTCTAG 886

RESULT 2  
US-09-695-481-5  
; Sequence 5, Application US/09695481  
; Patent No. 6534287  
; GENERAL INFORMATION:  
; APPLICANT: STORMANN, THOMAS M.  
; APPLICANT: LEVINTHAL, CYNTHIA  
; APPLICANT: STORJOHANN, LAURA  
; APPLICANT: HAMMERLAND, LANCE G.  
; APPLICANT: KRAPCHO, KAREN J.  
; APPLICANT: NPS PHARMACEUTICALS, INC.  
; TITLE OF INVENTION: A NOVEL HUMAN METABOTROPIC GLUTAMATE RECEPTOR  
; FILE REFERENCE: 1094.2.6  
; CURRENT APPLICATION NUMBER: US/09/695,481  
; CURRENT FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: 60/161,481  
; PRIOR FILING DATE: 1999-10-25  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 3129  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURES:  
; OTHER INFORMATION: Description of Artificial Sequence:Chimeric  
; OTHER INFORMATION: molecule comprising portions of human mGluR4 and  
; OTHER INFORMATION: the human calcium receptor.  
; NAME/KEY: CDS  
; LOCATION: ( )..(3129)  
US-09-695-481-5

Query Match 12.2%; Score 222; DB 4; Length 3129;  
Best Local Similarity 99.1%; Pred. No. 7,1e-88;  
Matches 422; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 464 TAGCCATTGAGTTCAGAAATTTGCTCCAGCTTTTCAACATACCTCAGATTGCTTACTCAG 523  
Db 461 TAGCCATTGAGTTCAGAAATTTGCTCCAGCTTTTCAACATACCTCAGATTGCTTACTCAG 520  
QY 524 CAACCATCATGAGATCTGAGTGAAGAAGCTGCTCAAAATTTTCATAGAGGTTGTGCTT 583  
Db 521 CAACCATCATGAGATCTGAGTGAAGAAGCTGCTCAAAATTTTCATAGAGGTTGTGCTT 580  
QY 584 CAGATGCTCAGCAGGCAAGGTCTCATGCTGATGATGAGAGGTGATGAGAGTCACTGACCTATG 643  
Db 581 CAGATGCTCAGCAGGCAAGGTCTCATGCTGATGATGAGAGGTGATGAGAGTCACTGACCTATG 640  
QY 644 TATCAGCCGTGACACAGAAAGCACTATGAGAAAGTGGAGTGAAGCTTCAAGATA 703  
Db 641 TATCAGCCGTGACACAGAAAGCACTATGAGAAAGTGGAGTGAAGCTTCAAGATA 700  
QY 704 TGTGAGGAGGAGGAGGATTTGATGCGCCCACTTTTCAAAATTTTCAAGTAATGCAAGGG 763  
Db 701 TGTGAGGAGGAGGAGGATTTGATGCGCCCACTTTTCAAAATTTTCAAGTAATGCAAGGG 760  
QY 764 AGCAGAGCTTTGATTAAGCTCTGTAAGAGCTCAACAAGTCACTTGCCCAAGGCCGGGTGG 823  
Db 761 AGCAGAGCTTTGATTAAGCTCTGTAAGAGCTCAACAAGTCACTTGCCCAAGGCCGGGTGG 820

QY 824 TGGCCTACTCTGTGAGGGGATGACGGGTGAGAGGTCTGATAGAGGCCATGAGGGCCTGG 883  
Db 821 TGGCCTACTCTGTGAGGGGATGACGGGTGAGAGGTCTGATAGAGGCCATGAGGGCCTGG 880  
QY 884 GTCTAG 889  
Db 881 GTCTAG 886

RESULT 3  
US-09-016-434-1133  
; Sequence 1133, Application US/09016434  
; Patent No. 6500938  
; GENERAL INFORMATION:  
; APPLICANT: Janice Au-Young  
; APPLICANT: Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
; NUMBER OF SEQUENCES: 1490  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/016,434  
; FILING DATE: HEREMITH  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0002 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 845-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 1133:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4078 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GENBANK  
; CLONE: g1408051  
US-09-016-434-1133

Query Match 12.2%; Score 222; DB 4; Length 4078;  
Best Local Similarity 99.1%; Pred. No. 7e-88;  
Matches 422; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 464 TAGCCATTGAGTTCAGAAATTTGCTCCAGCTTTTCAACATACCTCAGATTGCTTACTCAG 523  
Db 611 TAGCCATTGAGTTCAGAAATTTGCTCCAGCTTTTCAACATACCTCAGATTGCTTACTCAG 670  
QY 524 CAACCATCATGAGATCTGAGTGAAGAAGCTGCTCAAAATTTTCATAGAGGTTGTGCTT 583  
Db 671 CAACCATCATGAGATCTGAGTGAAGAAGCTGCTCAAAATTTTCATAGAGGTTGTGCTT 730  
QY 584 CAGATGCTCAGCAGGCAAGGTCTCATGCTGATGATGAGAGGTGATGAGAGTCACTGACCTATG 643  
Db 731 CAGATGCTCAGCAGGCAAGGTCTCATGCTGATGATGAGAGGTGATGAGAGTCACTGACCTATG 790

GenCore version 5.1.6  
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OM nucleic - nucleic search, using bw model

Run on: December 14, 2003, 09:48:38 ; Search time 118.716 Seconds  
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Title: US-10-027-923-1

Perfect score: 1823

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Scoring table: OLIGO\_NBC

Searched: 569978 seqs, 220691566 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0  
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Post-processing: Listing first 45 summaries

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2: /cgn2\_6/ptodata/2/ina/5B COMB.seq: \*  
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6: /cgn2\_6/ptodata/2/ina/backfile1.seq: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	222	12.2	2826	4 US-09-695-481-1	Sequence 1, Appl1
2	222	12.2	3129	4 US-09-695-481-5	Sequence 5, Appl1
3	222	12.2	4078	4 US-09-016-434-1133	Sequence 1133, Ap
4	222	12.2	4207	3 US-08-660-148-1	Sequence 1, Appl1
5	222	12.2	4207	3 US-08-660-148-3	Sequence 3, Appl1
6	222	12.2	4303	3 US-08-660-148-4	Sequence 4, Appl1
7	222	12.2	4303	3 US-08-660-148-6	Sequence 6, Appl1
8	171	9.4	3282	1 US-08-072-574-11	Sequence 11, Appl1
9	171	9.4	3282	1 US-08-486-270-11	Sequence 11, Appl1
10	171	9.4	3282	4 US-08-367-264-11	Sequence 11, Appl1
11	171	9.4	3282	4 US-09-153-757-11	Sequence 11, Appl1
12	171	9.4	3282	4 US-09-459-715-11	Sequence 11, Appl1
13	171	9.4	4085	1 US-08-072-574-7	Sequence 7, Appl1
14	171	9.4	4085	1 US-08-486-270-7	Sequence 7, Appl1
15	171	9.4	4085	3 US-08-367-264-7	Sequence 7, Appl1
16	171	9.4	4085	4 US-09-153-757-7	Sequence 7, Appl1
17	171	9.4	4085	4 US-09-459-715-7	Sequence 7, Appl1
18	171	9.4	4181	1 US-08-072-574-9	Sequence 9, Appl1
19	171	9.4	4181	1 US-08-486-270-9	Sequence 9, Appl1
20	171	9.4	4181	3 US-08-367-264-9	Sequence 9, Appl1
21	171	9.4	4181	4 US-09-153-757-9	Sequence 9, Appl1
22	171	9.4	4181	4 US-09-459-715-9	Sequence 9, Appl1
23	33	1.8	241	4 US-09-389-681-334	Sequence 334, App
24	33	1.8	241	4 US-09-620-4058-334	Sequence 334, App
25	33	1.8	241	4 US-09-433-8268-334	Sequence 334, App
26	33	1.8	241	4 US-09-604-2874-334	Sequence 334, App
27	33	1.8	940	2 US-08-471-717-1	Sequence 1, Appl1

28	33	1.8	981	3 US-08-915-225-1	Sequence 1, Appl1
29	33	1.8	1277	4 US-09-187-999-30	Sequence 30, Appl1
30	33	1.8	1413	4 US-09-504-445-1	Sequence 1, Appl1
31	33	1.8	1445	4 US-09-814-951A-1	Sequence 1, Appl1
32	33	1.8	1810	4 US-09-369-247-11	Sequence 11, Appl1
33	33	1.8	2051	4 US-09-399-913-52	Sequence 52, Appl1
34	33	1.8	2797	4 US-09-482-273-74	Sequence 74, Appl1
35	33	1.8	3080	4 US-09-489-041A-25	Sequence 25, Appl1
36	33	1.8	3080	4 US-09-245-281-25	Sequence 25, Appl1
37	33	1.8	3080	4 US-09-207-3598-25	Sequence 25, Appl1
38	33	1.8	3080	4 US-09-340-620A-25	Sequence 25, Appl1
39	33	1.8	3312	4 US-09-669-751-259	Sequence 259, App
40	33	1.8	3385	3 US-08-405-392-1	Sequence 1, Appl1
41	33	1.8	3385	3 US-08-487-691-1	Sequence 1, Appl1
42	33	1.8	3385	3 US-08-666-221B-3	Sequence 3, Appl1
43	33	1.8	3385	3 US-08-666-221B-9	Sequence 9, Appl1
44	33	1.8	3385	4 US-08-189-738A-1	Sequence 1, Appl1
45	33	1.8	3637	1 US-08-445-640-3	Sequence 3, Appl1

#### ALIGNMENTS

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RESULT 1
US-09-695-481-1
; Sequence 1, Application US/09695481
; Patent No. 6534287
; GENERAL INFORMATION:
; APPLICANT: STORMANN, THOMAS M.
; APPLICANT: LEVINTHAL, CYNTHIA
; APPLICANT: STORJOHAN, LAURA
; APPLICANT: HAMBERLAND, LANCE G.
; APPLICANT: KRAPCHO, KAREN J.
; APPLICANT: NPS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: A NOVEL HUMAN METABOTROPIC GLUTAMATE RECEPTOR
; FILE REFERENCE: 1094.2.6
; CURRENT APPLICATION NUMBER: US/09/695,481
; CURRENT FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 60/161,481
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2826
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2826)
US-09-695-481-1
Query Match 12.2%; Score 222; DB 4; Length 2826;
Best Local Similarity 99.1%; Pred. No. 7.1e+88;
Matches 422; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 464 TGGCCATTAGAGTCCGAAATTTGCTCAGCTTTTCAACCTACTGATTCCTACTGAG 523
DB 461 TAGCCATTAGAGTCCGAAATTTGCTCAGCTTTTCAACCTACTGATTCCTACTGAG 520
QY 524 CAACCATCATGATCATGATGATGATCAAGACTCTGTTCAAAATTTTCATGAGGGTTGCTT 583
DB 521 CAACCATCATGATCATGATGATGATCAAGACTCTGTTCAAAATTTTCATGAGGGTTGCTT 580
QY 584 CAGATCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 643
DB 581 CAGATCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 640
QY 644 TATCAGCCTTACACACACACACACACACACACACACACACACACACACACACACAC 703
DB 641 TATCAGCCTTACACACACACACACACACACACACACACACACACACACACACACAC 700
QY 704 TGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 763
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FT	CDS		460..4002	/tag= a	
FT				/product= "Human metabotropic glutamate receptor,	
FT				mglur5A"	
XX					
PN			US6211353-B1.		
PD			03-APR-2001.		
XX					
PP			07-JUN-1996;	96US-0660148.	
XX					
PR			29-JUL-1994;	94US-0282853.	
XX					
PA			(ELIL ) LILLY & CO ELI.		
PI			Burnett JP, Mayne NG, Sharp RL, Snyder YM;		
XX					
DR			WPI; 2001-289639/30.		
XX			P-PSD; AAE01156.		
PT			New isolated nucleic acids for producing human metabotropic glutamate receptors, which are useful for modulating the presynaptic release of glutamate or the postsynaptic sensitivity of the neuronal cell to glutamate excitation -		
PS			Claim 2; Column 59-68; 53pp; English.		
XX			The present sequence is a cDNA encoding human metabotropic glutamate receptor, mglur5A. L-glutamate, the most abundant neurotransmitter in the central nervous system (CNS), mediates excitatory pathway in mammals. L-glutamate is referred to as excitatory amino acid (EAA) and the receptors that respond to glutamate are EAA receptors. The receptors are useful for modulating the presynaptic release of glutamate and the postsynaptic sensitivity of the neuronal cell to glutamate excitation.		
CC			Note: The present sequence is stated as being the same as that shown as SEQ ID NO:1 (AADO5033) in column 7-18 of the specification. However the sequences differ at several positions.		
XX					
SQ			Sequence 4207 BP; 1011 A; 1120 C; 1112 G; 964 T; 0 other;		
Query Match			12.2%; Score 222; DB 22; Length 4207;		
Best Local Similarity			99.1%; Pred. No. 7,1e-77;		
Matches			422; Conservative 0; Mismatches 4; Indels 0; Gaps 0;		
QY			464 TAGCCATTGAGTCCAGAAATTTGCTCGACGCTTTTCACAATACCTCAATGCTTA CTGAG 523		
DB			920 TAGCCATTGAGTCCAGAAATTTGCTCGACGCTTTTCACAATACCTCAATGCTTA CTGAG 979		
QY			524 CAACCATCANTGATCTGAGTGAACAAGAATCTGTTCATAATATTTCATGAGGGTGTGCCTT 583		
DB			980 CAACCATGATGATCTGAGTGAACAAGAATCTGTTCATAATATTTCATGAGGGTGTGCCTT 1039		
QY			584 CAGATGCTCACAGGACAGTTCATGTGTGACATAGTAGAAGGTACAACTGACCTATG 643		
DB			1040 CAGATGCTCACAGGACAGGACAGTTCATGTGTGACATAGTAGAAGGTACAACTGACCTATG 1099		
QY			644 TATCAGCCGTACACACAGAAAGCACTATGAGAAAAGTGGAATGGAACCTTCAAAGATA 703		
DB			1100 TATCAGCCGTACACACAGAAAGCACTATGAGAAAAGTGGAATGGAACCTTCAAAGATA 1159		
QY			704 TGTCAGCAAGAAAGGAAATTTGCAATGCCCACTCTTACAAAAATCTACAGTAATGACGGG 763		
DB			1160. TGTCAGCAAGAAAGGAAATTTGCAATGCCCACTCTTACAAAAATCTACAGTAATGACGGG 1219		
QY			764 AGCAGAGCTTGTATAGCTGTGCGAAGAGCTCAACAAGTCACTTGCCCAAGGCCGGGGTG 823		
DB			1220 AGCAGAGCTTGTATAGCTGTGCGAAGAGCTCAACAAGTCACTTGCCCAAGGCCGGGGTG 1279		
QY			824 TGGCTACTTCTGTGAGGCGATGACGATGAGAGGTCTGCTGATGCGCATGAGCGCCTTGG 883		
DB			1280 TGGCTACTTCTGTGAGGCGATGACGATGAGAGGTCTGCTGATGCGCATGAGCGCCTTGG 1339		
QY			884 GTCTAG 889		

Db		 1340 GCTTAG 1345
	RESULT 15	
XX	AAD05030	
XX	AAD05030 standard; mRNA; 4207 BP.	
AC	AAD05030;	
XX		
DT	17-JUL-2001 (first entry)	
XX		
DE	Human metabotropic glutamate receptor, mGluR5A mRNA.	
KW	Human; metabotropic glutamate receptor; mGluR5A; excitatory amino acid,	
RN	EAA; central nervous system; CNS; presynaptic release; neurotransmitter;	
KM	postsynaptic sensitivity; glutamate excitation; 89.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	460..4002
FT	/tag= a	
FT	/product= "Human metabotropic glutamate receptor,	mGluR5A"
FT		
FN	US6211353-B1.	
XX		
PD	03-APR-2001.	
XX		
PE	07-JUN-1996; 96US-0660148.	
XX		
PR	29-JUL-1994; 94US-0282853.	
XX		
PA	(EHLI ) LILLY & CO E.L.I.	
PI	Burnett JP, Mayne NG, Sharp RL, Snyder YM;	
DR	WPI; 2001-289639/30.	
DR	P-PSDB; AAE01156.	
XX		
PT	New isolated nucleic acids for producing human metabotropic glutamate	
PT	receptors, which are useful for modulating the presynaptic release of	
PT	glutamate or the postsynaptic sensitivity of the neuronal cell to	
PT	glutamate excitation -	
XX		
PS	Claim 2; Column 43-46; 53pp; English.	
XX		
CC	The present sequence is a mRNA encoding human metabotropic glutamate	
CC	receptor, mGluR5A. D-glutamate, the most abundant neurotransmitter in	
CC	the central nervous system (CNS), mediates excitatory pathway in	
CC	mammals. D-glutamate is referred to as excitatory amino acid (EAA) and	
CC	the receptors that respond to glutamate are EAA receptors. The receptors	
CC	are useful for modulating the presynaptic release of glutamate and the	
CC	postsynaptic sensitivity of the neuronal cell to glutamate excitation.	
XX		
SQ	Sequence 4207 BP; 1010 A; 1121 C; 1112 G; 964 U; 0 other;	
	Query Match 12.2%; Score 222; DB 22; Length 4207;	
	Best Local Similarity 76.3%; Pred. No. 7.1e-77;	
	Matches 325; Conservative 97; Mismatches 4; Indels 0; Gaps 0;	
OY	464 TAGCATTCAGGTCAGGAATTGGTCTCGAGTTTCAACATACCTCAGATTGCTTACTACG 523 ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::	
Db	920 UAGGCCAUUCAGGUCUACAUAUUUGUCUGAGCUUUUCAACAUACCUCAGAUGUCUACUAG 979	
OY	524 CAACCATCATGATCTGTATGACAAAGACTCTGTTCATAATATTTTCATAGAGGTGTGCTT 583 ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::	
Db	980 CAACACCAUGAGUAGUACAAGACUCUGUTCCAUAUUVUUCUAGAAGGUUUGUCCUU 1039	
OY	584 CAGATGCTCAGCAGGCAAGGTCACATGTGTGACATATGGAAGAGGTACCACTGCATATG 643 ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::	
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QY 1384 GAGGACCTTATGCTTGGATGTTTAAAGACGATTCAGTGCAGTCTCTTACACC 1443  
 CC 1814 GAGGACCTTATGCTTGGATGTTTAAAGACGATTCAGTGCAGTCTCTTACACC 1873  
 Db 1444 TCCCGATTACCTGAGTATGTTCCCAAGACCTAACCAACATGATGATTTCTGGAT 1503  
 QY 1874 TCCCGATTACCTGAGTATGTTCCCAAGACCTAACCAACATGATGATTTCTGGAT 1933  
 Db 1504 TCGAAGCTAGACCTGAGTATGTTCCCAAGACCTAACCAACATGATGATTTCTGGAT 1563  
 QY 1934 TCGAAGCTAGACCTGAGTATGTTCCCAAGACCTAACCAACATGATGATTTCTGGAT 1993  
 Db 1564 CCGAATGCTCTTCACTCTGAGGCTATCTTTGCTGATTCATCTGACCA 1623  
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 QY 2054 GAGACAAATCAGAAATGTTTATCTGCTGAGAACCCCTTATCCATTAAGCCCTCT 2113  
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 QY 2234 AAAAAA 2241

## RESULT 10

ACAS6535

ID ACAS6535 standard; cDNA; 4078 BP.

ACAS6535;

06-JUN-2003 (first entry)

Human signalling pathway polynucleotide probe SEQ ID NO 1133.

Human; Probe; ss; array element; Parkinson's disease;

signalling pathway population; cancer; adenocarcinoma; leukaemia;

immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.

Homo sapiens.

US6500938-B1.

31-DEC-2002.

30-JAN-1998; 98US-0016434.

30-JAN-1998; 98US-0016434.

'INCY-') INCYTE GENOMICS INC.

Au-Young J, Seilhamer JF;

MPI, 2003-352189/33.

Combination of polynucleotide probes, useful as array elements in a

microarray for monitoring the expression of a number of target

polynucleotides

Claim 1; SEQ ID NO 1133; 65bp; English.

The invention relates to a combination which comprises a number of

polynucleotide probes comprising a sequence selected from one of the 1490

sequences mentioned in the specification. The combination is useful as an

of target polynucleotides. The microarray is particularly useful in the  
 diagnosis and treatment of cancer and immunopathology and neuropathology.  
 The microarray is useful in diagnostics and treatment regimens, drug  
 discovery and development, toxicological and carcinogenicity studies,  
 for immunology and pharmacogenomics. The microarray is also useful for  
 monitoring progression of diseases and for developing sophisticated  
 profiles for the effects of currently available therapeutic drugs. The  
 combination is also useful for purifying a subpopulation of mRNAs, cDNAs  
 and genomic fragments and in research and diagnostic applications. The  
 array can detect changes in expression in a large number of genes coding  
 for different signalling pathway populations which can be used to diagnose  
 various diseases including cancer e.g. adenocarcinoma and leukaemia,  
 immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease  
 and Parkinson's disease. The present sequence represents a polynucleotide  
 probe of the invention.  
 Note: The sequence data for this patent did not form part of the printed  
 CC specification but was obtained in electronic format directly from USPTO  
 at seqdata.uspto.gov/sequence.html?docid=06500938B1.

Sequence 4078 BP; 994 A; 1074 C; 1076 G; 934 T; 0 other;

Query Match 48.9%; Score 891.4; DB 25; Length 4078;

Best Local Similarity 98.3%; Pred. No. 1.3e-215;

Matches 901; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1 AAAAAATGCTCTTCTGTTGATTCCTGTCAGTCTTATCTTTGAAAGAAATGCTGGAGT 60  
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 QY 61 GCACAGTCCAGTGAAGAGAGGAGTGTGCTCACATGCTGGGTGACATCATTTATGAGCT 120  
 Db 208 GCACAGTCCAGTGAAGAGAGGAGTGTGCTCACATGCTGGGTGACATCATTTATGAGCT 267  
 QY 121 CTCCTTTCTGTTTCATGACCAAGCTTCTGTCAGGAAATTCATGAGAGAAAGTGGGCA 180  
 Db 268 CTCCTTTCTGTTTCATGACCAAGCTTCTGTCAGGAAATTCATGAGAGAAAGTGGGCG 327  
 QY 181 GTCCGTGAACAGTATGAGCATTCAGAGAGTGGAGCCATGCTGCATTCCTGGAAGATC 240  
 Db 328 GTCCGTGAACAGTATGAGCATTCAGAGAGTGGAGCCATGCTGCATTCCTGGAAGATC 387  
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 Db 388 AATTGAGACCCCACTCTTGGCCCAATCATCACTGGGCTGTGAGATTAAGGATTCCTGTC 447  
 QY 301 TGGCATTTGGCTGTGAGCCCTTAAGAGCAGCATTTGATTAAGAGATTCCTCATTTCT 360  
 Db 448 TGGCATTTGGCTGTGAGCCCTTAAGAGCAGCATTTGATTAAGAGATTCCTCATTTCT 507  
 QY 361 TCGAAGAGAGAGAGGCTTTGATGCTCTGTGAGATGAGTCTCTCTCTCCCTCCCTCC 420  
 Db 508 TCGAAGAGAGAGAGGCTTTGATGCTCTGTGAGATGAGTCTCTCTCTCCCTCCCTCC 567  
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 Db 808 GAGGCACTATGAGAAAGTGGATGAGAGCTTTCAAGATATGTCAGGAGAGAGG 867







PN US6211353-B1.  
 XX 03-APR-2001.  
 XX 07-JUN-1996; 96US-0660148.  
 XX 29-JUL-1994; 94US-0282853.  
 XX (ELIL ) LILLY & CO ELI.  
 PI Burnett JP, Mayne NG, Sharp RL, Snyder YM;  
 XX WPI; 2001-289639/30.  
 DR P-PSDB; AAE01156.  
 XX  
 PT New isolated nucleic acids for producing human metabotropic glutamate  
 PT receptors, which are useful for modulating the presynaptic release of  
 PT glutamate or the postsynaptic sensitivity of the neuronal cell to  
 PT glutamate excitation -  
 XX  
 PS Claim 2; Column 43-46; 53pp; English.  
 CC The present sequence is a mRNA encoding human metabotropic glutamate  
 CC receptor, mGluR5A. L-glutamate, the most abundant neurotransmitter in  
 CC the central nervous system (CNS), mediates excitatory pathway in  
 CC mammals. L-glutamate is referred to as excitatory amino acid (EAA) and  
 CC the receptors that respond to glutamate are EAA receptors. The receptors  
 CC are useful for modulating the presynaptic release of glutamate and the  
 CC postsynaptic sensitivity of the neuronal cell to glutamate excitation.  
 CC  
 XX Sequence 4207 BP; 1010 A; 1121 C; 1112 G; 964 U; 0 other;  
 SQ  
 Query Match 48.9%; Score 891.4; DB 22; Length 4207;  
 Best Local Similarity 73.9%; Pred. No. 1.4e-215;  
 Matches 678; Conservative 223; Mismatches 16; Indels 0; Gaps 0;  
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 QY 301 TGGCATTGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATTCCT 360  
 DB 757 UGGCAUUCGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATTC 816  
 QY 361 TCGGATTC 420  
 DB 817 UCGATTC 876  
 QY 421 AAGATTC 480  
 DB 877 AAGATTC 936  
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DB 997 AGUGACAAGACUCUGUCAAUUAUUGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1056  
 QY 601 AGTTCATGAGTGAAG 660  
 DB 1057 AGGAG 1116  
 QY 661 GAAAGCAATATGAG 720  
 DB 1117 GAAAGCAATATGAG 1176  
 QY 721 AATTGATGAG 780  
 DB 1177 AATGATGAG 1236  
 QY 781 CTGCTGAAG 840  
 DB 1237 CUGGAG 1296  
 QY 841 GGCATGAG 900  
 DB 1297 GGCATGAG 1356  
 QY 901 CTGCTTGTGAG 917  
 DB 1357 CUGGAG 1373  
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 AAD05033  
 ID AAD05033 standard; cDNA; 4207 BP.  
 XX  
 AC AAD05033;  
 XX  
 DT 17-JUL-2001 (first entry)  
 XX  
 DE Human metabotropic glutamate receptor, mGluR5A cDNA, alternative version.  
 XX  
 KW Human; metabotropic glutamate receptor; mGluR5A; excitatory amino acid;  
 KW EAA; central nervous system; CNS; presynaptic release; neurotransmitter;  
 KW postsynaptic sensitivity; glutamate excitation; 88.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key  
 FT misc\_feature  
 FT 416  
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 FT mGluR5A"  
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 FT specification (AAD05029)"  
 FT 4087  
 FT /tag= f  
 FT /note= "Nucleotide 'G' is present at this location  
 FT in the sequence shown in column 59-68 of the





GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 14, 2003, 04:35:06 ; Search time 118.716 Seconds  
(without alignments)  
6777.889 Million cell updates/sec

Title: US-10-027-923-1

Perfect score: 1823  
Sequence: 1 aaatgctctctctgtgtat.....aaaaaaaaaaaaaaaaaaaa 1823

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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3: /cgn2\_6/ptodata/2/ina/6A COMB.seq: \*  
4: /cgn2\_6/ptodata/2/ina/6B COMB.seq: \*  
5: /cgn2\_6/ptodata/2/ina/PTUS COMB.seq: \*  
6: /cgn2\_6/ptodata/2/ina/backfile1.seq: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed.  
and is derived by analysis of the total score distribution.

## SUMMARIES

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3	891.4	48.9	4207	3 US-08-660-148-3	Sequence 3, Appl
4	891.4	48.9	4303	3 US-08-660-148-4	Sequence 4, Appl
5	891.4	48.9	4303	3 US-08-660-148-6	Sequence 6, Appl
6	888.4	48.7	2826	4 US-09-695-481-1	Sequence 1, Appl
7	888.4	48.7	3129	4 US-09-695-481-5	Sequence 5, Appl
8	888.2	48.7	3282	1 US-08-072-574-11	Sequence 11, Appl
9	888.2	48.7	3282	1 US-08-486-270-11	Sequence 11, Appl
10	888.2	48.7	3282	4 US-08-367-264-11	Sequence 11, Appl
11	888.2	48.7	3282	4 US-09-153-757-11	Sequence 11, Appl
12	888.2	48.7	3282	4 US-09-459-715-11	Sequence 11, Appl
13	888.2	48.7	4085	1 US-08-072-574-7	Sequence 7, Appl
14	888.2	48.7	4085	1 US-08-486-270-7	Sequence 7, Appl
15	888.2	48.7	4085	3 US-08-367-264-7	Sequence 7, Appl
16	888.2	48.7	4085	4 US-09-153-757-7	Sequence 7, Appl
17	888.2	48.7	4085	4 US-09-459-715-7	Sequence 7, Appl
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19	888.2	48.7	4181	1 US-08-486-270-9	Sequence 9, Appl
20	888.2	48.7	4181	3 US-08-367-264-9	Sequence 9, Appl
21	888.2	48.7	4181	4 US-09-153-757-9	Sequence 9, Appl
22	888.2	48.7	4181	4 US-09-459-715-9	Sequence 9, Appl
23	458.2	25.1	3321	1 US-08-486-270-1	Sequence 1, Appl
24	458.2	25.1	3321	3 US-08-367-264-1	Sequence 1, Appl
25	458.2	25.1	3321	4 US-09-153-757-1	Sequence 1, Appl
26	458.2	25.1	3321	4 US-09-459-715-1	Sequence 1, Appl
27	458.2	25.1	3582	4 US-08-538-526-2	Sequence 2, Appl

28	458.2	25.1	4074	4 US-09-016-434-1475	Sequence 1475, Ap
29	449.2	24.6	3219	4 US-08-687-289A-3	Sequence 3, Appl
30	449.2	24.6	3219	4 US-09-435-897-3	Sequence 3, Appl
31	449.2	24.6	3384	2 US-08-687-289A-1	Sequence 1, Appl
32	449.2	24.6	3384	4 US-09-435-897-1	Sequence 1, Appl
33	449.2	24.6	4300	1 US-08-041-538-1	Sequence 1, Appl
34	449.2	24.6	4300	1 US-08-463-642-1	Sequence 1, Appl
35	449.2	24.6	4300	1 US-08-455-602-1	Sequence 1, Appl
36	449.2	24.6	4300	2 US-08-465-157-1	Sequence 1, Appl
37	449.2	24.6	5236	5 PCT-US91-09422-1	Sequence 1, Appl
38	449.2	24.6	5236	5 PCT-US91-09422-16	Sequence 16, Appl
39	444.4	24.4	3219	2 US-08-687-289A-4	Sequence 4, Appl
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41	437.4	24.0	3330	1 US-08-072-574-1	Sequence 1, Appl
42	144.2	7.9	4095	5 PCT-US91-09422-18	Sequence 18, Appl
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44	143.6	7.9	2736	4 US-09-817-464-1	Sequence 0, Appl
45	143.6	7.9	3431	4 US-09-641-318-1	Sequence 1, Appl

## ALIGNMENTS

RESULT 1  
US-09-016-434-1133  
Sequence 1133, Application US/09016434  
Patent No. 6500938  
GENERAL INFORMATION:  
APPLICANT: Janice Au-Young  
APPLICANT: Jeffrey J. Sellhammer  
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
NUMBER OF SEQUENCES: 1490  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 PORTER DRIVE  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/016,434  
FILING DATE: HEREWITH  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Zeller, Karen J.  
REGISTRATION NUMBER: 37,071  
REFERENCE/DOCKET NUMBER: PA-0002 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 855-0555  
TELEFAX: (650) 845-4166  
INFORMATION FOR SEQ ID NO: 1133:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4078 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GENBANK  
CLONE: g1408051  
US-09-016-434-1133  
Query Match 48.9%; Score 891.4; DB 4; Length 4078;  
Best Local Similarity 98.3%; Pred. No. 3.3e-211;

Matches 901; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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QY 1 AAAATGTCCTTCTGTTGATTCCTGTCAGTCTTACTTTTGAAGAAAGATGTCGGAGT 60
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QY 61 GCACAGTCAGTGAAGAGGAGTGTGGCTCACTGTCGGTGCATCATTTATTTGAGT 120
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RESULT 2  
US-08-660-148-1  
; Sequence 1, Application US/08660148  
; Patent No. 6211353  
; GENERAL INFORMATION:  
; APPLICANT: Burnett, J. P.

```

? APPLICANT: Mayne, Nancy G.
? APPLICANT: Sharp, Robert L.
? APPLICANT: Snyder, Yvonne M.
? TITLE OF INVENTION: EXCITATORY AMINO RECEPTOR PROTEIN AND
? TITLE OF INVENTION: RELATED NUCLEIC ACID COMPOUNDS
? NUMBER OF SEQUENCES: 6
? CORRESPONDENCE ADDRESS:
? ADDRESS: Eli Lilly and Company
? STREET: Lilly Corporate Center
? CITY: Indianapolis
? STATE: Indiana
? COUNTRY: United States of America
? ZIP: 46285
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/660,148
? FILING DATE:
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US/08/282,853
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:
? NAME: Gaylo, Paul J.
? REGISTRATION NUMBER: 36,808
? REFERENCE/DOCKET NUMBER: X-9419
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (317) 276-0756
? TELEFAX: (317) 276-3861
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 4207 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 460..3999
? US-08-660-148-1
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Query Match 48.9%; Score 891.4; DB 3; Length 4207;
Best Local Similarity 98.3%; Pred. No. 3.3e-211;
Matches 901; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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QY 301 TGGCATTGCGCTGTGGCTTGAAGCAGAGCATTTGATTAAGAGATTCCTCATTTCT 360
DB 757 TGGCATTGCGCTGTGGCTTGAAGCAGAGCATTTGATTAAGAGATTCCTCATTTCT 816
QY 361 TCGGAAGAAGAAAGGGCTTGTATGCTGTGTGATAGGCTTCCTCTTCCCTCCCTCC 420

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QY 841 GGCATGACGGTGAAGAGTCTGTCATGAGCCATGAGGGCCGAGGTCTAGTGGAGAAATT 900  
DB 1297 GGCATGACGGTGAAGAGTCTGTCATGAGCCATGAGGGCCGAGGTCTAGTGGAGAAATT 1356  
QY 901 CTGCTTCTGGGACAGGA 917  
DB 1357 CUGCUCUGGCGAGUGA 1373

RESULT 4  
US-08-660-148-4  
Sequence 4, Application US/08660148  
Patent No. 6211353  
GENERAL INFORMATION:  
APPLICANT: Burnette, J. P.  
APPLICANT: Mayne, Nancy G.  
APPLICANT: Sharp, Robert L.  
APPLICANT: Snyder, Yvonne M.  
TITLE OF INVENTION: EXCITATORY AMINO RECEPTOR PROTEIN AND  
TITLE OF INVENTION: RELATED NUCLEIC ACID COMPOUNDS  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Eli Lilly and Company  
STREET: Lilly Corporate Center  
CITY: Indianapolis  
STATE: Indiana  
COUNTRY: United States of America  
ZIP: 46285  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/660,148  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/282,853  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Gaylo, Paul J.  
REGISTRATION NUMBER: 36,808  
REFERENCE/DOCKET NUMBER: X-9419  
TELEPHONE: (317) 276-0756  
TELEFAX: (317) 276-3861  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4303 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 460..4095  
US-08-660-148-4

Query Match 48.9%; Score 891.4; DB 3; Length 4303;  
Best Local Similarity 98.3%; Pred. No. 3,3e-211;  
Matches 901; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1 AAATGCTCTTCTGTTGATCTGTCAGTCTTAATTGAAAGAGATGTCGGTGGAGT 60  
DB 457 AAATGCTCTTCTGTTGATCTGTCAGTCTTAATTGAAAGAGATGTCGGTGGAGT 516  
QY 61 GCACAGTCCGATGAGAGAGTGGTGGTCCATGATGCTGGTGGATCATCATTTTGAAGCT 120  
DB 517 GCACAGTCCGATGAGAGAGTGGTGGTCCATGATGCTGGTGGATCATCATTTTGAAGCT 576  
QY 121 CTCCTTTCTGTCATCACGAGCTACTGTGAGAGAGTTCATGAGAGAGTGTGGGCA 180

DB 577 CTCCTTTCTGTCATCACGAGCTACTGTGAGAGAGTTCATGAGAGAGTGTGGGCG 636  
QY 181 GTCCGTAAGACATGATGGCATTGAGAGATGAGAGCCATGCTGATACCTCTGAAAGATC 240  
DB 637 GTCCGTAAGACATGATGGCATTGAGAGATGAGAGCCATGCTGATACCTCTGAAAGATC 636  
QY 241 AATTGAGACCCACACTCTGGCCCAATCATCACTGGGCTGTGAGATTAAGGATTCCTGTC 300  
DB 697 AATTGAGACCCACACTCTGGCCCAATCATCACTGGGCTGTGAGATTAAGGATTCCTGTC 756  
QY 301 TGGCATTGGGCTGGGCTGAGAGAGAGATGAGAGATGAGATGAGATGAGATGAGATGAG 360  
DB 757 TGGCATTGGGCTGGGCTGAGAGAGAGATGAGAGATGAGATGAGATGAGATGAGATGAG 816  
QY 361 TCGAAGAGAGAGAGAGGCTGTGATGCTGTGAGATGAGATGAGATGAGATGAGATGAG 420  
DB 817 TCGAAGAGAGAGAGAGGCTGTGATGCTGTGAGATGAGATGAGATGAGATGAGATGAG 876  
QY 421 AAGAAGCCATAGTAGAGGAGTCAATGGGCTGTTCCAGTCTTAGCATTGAGATGAGTCCAG 480  
DB 877 AAGAAGCCATAGTAGAGGAGTCAATGGGCTGTTCCAGTCTTAGCATTGAGATGAGTCCAG 936  
QY 481 AATTGCTCCAGCTTTTCAACATACCTCAGATTTGTTACTCAGCAACCATCATGATCTG 540  
DB 937 AATTGCTCCAGCTTTTCAACATACCTCAGATTTGTTACTCAGCAACCATCATGATCTG 996  
QY 541 AGTGAAGACCTGTGTTCAATTTTCAATGAGAGGTTGCTTCAATGATGCTCAGAGGCA 600  
DB 997 AGTGAAGACCTGTGTTCAATTTTCAATGAGAGGTTGCTTCAATGATGCTCAGAGGCA 1056  
QY 601 AGGTCCATGTTGAGATGAGAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAG 660  
DB 1057 AGGTCCATGTTGAGATGAGAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAG 1116  
QY 661 GAAGGACATGATGAGAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 720  
DB 1117 GAAGGACATGATGAGAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 1176  
QY 721 AATTGATGAGCCCACTCTTCAAAATCTACAGTAATGACAGAGGAGTGAATGAG 780  
DB 1177 AATTGATGAGCCCACTCTTCAAAATCTACAGTAATGACAGAGGAGTGAATGAG 1236  
QY 781 CTGCTGAAGAGTCAAGTCACTTGGCCAGAGCCGAGTGGTGGTCTTCTGAG 840  
DB 1237 CTGCTGAAGAGTCAAGTCACTTGGCCAGAGCCGAGTGGTGGTCTTCTGAG 1296  
QY 841 GGCATGACGGTGAAGAGTCTGTCATGAGCCATGAGGCGCTGGGTCTAGTGGAGAAATT 900  
DB 1297 GGCATGACGGTGAAGAGTCTGTCATGAGCCATGAGGCGCTGGGTCTAGTGGAGAAATT 1356  
QY 901 CTGCTTCTGGGACAGGA 917  
DB 1357 CTGCTTCTGGGACAGGA 1373

RESULT 5  
US-08-660-148-6  
Sequence 6, Application US/08660148  
Patent No. 6211353  
GENERAL INFORMATION:  
APPLICANT: Burnette, J. P.  
APPLICANT: Mayne, Nancy G.  
APPLICANT: Sharp, Robert L.  
APPLICANT: Snyder, Yvonne M.  
TITLE OF INVENTION: EXCITATORY AMINO RECEPTOR PROTEIN AND  
TITLE OF INVENTION: RELATED NUCLEIC ACID COMPOUNDS  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Eli Lilly and Company  
STREET: Lilly Corporate Center  
CITY: Indianapolis  
STATE: Indiana



```

COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,148
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/282,853
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: GAYLO, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-9419
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 4303 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: mRNA
US-08-660-148-6

Query Match      48.9%; Score 891.4; DB 3; Length 4303;
Best Local Similarity 73.9%; Pred. No. 3,3e-211;
Matches 678; Conservative 223; Mismatches 16; Indels 0; Gaps 0;

QY 1 AAAATGCTCTTCTGTGATCTGTCAAGTCTTGAAGAAGATGCTGGAGAT 60
DB 457 AAAATGCTCTTCTGTGATCTGTCAAGTCTTGAAGAAGATGCTGGAGAT 516
QY 61 GCACATCCAGTGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120
DB 517 GCACATCCAGTGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 576
QY 121 CTCTTCTGTTGATCATGACGACCTACTGTCGAGGAGGAGGAGGAGGAGGAG 180
DB 577 CUCUUUCUUGUUUUAUACACGACCUACUGUGGACAAAGUUUAUAGAGUUU 636
QY 181 GTCCGTGAACAGTATGAGATTGAGAGAGTGAAGAGGAGGAGGAGGAGGAG 240
DB 637 GUCCGUAACAGAUUGGACAUUAGAGAGGAGGAGGAGGAGGAGGAGGAG 696
QY 241 AATTGAGACCCCACTCTTGGCCCAATCATCACTGGGCTGTGAATTAAGGAT 300
DB 697 AAUUCAGACCCCACTCTTGGCCCAATCATCACTGGGCTGTGAATTAAGGAT 756
QY 301 TGGCATTTGGCTGTGGCCCTTGAAGAGAGGAGGAGGAGGAGGAGGAGGAG 360
DB 757 UGCAUUCUGGCTUUGGCTTGAAGAGAGGAGGAGGAGGAGGAGGAGGAG 816
QY 361 TCGAAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
DB 817 UCGAAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 876
QY 421 AAGAAGCCCACTAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
DB 877 AAGAAGCCCACTAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 936
QY 481 AATTGCTCAGGCTTTTCAACATACCTCAGATTGCTTACTCAGAAACCATGAT 540
DB 937 AAUUCGUCAGGCTTTCACATACCTCAGATTGCTTACTCAGAAACCATGAT 996
QY 541 AGTGAAGAAGCTGTCTTCAATAATTTTCATGAGGAGGAGGAGGAGGAGGAG 600
DB 997 AGTGAAGAAGCTGTCTTCAATAATTTTCATGAGGAGGAGGAGGAGGAGGAG 1056

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QY 601 AGTCCATGTTGAGACATAGTGAAGAGTCAACATGAGCCTATGTACAGCCGTCACACA 660
DB 1057 AGGCGCAUGGUGACAUUAGUAGAGGUGACACUGGACCUUAGUUAACACCGGACACA 1116
QY 661 GAAGGCACTATGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
DB 1117 GAAGGCACTATGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1176
QY 721 AATTGATGCCCACTCTTACAAATCTACAGTATGACAGGAGGAGGAGGAGGAG 780
DB 1177 AUUGCAUCCGCCCACTCTTACAAATCTACAGTATGACAGGAGGAGGAGGAGGAG 1236
QY 781 CAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
DB 1237 CAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1296
QY 841 GGCATGACGAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
DB 1297 GGCATGACGAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1356
QY 901 CTGCTTCTGGGACAGGAG 917
DB 1357 CUGCUCUGGAGGAGUGA 1373

RESULT 6
US-09-695-481-1
Sequence 1, Application US/09695481
Patent No. 6534287
GENERAL INFORMATION:
APPLICANT: STORMANN, THOMAS M.
APPLICANT: LEVINTHAL, CYNTHIA
APPLICANT: STOROHAN, LAURA
APPLICANT: HAMMERLAND, LANCE G.
APPLICANT: KRAPCHO, KAREN J.
APPLICANT: NPS PHARMACEUTICALS, INC.
TITLE OF INVENTION: A NOVEL HUMAN METABOTROPIC GLUTAMATE RECEPTOR
FILE REFERENCE: 1094.2.6
CURRENT APPLICATION NUMBER: US/09/695,481
CURRENT FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: 60/161,481
PRIOR FILING DATE: 1999-10-25
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 2826
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(2826)
US-09-695-481-1

Query Match      48.7%; Score 888.4; DB 4; Length 2826;
Best Local Similarity 98.2%; Pred. No. 1.6e-210;
Matches 898; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 4 ATGATCTCTTCTGTGATCTGTGATCTGTGATCTGTGATCTGTGATCTGTGAT 63
DB 1 ATGATCTCTTCTGTGATCTGTGATCTGTGATCTGTGATCTGTGATCTGTGAT 60
QY 64 CAGTCAAGTGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 123
DB 61 CAGTCAAGTGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120
QY 124 TTTTCTGTTCAATCAGAGGCTCTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 183
DB 121 TTTTCTGTTCAATCAGAGGCTCTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
QY 184 CGTGAACAGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 243
DB 181 CGTGAACAGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240

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QY 244 TCAGACCCCACTCTTGGCCCAATCACACTGGGCTGTGAGATTAAGGAATTCCTGCTGG 303  
Db 241 TCAGACCCCACTCTTGGCCCAATCACACTGGGCTGTGAGATTAAGGAATTCCTGCTGG 300  
QY 304 CATTGGCTGTGGCCCTTAGAGACAGAGCATTAAGTTCAATAAGATTCCCTCATTTCTTG 363  
Db 301 CATTGGCTGTGGCCCTTAGAGACAGAGCATTAAGTTCAATAAGATTCCCTCATTTCTTG 360  
QY 364 GAAGAGGAAAGAGGCTGTGATGCTGTGTGATGAGTCCCTCTTCTTCCCTCCGCTCCAG 423  
Db 361 GAAGAGGAAAGAGGCTGTGATGCTGTGTGATGAGTCCCTCTTCTTCCCTCCGCTCCAG 420  
QY 424 AAGCCCATAGAGGAGGCTATTGGGCTGTGTCCAGTTCTTTAGCCATTGAGTCCAGAAAT 483  
Db 421 AAGCCCATAGAGGAGGCTATTGGGCTGTGTCCAGTTCTTTAGCCATTGAGTCCAGAAAT 480  
QY 484 TTGCTCCAGCTTTTCAACATACCTCAGATTGCTTACTCAGCAACCATCATGATCTGAGT 543  
Db 481 TTGCTCCAGCTTTTCAACATACCTCAGATTGCTTACTCAGCAACCATCATGATCTGAGT 540  
QY 544 GACAAAGCTGTGTTCAATATTTTCAATGAGGTTGTGCTTCAATGCTCAGCAAGGCAAG 603  
Db 541 GACAAAGCTGTGTTCAATATTTTCAATGAGGTTGTGCTTCAATGCTCAGCAAGGCAAG 600  
QY 604 TCCATGTTGACATATGAGAGAGGTACAACTGACCTATGATCAGCCGTACACAGAA 663  
Db 601 GGCATGTGTGACATATGAGAGAGGTACAACTGACCTATGATCAGCCGTACACAGAA 660  
QY 664 GGCATATGAGAGAGGTGAGATGGAAGCCTTCAAGATATGTCAGGAAAGAGGATTT 723  
Db 661 GGCATATGAGAGAGGTGAGATGGAAGCCTTCAAGATATGTCAGGAAAGAGGATTT 720  
QY 724 TGCATGCCCCACTTTTCAAAATTTAATGATATGACAGGAGGAGGACCTTTGATTAACCTG 783  
Db 721 TGCATGCCCCACTTTTCAAAATTTAATGATATGACAGGAGGAGGACCTTTGATTAACCTG 780  
QY 784 CTGAAGAAGCTCAACAAGTCACTTGGCCCAAGGCGGGGTGTGAGCTTCTGTTGAGGGC 843  
Db 781 CTGAAGAAGCTCAACAAGTCACTTGGCCCAAGGCGGGGTGTGAGCTTCTGTTGAGGGC 840  
QY 844 ATGACGGTGAAGAGTCTGCTGATGAGGCAATGAGGCGCTGAGTCTAGTGGAGAAATTTCTG 903  
Db 841 ATGACGGTGAAGAGTCTGCTGATGAGGCAATGAGGCGCTGAGTCTAGTGGAGAAATTTCTG 900  
QY 904 CTTCTGGGCAAGGA 917  
Db 901 CTTCTGGGCAAGTA 914

RESULT 7  
US-09-695-481-5  
Sequence 5, Application US/09695481  
Patent No. 6534287  
GENERAL INFORMATION:  
APPLICANT: STORMANN, THOMAS M.  
APPLICANT: LEVINTHAL, CYNTHIA  
APPLICANT: STORJOHANN, LAURA  
APPLICANT: HAMERLAND, LANCE G.  
APPLICANT: KRAPCHO, KAREN J.  
APPLICANT: NPS PHARMACEUTICALS, INC.  
TITLE OF INVENTION: A NOVEL HUMAN METABOTROPIC GLUTAMATE RECEPTOR  
FILE REFERENCE: 1094.2.6  
CURRENT APPLICATION NUMBER: US/09/695,481  
CURRENT FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: 60/161,481  
PRIOR FILING DATE: 1999-10-25  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 5  
LENGTH: 3129  
TYPE: DNA  
ORGANISM: Artificial Sequence

FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:Chimeric  
OTHER INFORMATION: molecule comprising portions of human mglur5d and  
OTHER INFORMATION: the human calcium receptor.  
NAME/KEY: CDS  
LOCATION: (1..3129)  
US-09-695-481-5  
Query Match 48.7%; Score 888.4; DB 4; Length 3129;  
Best Local Similarity 98.2%; Pred. No. 1.6e-210;  
Matches 898; Conservative 0; Mismatches 16; Indels 0; Gaps 0;  
QY 4 ATGGCTCTTCTGTGATTCCTGTCAGTCTTATCTTTGAAAGAGATGTCGGTGGAGTGC 63  
Db 1 ATGGCTCTTCTGTGATTCCTGTCAGTCTTATCTTTGAAAGAGATGTCGGTGGAGTGC 60  
QY 64 CAGTCCAGTGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 123  
Db 61 CAGTCCAGTGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120  
QY 124 TTTTCTGTTTCATCAGCAGCCTACTGTGAGAGGAGTTCATGAGAGAGAGAGTGTGGGAGTTC 183  
Db 121 TTTTCTGTTTCATCAGCAGCCTACTGTGAGAGGAGTTCATGAGAGAGAGTGTGGGAGTTC 180  
QY 184 CGTGAACAGTANGGCAATTCAGAGAGTGAAGGCCATGCTGCAATCCCTGGAAGATCAAT 243  
Db 181 CGTGAACAGTANGGCAATTCAGAGAGTGAAGGCCATGCTGCAATCCCTGGAAGATCAAT 240  
QY 244 TCAGACCCCACTCTTGGCCCAATCACACTGGGCTGTGAGATTAAGGAATTCCTGCTGG 303  
Db 241 TCAGACCCCACTCTTGGCCCAATCACACTGGGCTGTGAGATTAAGGAATTCCTGCTGG 300  
QY 304 CATTGGCTGTGGCCCTTAGAGACAGAGCATTAAGTTCAATAAGATTCCCTCATTTCTTG 363  
Db 301 CATTGGCTGTGGCCCTTAGAGACAGAGCATTAAGTTCAATAAGATTCCCTCATTTCTTG 360  
QY 364 GAAGAGGAAAGAGGCTGTGATGCTGTGTGATGAGTCCCTCTTCTTCCCTCCGCTCCAG 423  
Db 361 GAAGAGGAAAGAGGCTGTGATGCTGTGTGATGAGTCCCTCTTCTTCCCTCCGCTCCAG 420  
QY 424 AAGCCCATAGAGGAGGCTATTGGGCTGTGTCCAGTTCTTTAGCCATTGAGTCCAGAAAT 483  
Db 421 AAGCCCATAGAGGAGGCTATTGGGCTGTGTCCAGTTCTTTAGCCATTGAGTCCAGAAAT 480  
QY 484 TTGCTCCAGCTTTTCAACATACCTCAGATTGCTTACTCAGCAACCATCATGATCTGAGT 543  
Db 481 TTGCTCCAGCTTTTCAACATACCTCAGATTGCTTACTCAGCAACCATCATGATCTGAGT 540  
QY 544 GACAAAGCTGTGTTCAAAATTTTCAATGAGGTTGTGCTTCAATGCTCAGCAAGGCAAG 603  
Db 541 GACAAAGCTGTGTTCAAAATTTTCAATGAGGTTGTGCTTCAATGCTCAGCAAGGCAAG 600  
QY 604 TCCATGTTGACATATGAGAGAGGTACAACTGACCTATGATCAGCCGTACACAGAA 663  
Db 601 GGCATGTGTGACATATGAGAGAGGTACAACTGACCTATGATCAGCCGTACACAGAA 660  
QY 664 GGCATATGAGAGAGGTGAGATGGAAGCCTTCAAGATATGTCAGGAAAGAGGATTT 723  
Db 661 GGCATATGAGAGAGGTGAGATGGAAGCCTTCAAGATATGTCAGGAAAGAGGATTT 720  
QY 724 TGCATGCCCCACTTTTCAAAATTTTCAATGAGGTTGTGCTTCAATGCTCAGCAAGGCAAG 783  
Db 721 TGCATGCCCCACTTTTCAAAATTTTCAATGAGGTTGTGCTTCAATGCTCAGCAAGGCAAG 780  
QY 784 CTGAAGAAGCTCAACAAGTCACTTGGCCCAAGGCGGGGTGTGAGCTTCTGTTGAGGGC 843  
Db 781 CTGAAGAAGCTCAACAAGTCACTTGGCCCAAGGCGGGGTGTGAGCTTCTGTTGAGGGC 840  
QY 844 ATGACGGTGAAGAGTCTGCTGATGAGGCAATGAGGCGCTGAGTCTAGTGGAGAAATTTCTG 903  
Db 841 ATGACGGTGAAGAGTCTGCTGATGAGGCAATGAGGCGCTGAGTCTAGTGGAGAAATTTCTG 900  
QY 904 CTTCTGGGCAAGGA 917



OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,270  
FILING DATE: 02-JUN-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/072,574  
FILING DATE: 04-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen E.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: PP41 9772  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-546-4737  
TELEFAX: 619-546-9392  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3282 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 370..3003  
OTHER INFORMATION: /product= "HUMAN MGLUR5C"  
OTHER INFORMATION: /note= "Variant of MGLUR5A with truncated 3' end."  
US-08-486-270-11

Query Match 48.7%; Score 888.2; DB 1; Length 3282;

Best Local Similarity 98.0%; Pred. No. 1,9e-210;

Matches 89; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 1 AAAATGCTCTTCTGTTGATCTGTGCTTACTTTTGAAGAAGATGCTGGAGT 60  
DB 367 AAAATGCTCTTCTGTTGATCTGTGCTTACTTTTGAAGAAGATGCTGGAGT 426  
QY 61 GCACAGTCAGTAGT 120  
DB 427 GCACAGTCAGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 486  
QY 121 CTCTTTCTGTTGATCTGTGCTTACTTTTGAAGAAGATGCTGGAGT 180  
DB 487 CTCTTTCTGTTGATCTGTGCTTACTTTTGAAGAAGATGCTGGAGT 546  
QY 181 GTCCGTGACAGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATC 240  
DB 547 GTCCGTGACAGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATC 606  
QY 241 AATTGACAGCCACACTTGTGCTTACTTTTGAAGAAGATGCTGGAGT 300  
DB 607 AATTGACAGCCACACTTGTGCTTACTTTTGAAGAAGATGCTGGAGT 666  
QY 301 TGGCATTCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 360  
DB 667 TGGCATTCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 726  
QY 361 TCGAAGT 420  
DB 727 TCGAAGT 786  
QY 421 AAGAAGCCATAGT 480  
DB 787 AAGAAGCCATAGT 846  
QY 481 AATTGCTCAGCTTTCAACATCTCAAGTCTTACTTCAAGCAACATGATGATG 540  
DB 847 AATTGCTCAGCTTTCAACATCTCAAGTCTTACTTCAAGCAACATGATGATG 906  
QY 541 AGTGACAAGACTCTGTTCAATATTTTCAATGAGAGGTTGCTTCAATGCTCAGCAGCA 600  
DB 907 AGTGACAAGACTCTGTTCAATATTTTCAATGAGAGGTTGCTTCAATGCTCAGCAGCA 966

QY 601 AGTCCATGATGAGCATAGTAAGAGAGTACAACTGACCTATGATACACCGTACACACA 660  
DB 967 AGGCGCATGATGAGCATAGTAAGAGAGTACAACTGACCTATGATACACCGTACACACA 1026  
QY 661 GAAGCACTATGAGT 720  
DB 1027 GAAGCACTATGAGT 1086  
QY 721 AATTGATGCGCCACTTTCACAAATCTACAGTAAGCAGGAGAGAGAGAGAGAGT 780  
DB 1087 AATTGATGCGCCACTTTCACAAATCTACAGTAAGCAGGAGAGAGAGAGAGT 1146  
QY 781 CTGCTGAAGAGCTCAAGTCACTTGCCCAAGGCCGGGTGAGCTTCTGTGAG 840  
DB 1147 CTGCTGAAGAGCTCAAGTCACTTGCCCAAGGCCGGGTGAGCTTCTGTGAG 1206  
QY 841 GGCATGACGGTAGAGAGTCTGTGATGACATGAGCGCTGGGTCTAGTGGAGAAATT 900  
DB 1207 GGCATGACGGTAGAGAGTCTGTGATGACATGAGCGCTGGGTCTAGTGGAGAAATT 1266  
QY 901 CTGCTTCTGGCAGGGA 917  
DB 1267 CTGCTTCTGGCAGTGA 1283

RESULT 10  
US-08-367-264-11  
Sequence 11, Application US/08367264  
Patent No. 6001581  
GENERAL INFORMATION:  
APPLICANT: Daggett, Lorrie  
APPLICANT: Ellis, Steven B.  
APPLICANT: Liaw, Chen  
APPLICANT: Pontsler, Aaron  
APPLICANT: Johnson, Edwin C.  
APPLICANT: Hees, Stephen D.  
TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,  
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME AND USES THEREOF  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Pretty, Schroeder, Brueggemann & Clark  
STREET: 444 South Flower Street, Suite 2000  
CITY: Los Angeles  
STATE: CA  
COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/367,264  
FILING DATE: 02-JUN-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/072,574  
FILING DATE: 04-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen E.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: PP41 9772  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-546-4737  
TELEFAX: 619-546-9392  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3282 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA

FEATURE:  
NAME/KEY: CDS  
LOCATION: 370..3003  
OTHER INFORMATION: /product= "HUMAN MGLUR5C"  
OTHER INFORMATION: /note= "variant of MGLUR5A with truncated 3' end."  
US-08-367-264-11

Query Match  
Best Local Similarity 98.0%; Pred. No. 1.9e-210;  
Matches 899; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

48.7%; Score 888.2; DB 3; Length 3282;

1 AAAATGCTCTTCTGTTGATCTCTGCACTCTTACCTTTGAAAGAGATGTCCTGGAGT 60  
367 AAAATGCTCTTCTGTTGATCTCTGCACTCTTACCTTTGAAAGAGATGTCCTGGAGT 426  
61 GCAAGCTCAGTGAAG 120  
427 GCAAGCTCAGTGAAG 486  
121 CTCTTTCTGTTCACTCAGCAGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180  
487 CTCTTTCTGTTCACTCAGCAGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 546  
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847 AATTGCTCAGCTCTGTTGATCTCTGCACTCTTACCTTTGAAAGAGATGTCCTGG 906  
541 AATTGCTCAGCTCTGTTGATCTCTGCACTCTTACCTTTGAAAGAGATGTCCTGG 600  
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601 AATTGCTCAGCTCTGTTGATCTCTGCACTCTTACCTTTGAAAGAGATGTCCTGG 660  
967 AATTGCTCAGCTCTGTTGATCTCTGCACTCTTACCTTTGAAAGAGATGTCCTGG 1026  
661 AATTGCTCAGCTCTGTTGATCTCTGCACTCTTACCTTTGAAAGAGATGTCCTGG 720  
1027 AATTGCTCAGCTCTGTTGATCTCTGCACTCTTACCTTTGAAAGAGATGTCCTGG 1086  
721 AATTGCTCAGCTCTGTTGATCTCTGCACTCTTACCTTTGAAAGAGATGTCCTGG 780  
1087 AATTGCTCAGCTCTGTTGATCTCTGCACTCTTACCTTTGAAAGAGATGTCCTGG 1146  
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DB 1267 CTGCTTCTGGGAGTGA 1283

RESULT 11  
US-09-153-757-11  
Sequence 11, Application US/09153757  
Patent No. 6413764  
GENERAL INFORMATION:  
APPLICANT: Daggett, Lorrie  
Ellis, Steven B.  
Law, Chen  
Pontsler, Aaron  
Johnson, Edwin C.  
Hess, Stephen D.  
TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,  
NUCLEIC ACIDS ENCODING SAME AND USES THEREOF  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESS: Precity, Schroeder, Brueggemann & Clark  
STREET: 444 South Flower Street, Suite 2000  
CITY: Los Angeles  
STATE: CA  
COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09153, 757  
FILING DATE: 15-Sep-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/486, 270  
FILING DATE: 02-JUN-1994  
APPLICATION NUMBER: US 08/072, 574  
FILING DATE: 04-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen E.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: FP41 9772  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-546-4737  
TELEFAX: 619-546-9392  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3282 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 370..3003  
OTHER INFORMATION: /product= "HUMAN MGLUR5C"  
/note= "variant of MGLUR5A with truncated 3' end."  
SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-09-153-757-11

Query Match  
Best Local Similarity 98.0%; Pred. No. 1.9e-210;  
Matches 899; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

48.7%; Score 888.2; DB 4; Length 3282;

1 AAAATGCTCTTCTGTTGATCTCTGCACTCTTACCTTTGAAAGAGATGTCCTGGAGT 60  
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61 GCAAGCTCAGTGAAG 120  
427 GCAAGCTCAGTGAAG 486  
121 CTCTTTCTGTTCACTCAGCAGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180

487 CTCCTTTCTGTTATATACAGCTTCTGATGACAAAGTTTATATAGAGAAAGTGTGGGGC 546  
181 GTCCGTGAACAGATAGGATTCAGAGAGTGAAGGCAATGCTGATACCTTGAAGAGATC 240  
547 GTCCGTGAACAGATAGGATTCAGAGAGTGAAGGCAATGCTGATACCTTGAAGAGATC 606  
241 AATTCAGACCCCACTTCTTGGCCCAATCACTGGGCTGTGAATGAAGGATTCCTG 300  
607 AATTCAGACCCCACTTCTTGGCCCAATCACTGGGCTGTGAATGAAGGATTCCTG 666  
301 TGGCATTGCGCTGTGGCCCTAGAGACAGAGATTAAGTTCAATTAAGATTCCTCATTTCT 360  
667 TGGCATTGCGCTGTGGCCCTAGAGACAGAGATTAAGTTCAATTAAGATTCCTCATTTCT 726  
727 TCAGAGAGAGAAAGGCTTGTGATGCTGTGATGCTGCTCTCTCTCTCTCTCTCTCT 786  
421 AAGAGCCCATATAGAGGCTTGTGATGCTGTGATGCTGCTCTCTCTCTCTCTCTCTCT 480  
787 AAGAGCCCATATAGAGGCTTGTGATGCTGTGATGCTGCTCTCTCTCTCTCTCTCTCT 846  
481 AATTTGCTCAGCTTTTCAACATACCTCAGATTGCTTACTCAGCAACCATCATGATCTG 540  
847 AATTTGCTCAGCTTTTCAACATACCTCAGATTGCTTACTCAGCAACCATCATGATCTG 906  
541 AGTGACAGAGCTGTGTTCAAAATATTTTCAATGAGGCTGTGCTTCAATGCTCAGAGCA 600  
907 AGTGACAGAGCTGTGTTCAAAATATTTTCAATGAGGCTGTGCTTCAATGCTCAGAGCA 966  
601 AGGTCCATGCTGACATAGTGAAGAGGTACAACTGACCTTATGATACAGCCCTTACACA 660  
967 AGGTCCATGCTGACATAGTGAAGAGGTACAACTGACCTTATGATACAGCCCTTACACA 1026  
661 GAAGGCACTATGAGAGAGGTGAGATGAGACCTTCAAAATATGTCAGAGGAGAGAGG 720  
1027 GAAGGCACTATGAGAGAGGTGAGATGAGACCTTCAAAATATGTCAGAGGAGAGAGG 1086  
721 AATTCATGCGCCACTCTTCAAAATATGTCAGATGATGAGAGGAGAGAGGAGAGGATG 780  
1087 AATTCATGCGCCACTCTTCAAAATATGTCAGATGATGAGAGGAGAGGAGAGGATG 1146  
781 CTCTGTAAGAGCTCAAACTCACTTGGCCAGAGGCTGTGCTGCTGCTGCTGCTGCTG 840  
1147 CTCTGTAAGAGCTCAAACTCACTTGGCCAGAGGCTGTGCTGCTGCTGCTGCTGCTG 1206  
841 GGCATGACGCTGAGAGGCTGTGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 900  
1207 GGCATGACGCTGAGAGGCTGTGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 1266  
901 CTGCTTCTGGGCAAGGA 917  
1267 CTGCTTCTGGGCAAGTGA 1283

RESULT 12

US-09-459-715-11

Sequence 11, Application US/09459715

Patent No. 6485919

GENERAL INFORMATION:

APPLICANT: Daggett, Lorrie

Ellis, Steven B.

Liaw, Chen

Pontsler, Aaron

Johnson, Edwin C.

Hess, Stephen D.

TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,

NUCLEIC ACIDS ENCODING SAME AND USES THEREOF

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSER: Pretty, Schroeder, Brueggemann &amp; Clark

STREET: 444 South Flower Street, Suite 2000

CITY: Los Angeles  
STATE: CA  
COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/459,715  
FILING DATE: 13-Dec-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/367,264  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen E.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: PP41 9772  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-546-4737  
TELEFAX: 619-546-5392  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3282 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
MOLECULE TYPE: cDNA  
FEATURES:  
NAME/KEY: CDS  
LOCATION: 370..3003  
OTHER INFORMATION: /product= "HUMAN MGLUR5C"  
/note= "variant of MGLUR5A with truncated 3' end."  
SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-09-459-715-11  
Query Match 48.7%; Score 888.2; DB 4; Length 3282;  
Best Local Similarity 98.0%; Pred. No. 1.9e-210;  
Matches 899; Conservative 0; Mismatches 18; Indels 0; Gaps 0;  
1 AAAATGTCCTTCTGTTGATTCCTGATGCTTACTTTTGAAGAGATGTCCTGGAGT 60  
367 AAAATGTCCTTCTGTTGATTCCTGATGCTTACTTTTGAAGAGATGTCCTGGAGT 426  
61 GCAAGTCCAGTGAAGAGAGGCTGTGCTCAGATGCTGGGTGACATCATTTAGAGCT 120  
427 GCAAGTCCAGTGAAGAGAGGCTGTGCTCAGATGCTGGGTGACATCATTTAGAGCT 486  
121 CTCCTTCTGTTGATTCACAGAGCTTCTGAGAGAGTTCATGAGAGAGAGTGGAGCA 180  
487 CTCCTTCTGTTGATTCACAGAGCTTCTGAGAGAGTTCATGAGAGAGAGTGGAGCA 546  
181 GTCCGTGAACAGATAGGATTCAGAGAGTGAAGGCAATGCTGATACCTTGAAGAGATC 240  
547 GTCCGTGAACAGATAGGATTCAGAGAGTGAAGGCAATGCTGATACCTTGAAGAGATC 606  
607 AATTCAGACCCCACTTCTTGGCCCAATCACTGGGCTGTGAATGAAGGATTCCTG 666  
241 AATTCAGACCCCACTTCTTGGCCCAATCACTGGGCTGTGAATGAAGGATTCCTG 300  
301 TGGCATTGCGCTGTGGCCCTAGAGACAGAGATTAAGTTCAATTAAGATTCCTCATTTCT 360  
667 TGGCATTGCGCTGTGGCCCTAGAGACAGAGATTAAGTTCAATTAAGATTCCTCATTTCT 726  
727 TCAGAGAGAGAAAGGCTTGTGATGCTGTGATGCTGCTCTCTCTCTCTCTCTCTCT 786  
421 AAGAGCCCATATAGAGGCTTGTGATGCTGTGATGCTGCTCTCTCTCTCTCTCTCTCT 480  
787 AAGAGCCCATATAGAGGCTTGTGATGCTGTGATGCTGCTCTCTCTCTCTCTCTCTCT 846

QY 481 AATTGCTCAGCTTTTCAACATACCTCAGATTTGTTACTCAGCAACCATCATGATCTG 540  
DB 847 AATTGCTCAGCTTTTCAACATACCTCAGATTTGTTACTCAGCAACCATCATGATCTG 906  
QY 541 AGTACAGAGCTCTGTTCAAAATATTTTCATGAGGGTGTGCTTCAGATGCTCAGCAGCA 600  
DB 907 AGTACAGAGCTCTGTTCAAAATATTTTCATGAGGGTGTGCTTCAGATGCTCAGCAGCA 966  
QY 601 AGTCCATGCTGACATATGTAAGAGGTACATCTGACCTTATGATCAGCCGTACACACA 660  
DB 967 AGGGCCATGCTGACATATGTAAGAGGTACATCTGACCTTATGATCAGCCGTACACACA 1026  
QY 661 GAAGCACTATGTAAGAGGTGTAAGAGGTGTAAGAGGTGTAAGAGGTGTAAGAGGTGTA 720  
DB 1027 GAAGCACTATGTAAGAGGTGTAAGAGGTGTAAGAGGTGTAAGAGGTGTAAGAGGTGTA 1086  
QY 721 ATTGATGCGCCCACTCTTACAAATCTACATATGACAGGAGGAGCAGCTTTGATTAAG 780  
DB 1087 ATTGATGCGCCCACTCTTACAAATCTACATATGACAGGAGGAGCAGCTTTGATTAAG 1146  
QY 781 CTGCTGAAGAGCTCAAGTCACTTGGCCCAAGCCCGGGTGGTGGCTTACTTGTGAG 840  
DB 1147 CTGCTGAAGAGCTCAAGTCACTTGGCCCAAGCCCGGGTGGTGGCTTACTTGTGAG 1206  
QY 841 GGCATGACGGTGAAGAGGTCTGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900  
DB 1207 GGCATGACGGTGAAGAGGTCTGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1266  
QY 901 CTGCTTCTGGGAGGAGA 917  
DB 1267 CTGCTTCTGGGAGGAGA 1283

RESULT 13  
US-08-072-574-7  
Sequence 7, Application US/08072574  
Patent No. 5521297  
GENERAL INFORMATION:  
APPLICANT: Daggett, Lorrie  
APPLICANT: Ellis, Steven B.  
APPLICANT: Liaw, Chen  
APPLICANT: Pontler, Aaron  
TITLE OF INVENTION: HUMAN MATABOTROPIC GLUTAMATE RECEPTORS,  
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME AND USES THEREOF  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESSES:  
ADDRESSES: Pretty, Schroeder, Brueggemann & Clark  
STREET: 444 South Flower Street, Suite 2000  
CITY: Los Angeles  
STATE: CA  
COUNTRY: USA  
ZIP: 00719  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/072,574  
FILING DATE: 19930604  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen E.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: P41 9383  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 213-622-7700  
TELEFAX: 213-489-4210  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4085 base pairs  
TYPE: nucleic acid

STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 370..3912  
OTHER INFORMATION: /product= "HUMAN MGLUR5A"  
US-08-072-574-7

Query Match 48.7%; Score 888.2; DB 1; Length 4085;  
Best Local Similarity 98.0%; Pred. No. 2e-210;  
Matches 899; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 1 AAAATGCTCTCTGTTGATCCGTGAGCTTACTTTGAAAGAAATGTCGCGGAGT 60  
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DB 427 GCACAGTCCAGTGAAGAGAGGTGTGCTCAATGCTGGTGAATCATTTATGAGCT 486  
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DB 487 CTCTTTTCTGTTCAATCAAGCTTACTGTGACGAAGTTCAATGAGAGAAATGTGGGCG 546  
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DB 547 GTCCCGTAACATATGAGGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 606  
QY 241 AATTGAGACCCCACTTGTGCCCAATCACTGGGCTGTGAGATTAAGGATTCCTGC 300  
DB 607 AATTGAGACCCCACTTGTGCCCAATCACTGGGCTGTGAGATTAAGGATTCCTGC 666  
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DB 727 TCGAAGAGAGAGAGAGGTGTGATGCTGTGAGAGAGAGAGAGAGAGAGAGAGAG 786  
QY 421 AAGAAGCCCATATGAGAGAGGTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480  
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QY 481 AATTGCTCAGCTTTTCAACATACCTCAGATTTGTTACTCAGCAACCATCATGATCTG 540  
DB 847 AATTGCTCAGCTTTTCAACATACCTCAGATTTGTTACTCAGCAACCATCATGATCTG 906  
QY 541 AGTACAGAGCTCTGTTCAAAATATTTTCATGAGGGTGTGCTTCAGATGCTCAGCAGCA 600  
DB 907 AGTACAGAGCTCTGTTCAAAATATTTTCATGAGGGTGTGCTTCAGATGCTCAGCAGCA 966  
QY 601 AGTCCATGCTGACATATGTAAGAGGTACATCTGACCTTATGATCAGCCGTACACACA 660  
DB 967 AGGGCCATGCTGACATATGTAAGAGGTACATCTGACCTTATGATCAGCCGTACACACA 1026  
QY 661 GAAGCACTATGTAAGAGGTGTAAGAGGTGTAAGAGGTGTAAGAGGTGTAAGAGGTGTA 720  
DB 1027 GAAGCACTATGTAAGAGGTGTAAGAGGTGTAAGAGGTGTAAGAGGTGTAAGAGGTGTA 1086  
QY 721 ATTGATGCGCCCACTCTTACAAATCTACATATGACAGGAGGAGCAGCTTTGATTAAG 780  
DB 1087 ATTGATGCGCCCACTCTTACAAATCTACATATGACAGGAGGAGCAGCTTTGATTAAG 1146  
QY 781 CTGCTGAAGAGCTCAAGTCACTTGGCCCAAGCCCGGGTGGTGGCTTACTTGTGAG 840  
DB 1147 CTGCTGAAGAGCTCAAGTCACTTGGCCCAAGCCCGGGTGGTGGCTTACTTGTGAG 1206  
QY 841 GGCATGACGGTGAAGAGGTCTGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900  
DB 1207 GGCATGACGGTGAAGAGGTCTGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1266

QY 901 CTGCTTCTGGGCGAGGA 917  
Db 1267 CTGCTTCTGGGCGAGGA 1283

## RESULT 14

US-08-486-270-7  
Sequence 7, Application US/08486270  
Patent No. 5807689

## GENERAL INFORMATION:

APPLICANT: Daggett, Lorrie  
APPLICANT: Ellis, Steven B.  
APPLICANT: Liaw, Chen  
APPLICANT: Pontsler, Aaron  
APPLICANT: Hesse, Stephen D.  
TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,  
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME AND USES THEREOF  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
STREET: 444 South Flower Street, Suite 2000  
CITY: Los Angeles  
STATE: CA  
COUNTRY: USA  
ZIP: 90071

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,270  
FILING DATE: 02-JUN-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/072,574  
FILING DATE: 04-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen B.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: FP41 9772  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-546-4737  
TELEFAX: 619-546-9392

## INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:  
LENGTH: 4085 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
FEATURE:

NAME/KEY: CDS  
LOCATION: 370..3912  
OTHER INFORMATION: /product= "HUMAN MGLUR5A"  
US-08-486-270-7

Query Match 48.7%; Score 888.2; DB 1; Length 4085;  
Best Local Similarity 98.0%; Pred. No. 2e-210;  
Matches 899; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 1 AAAATGCTCTTCTGTTGATCTGTCACTTACTTTGAAAGAGATGTCGGAGCT 60  
Db 367 AAAATGCTCTTCTGTTGATCTGTCACTTACTTTGAAAGAGATGTCGGAGCT 426  
QY 61 GCACAGTCAGTGAGAGGGGTGGCTCAATGCTGGGTGACATCATTAATTGAGCT 120  
Db 427 GCACAGTCAGTGAGAGGGGTGGCTCAATGCTGGGTGACATCATTAATTGAGCT 486  
QY 121 CTCCTTTCTGTTCAATCAAGCTTACTGTGAGCAAGTTCAATGAGAGAGTGTGGGCA 180  
Db 487 CTCCTTTCTGTTCAATCAAGCTTACTGTGAGCAAGTTCAATGAGAGAGTGTGGGCG 546

QY 181 GTCCGGAACAGATGAGCATTTAGAGAGTGAAGGCCATGCTGATACCTTGAAAGATC 240  
Db 547 GTCCGGAACAGATGAGCATTTAGAGAGTGAAGGCCATGCTGATACCTTGAAAGATC 606  
QY 241 AATTGACACCCCACTCTTGGCCCAATCACTGGGCTGTGAGTAAGAGATTCCTG 300  
Db 607 AATTGACACCCCACTCTTGGCCCAATCACTGGGCTGTGAGTAAGAGATTCCTG 666  
QY 301 TGGCATTTGGCTGTGGCCCTTAGAGCGAGCATTTGATTAAGATTCCTCATTTCT 360  
Db 667 TGGCATTTGGCTGTGGCCCTTAGAGCGAGCATTTGATTAAGATTCCTCATTTCT 726  
QY 361 TCGAAGAGAGAGAGGGCTTGGATATCTGTGATGAGCTCTCTCTTCTCCGCTCC 420  
Db 727 TCGAAGAGAGAGAGGGCTTGGATATCTGTGATGAGCTCTCTCTTCTCCGCTCC 786  
QY 421 AAGAACCCCATAGTAGGGGTCAATTTGGGCTGTGCAATTTAGCCATTCAGTCCAG 480  
Db 787 AAGAACCCCATAGTAGGGGTCAATTTGGGCTGTGCAATTTAGCCATTCAGTCCAG 846  
QY 481 AATTGCTCAGCTTTTCAACATACCTCAGATTTGCTTACTCAGCAACAGCATGATCTG 540  
Db 847 AATTGCTCAGCTTTTCAACATACCTCAGATTTGCTTACTCAGCAACAGCATGATCTG 906  
QY 541 AGTGAAGAAGCTGTTCAAAATATTTCATGAGGGTGTGCTTCAGATGCTCAGAGGCA 600  
Db 907 AGTGAAGAAGCTGTTCAAAATATTTCATGAGGGTGTGCTTCAGATGCTCAGAGGCA 966  
QY 601 AGGTCCATGTGACATAGTAAGAGGTACATCTGACCTATGATCAAGCCGTACACACA 660  
Db 967 AGGTCCATGTGACATAGTAAGAGGTACATCTGACCTATGATCAAGCCGTACACACA 1026  
QY 661 GAAGGCACTATGAGAAAGTGGATGAGAAAGCTTCAAGATTTGTCAGGAAGAGAGG 720  
Db 1027 GAAGGCACTATGAGAAAGTGGATGAGAAAGCTTCAAGATTTGTCAGGAAGAGAGG 1086  
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Db 1147 CTGCTGAAGAGCTCAAGTCACTTGCCCAAGGCCGGGTGTGAGCTTCTGTGAG 1206  
QY 841 GGCATGACGGTGAAGGTCTGCTGATGAGGCGATGAGGCGCTGGGTCTAGTGGAGATTT 900  
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QY 901 CTGCTTCTGGGCGAGGA 917  
Db 1267 CTGCTTCTGGGCGAGGA 1283

## RESULT 15

US-08-367-264-7  
Sequence 7, Application US/08367264  
Patent No. 6001581

## GENERAL INFORMATION:

APPLICANT: Daggett, Lorrie  
APPLICANT: Ellis, Steven B.  
APPLICANT: Liaw, Chen  
APPLICANT: Pontsler, Aaron  
APPLICANT: Johnson, Edwin C.  
TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,  
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME AND USES THEREOF  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
STREET: 444 South Flower Street, Suite 2000  
CITY: Los Angeles  
STATE: CA



COUNTRY: USA  
 ZIP: 90071  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/367,264  
 FILING DATE: 02-JUN-1994  
 CLASSIFICATION: 435  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/072,574  
 FILING DATE: 04-JUN-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Reiter, Stephen E.  
 REGISTRATION NUMBER: 31,192  
 REFERENCE/DOCKET NUMBER: PP41 9772  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 619-546-4737  
 TELEFAX: 619-546-9392  
 INFORMATION FOR SEQ. ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 4085 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: both  
 TOPOLOGY: both  
 MOLECULE TYPE: cDNA  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 370..3912  
 OTHER INFORMATION: /product= "HUMAN MGLUR5A"  
 US-08-367-264-7

Query Match 48.7%; Score 888.2; DB 3; Length 4085;  
 Best Local Similarity 98.0%; Pred. No. 2e-210;  
 Matches 899; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 1 AAAATGTCCTCTGTGATCCGTGACGCTTACTTTGAAAGAAAGATGCCGTGGAGT 60  
 DB 367 AAAATGTCCTCTGTGATCCGTGACGCTTACTTTGAAAGAAAGATGCCGTGGAGT 426  
 QY 61 GCACAGTCCAGTGAAGAGAGGAGTGTGCTCAATGCTGGGTGACATCATTTATTTGAGCT 120  
 DB 427 GCACAGTCCAGTGAAGAGAGGAGTGTGCTCAATGCTGGGTGACATCATTTATTTGAGCT 486  
 QY 121 CTCTTTTCTGTTTCATCAACAGCCTACTGTGAGCAAGATTCTATGAGAGAAAGTGGGCA 180  
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 QY 181 GTCCGTGAACAGTATGGCATTTGAGAGAGGAGCCATGTGATACCTTGGAAAGATC 240  
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QY 541 AGTGAAGAAGCTCTGTTCAAAATATTTCATGAGGAGTGTGCTTCAGATGCTCAGACGCA 600  
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 QY 601 AGGTCCATGATGAGACATAGTGAAGAGTCAACCTGACCTTATGATCAAGCCGTACACCA 660  
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 QY 781 CTGCTGAAGAAGTCACAAGTCACTTGCCCAAGGCCGGGTGTGCTTACTTCTGTAG 840  
 DB 1147 CTGCTGAAGAAGTCACAAGTCACTTGCCCAAGGCCGGGTGTGCTTACTTCTGTAG 1206  
 QY 841 GGCATGACGTTGAGAGAGTCTGCTGATGACCATGAGGCGCTGGGTCTAGTGGAGATTT 900  
 DB 1207 GGCATGACGTTGAGAGAGTCTGCTGATGACCATGAGGCGCTGGGTCTAGTGGAGATTT 1266  
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 DB 1267 CTGCTTCTGGGCAAGTGA 1283

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 14, 2003, 06:02:02 ; Search time 602.28 Seconds  
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Title: US-10-027-923-1

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Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 2201672 seqs, 166179959 residues

Total number of hits satisfying chosen parameters: 4403344

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	1787.6	98.1	1788	US-09-822-830A-61	Sequence 61, Appl1
3	1110	60.9	1110	US-10-027-923-3	Sequence 3, Appl1
4	891.4	48.9	489	US-10-225-567A-177	Sequence 177, Appl1
5	888.4	48.7	2826	US-10-346-241-1	Sequence 1, Appl1
6	888.4	48.7	3129	US-10-346-241-5	Sequence 5, Appl1
7	458.2	25.1	2634	US-09-826-509-346	Sequence 346, Appl1
8	458.2	25.1	3295	US-10-101-510-258	Sequence 258, Appl1
9	458.2	25.1	6619	US-10-225-567A-169	Sequence 169, Appl1
10	449.2	24.6	3219	US-10-300-473-3	Sequence 3, Appl1
11	449.2	24.6	3384	US-10-300-473-1	Sequence 1, Appl1
12	444.4	24.4	3219	US-10-300-473-4	Sequence 4, Appl1
13	263	14.4	687	US-10-027-632-211781	Sequence 211781, Appl1
14	263	14.4	687	US-10-027-632-211782	Sequence 211782, Appl1
15	263	14.4	687	US-10-027-632-211781	Sequence 211781, Appl1

16	263	14.4	687	US-10-027-632-211782	Sequence 211782, Appl1
17	197.8	10.9	2629	US-10-157-031-378	Sequence 378, Appl1
18	145.8	8.0	3867	US-10-255-149-1	Sequence 0, Appl1
19	143.6	7.9	2736	US-09-817-464-1	Sequence 1, Appl1
20	143.6	7.9	2736	US-10-331-289-1	Sequence 14, Appl1
21	143.6	7.9	3884	US-09-820-809-14	Sequence 175, Appl1
22	143.6	7.9	3884	US-10-225-567A-175	Sequence 179, Appl1
23	138.6	7.6	6122	US-10-225-567A-179	Sequence 3, Appl1
24	131.6	7.2	2621	US-10-251-661-3	Sequence 171, Appl1
25	131.6	7.2	2621	US-10-225-567A-171	Sequence 1, Appl1
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33	118.8	6.5	2748	US-10-083-168-70	Sequence 70, Appl1
34	118.8	6.5	2748	US-10-083-168-72	Sequence 72, Appl1
35	118.8	6.5	2748	US-09-817-464-13	Sequence 13, Appl1
36	118.8	6.5	2766	US-10-331-289-13	Sequence 13, Appl1
37	118.8	6.5	3804	US-09-817-464-3	Sequence 3, Appl1
38	118.8	6.5	3804	US-10-331-289-3	Sequence 3, Appl1
39	118.8	6.5	4312	US-10-225-567A-181	Sequence 181, Appl1
40	114.8	6.3	3321	US-10-353-690-85	Sequence 85, Appl1
41	114.8	6.3	3321	US-10-225-567A-183	Sequence 183, Appl1
42	92	5.0	2595	US-10-151-208-13	Sequence 13, Appl1
43	85.8	4.7	600	US-10-029-386-9681	Sequence 9681, Appl1
44	84	4.6	227	US-10-029-386-23381	Sequence 23381, Appl1
45	83.8	4.6	3361	US-10-002-854-1	Sequence 1, Appl1

#### ALIGNMENTS

RESULT 1  
US-10-027-923-1  
; Sequence 1, Application US/10027923  
; Publication No. US20020142330A1  
; GENERAL INFORMATION:  
; APPLICANT: Brian Galtner Bates  
; APPLICANT: Kamalaka Gulukota  
; APPLICANT: Yuhong Xie  
; APPLICANT: Janet Elizabeth Paulsen  
; TITLE OF INVENTION: NOVEL GLUTAMATE RECEPTOR MODULATORY PROTEINS AND  
; FILE REFERENCE: NUCLEIC ACID MOLECULES AND USES THEREFOR  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR FILING DATE: 2000-12-22  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 1823  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; . NAME/KEY: CDS  
; . LOCATION: (4)..(1110)  
US-10-027-923-1  
Query Match 100.0%; Score 1822.6; DB 14; Length 1823;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1823; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 AAATGCTCTCTGTGATCCGTGAGCTTACTTTGAAAGAGATGCGGGAGT 60  
QY GCACATCCAGTGAAGAGAGGAGTGTGCTCAATCTGGGTGACATCATTTATGGAGCT 120  
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QY 1801 AAAAAAAAAAAAAAAAAAAAAA 1823  
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RESULT 2  
US-09-822-830A-61  
Sequence 61, Application US/09822830A  
Patent No. US20020142952A1  
GENERAL INFORMATION:  
APPLICANT: Genetics Institute, Inc.  
APPLICANT: Wong, Gordon G.  
APPLICANT: Clark, Hilary  
APPLICANT: Fechtel, Kim  
APPLICANT: Agostino, Michael J.  
APPLICANT: Howes, Steven H.  
APPLICANT: Resnick, Richard J.  
APPLICANT: Gulukota, Kamalakar  
APPLICANT: Graham, James R.  
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS  
FILE REFERENCE: GIN 6402  
CURRENT FILING DATE: 2001-03-29  
PRIORITY FILING DATE: 2000-04-06  
PRIORITY FILING DATE: 2000-04-06  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 61  
LENGTH: 1788  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-822-830A-61

Query Match 98.1%; Score 1787.6; DB 10; Length 1788;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1787; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GGTCTTCTGTTGATCTGTCAGTCTTACTTTTGAAGAAGATGTCGAGAGTCA 60  
QY 66 GTCCAGTGAAGAGAGGTGGTGGTCACTGCTGGGGATCATATTTGAGACTCTT 125  
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QY 906 TCTGGGAGAGAAACCAAGATCCATCTTATGAGATCTCAAGAAACGATCTTATGGA 965  
DB 901 TCTGGGAGAGAAACCAAGATCCATCTTATGAGATCTCAAGAAACGATCTTATGGA 960  
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DB 961 AGACAGAGAGAAATGCAAGGCTCTTCAAGGCTTTGAGAGATATTTACAGAG 1020  
QY 1026 TGAATGCTGCTGCTGAGCAATGCCCCAGCTCTGAATCTAGAGTCAAGTCAAGGCCCAT 1085

DB 1021 TGAATGCTGCTGCTGAGCAATGCCCCAGCTCTGAATCTAGAGTCAAGTCAAGGCCCAT 1080  
QY 1086 CATGAGCTGAGAGAGAGGCTCATATTTCTGAGAGATTAATCTGATTAATGA 1145  
DB 1081 CATGAGCTGAGAGAGAGGCTCATATTTCTGAGAGATTAATCTGATTAATGA 1140  
QY 1146 AGCCAAAGCTCATATCTTCTGATGAGAGATTTGAGAGAACTTTGATGATGAGCCG 1205  
DB 1141 AGCCAAAGCTCATATCTTCTGATGAGAGATTTGAGAGAACTTTGATGATGAGCCG 1200  
QY 1206 TCAAAATGAGCCCATATCACTGCAACACTCAAGATTTCTTCAATGAGGCTCTCAGAC 1265  
DB 1201 TCAAAATGAGCCCATATCACTGCAACACTCAAGATTTCTTCAATGAGGCTCTCAGAC 1260  
QY 1266 TTTCACCTCTGGCAAGATTAATCTGAGAGGCTCCATGAGGAGACTCTTGAATTTGGGCTTT 1325  
DB 1261 TTTCACCTCTGGCAAGATTAATCTGAGAGGCTCCATGAGGAGACTCTTGAATTTGGGCTTT 1320  
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QY 1386 GGGACTCTTTAGTCTTGGAGTTGTTAAGAGCAATTCAGTGAAGTCTCTTTACCACTTC 1445  
DB 1381 GGGACTCTTTAGTCTTGGAGTTGTTAAGAGCAATTCAGTGAAGTCTCTTTACCACTTC 1440  
QY 1446 CCGAGTTACCTGAGATATGTCGAAGAGCTTCAACATCATGATGATTTCTGAGATTG 1505  
DB 1441 CCGAGTTACCTGAGATATGTCGAAGAGCTTCAACATCATGATGATTTCTGAGATTG 1500  
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QY 1566 TAAATGCTCTTCTCACTCTCTCAGAGGCTATCTTTGCTGATTCATCTGACAGGA 1625  
DB 1561 TAAATGCTCTTCTCACTCTCTCAGAGGCTATCTTTGCTGATTCATCTGACAGGA 1620  
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DB 1621 GACAAATCAAGAAATGTTTATGCTGAGAGAGCCCTTATTCATTAAGCCCTCTTC 1680  
QY 1686 CTGAGCTTATTAACAGAGCAAAATAGGTTCTGTTTATGCTGTAATGCAATTCAT 1745  
DB 1681 CTGAGCTTATTAACAGAGCAAAATAGGTTCTGTTTATGCTGTAATGCAATTCAT 1740  
QY 1746 GTTATTAACCTCAATTAATGTTTACTATTAATGAGTAAMCAG 1793  
DB 1741 GTTATTAACCTCAATTAATGTTTACTATTAATGAGTAAMCAG 1788

RESULT 3  
US-10-027-923-3  
; Sequence 3, Application US/10027923  
; Publication No. US20020142330A1  
; GENERAL INFORMATION:  
; APPLICANT: Brian Galcher Bates  
; APPLICANT: Kamalaka Gulukota  
; APPLICANT: Yuhong Xie  
; APPLICANT: Janet Elizabeth Paulsen  
; TITLE OF INVENTION: NOVEL GLUTAMATE RECEPTOR MODULATORY PROTEINS AND  
; FILE REFERENCE: GNN-024  
; CURRENT APPLICATION NUMBER: US/10/027,923  
; PRIOR APPLICATION NUMBER: 2001-12-21  
; PRIOR FILING DATE: 2000-12-22  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 1110  
; TYPE: DNA



QY 481 AATTTCCTCAGCTTTTCAACATACCTCAGATTGCTTACTCAGCAACCATCATGATCTG 540  
DB 628 AATTTCCTCAGCTTTTCAACATACCTCAGATTGCTTACTCAGCAACCATCATGATCTG 687  
QY 541 AGTGACAAGACTCTGTTCAATATTTTCATGAGGGTGTGCTTCAGATGCTCAGCAGGCA 600  
DB 688 AGTGACAAGACTCTGTTCAATATTTTCATGAGGGTGTGCTTCAGATGCTCAGCAGGCA 747  
QY 601 AGGTTCATGTTGACATATGTAAGAGGTTCAACTGAGCCATATGATCAGCCGATCAACA 660  
DB 748 AGGGCCATGTTGACATATGTAAGAGGTTCAACTGAGCCATATGATCAGCCGATCAACA 807  
QY 661 GAAGCACTATGAGAAAGTGGATGAGAGCTTCAAGATATGTCAGCAAGAGAGG 720  
DB 808 GAAGCACTATGAGAAAGTGGATGAGAGCTTCAAGATATGTCAGCAAGAGAGG 867  
QY 721 ATTTCATGCTCCCTCTTCAAAATCTACATATGACAGGGAGAGCAAGCTTTGATAG 780  
DB 868 ATTTCATGCTCCCTCTTCAAAATCTACATATGACAGGGAGAGCAAGCTTTGATAG 927  
QY 781 CTGCTGAGAGAGCTCAAGTCACTTGCCCAAGGCCCGGTGTGCTTACTTCTGTAG 840  
DB 928 CTGCTGAGAGAGCTCAAGTCACTTGCCCAAGGCCCGGTGTGCTTACTTCTGTAG 987  
QY 841 GGCATGACGGTGAAGAGTCTGCTGATGAGCCATGAGGCGCTGAGCTTATGAGAGATT 900  
DB 988 GGCATGACGGTGAAGAGTCTGCTGATGAGCCATGAGGCGCTGAGCTTATGAGAGATT 1047  
QY 901 CTGCTTCTGGGCAAGGA 917  
DB 1048 CTGCTTCTGGGCAAGGA 1064

## RESULT 5

US-10-346-241-1  
; Sequence 1, Application US/10346241  
; Publication No. US20030157647A1  
; GENERAL INFORMATION:  
; APPLICANT: STORMANN, THOMAS M.  
; APPLICANT: LEVINTHAL, CYNTHIA  
; APPLICANT: STOROHANN, LAURA  
; APPLICANT: HAMMERLAND, LANCE G.  
; APPLICANT: KRAPCHO, KAREN J.  
; APPLICANT: NPS PHARMACEUTICALS, INC.  
; TITLE OF INVENTION: A NOVEL HUMAN METABOTROPIC GLUTAMATE RECEPTOR  
; FILE REFERENCE: 1094.2.6  
; CURRENT APPLICATION NUMBER: US/10/346,241  
; CURRENT FILING DATE: 2003-01-17  
; PRIOR APPLICATION NUMBER: US/09/695,481  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: 60/161,481  
; PRIOR FILING DATE: 1999-10-25  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: Patent Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 2826  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(2826)  
US-10-346-241-1

Query Match 48.7%; Score 888.4; DB 13; Length 2826;  
Best Local Similarity 98.2%; Pred. No. 1.9e-234;  
Matches 898; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 4 ATGGCTCTCTGTGATCTCTGCAAGCTTACTTTTAAAGAAATGTCCTGGAGATGCA 63  
DB 1 ATGGCTCTCTGTGATCTCTGCAAGCTTACTTTTAAAGAAATGTCCTGGAGATGCA 60  
QY 64 CAGTCAGTGAAGAGGGTGTGCTCAATGCTGGTGAACATTAATTGAGCTCTC 123

DB 61 CAGTCAGTGAAGAGGGTGTGCTCAATGCTGGTGAACATTAATTGAGCTCTC 120  
QY 124 TTTTCGTTCATCACACAGCTTCTGTGAGAGAACTTCATGAGAGAGTGTGGGGCAGTC 183  
DB 121 TTTTCGTTCATCACACAGCTTCTGTGAGAGAACTTCATGAGAGAGTGTGGGGCAGTC 180  
QY 184 CGTGAACTATGAGCACTTTCAGAGAGTGAAGCCATGCTCATACCTCTGAAAGATCAAT 243  
DB 181 CGTGAACTATGAGCACTTTCAGAGAGTGAAGCCATGCTCATACCTCTGAAAGATCAAT 240  
QY 244 TGAAGCCCACTCTTGGCCCAACATCACATGAGGCTGTGAATTAAGGATTCCTGCTGG 303  
DB 241 TGAAGCCCACTCTTGGCCCAACATCACATGAGGCTGTGAATTAAGGATTCCTGCTGG 300  
QY 304 CATGGGCTGTGGCCCTTAAGAGAGCATTTAGTTTATTAAGATTCCTCATTTTCTTG 363  
DB 301 CATGGGCTGTGGCCCTTAAGAGAGCATTTAGTTTATTAAGATTCCTCATTTTCTTG 360  
QY 364 GAAGAGAGAGGGCTTGTGATGCTCTGTGAGATGAGCTCTCTCTTCTTCCGCTCAAG 423  
DB 361 GAAGAGAGAGGGCTTGTGATGCTCTGTGAGATGAGCTCTCTCTTCTTCCGCTCAAG 420  
QY 424 AAGCCATATGAGGGGTCAATGGGCTGTGATGAGCTTCAAGCTTCAAGTCCAGAT 483  
DB 421 AAGCCATATGAGGGGTCAATGGGCTGTGATGAGCTTCAAGCTTCAAGTCCAGAT 480  
QY 484 TTGCTCAGCTTTTCAACATACCTCAGATGCTTATCTCAGCAACCATATGATCTGAT 543  
DB 481 TTGCTCAGCTTTTCAACATACCTCAGATGCTTATCTCAGCAACCATATGATCTGAT 540  
QY 544 GACAAGACTCTGTTCAAAATATTTCAATGAGGGTGTGCTTCAAGATGCTCAGCAGCAAG 603  
DB 541 GACAAGACTCTGTTCAAAATATTTCAATGAGGGTGTGCTTCAAGATGCTCAGCAGCAAG 600  
QY 604 TCCATGTTGAGCATATGTAAGAGTACAATGAGCCATATGATCAGCCGATCAACAGAA 663  
DB 601 GGCATGTTGAGCATATGTAAGAGTACAATGAGCCATATGATCAGCCGATCAACAGAA 660  
QY 664 GGCATGTTGAGCATATGTAAGAGTACAATGAGCCATATGATCAGCCGATCAACAGAA 723  
DB 661 GGCATGTTGAGCATATGTAAGAGTACAATGAGCCATATGATCAGCCGATCAACAGAA 720  
QY 724 TGCATGCCCCCTCTTCAAAAATCTACAGTAATGAGGGAGAGAGCTTTGTAAGCTG 783  
DB 721 TGCATGCCCCCTCTTCAAAAATCTACAGTAATGAGGGAGAGAGCTTTGTAAGCTG 780  
QY 784 CTGAAGAGCTCAAGAGTCACTTGGCCCAAGGCCCGGTGTGAGCTTCTGTGAGGCG 843  
DB 781 CTGAAGAGCTCAAGAGTCACTTGGCCCAAGGCCCGGTGTGAGCTTCTGTGAGGCG 840  
QY 844 ATGACGGTGAAGAGTGTGCTGATGAGCCATGAGGCGCTTGGTCTATGAGAGATTCTG 903  
DB 841 ATGACGGTGAAGAGTGTGCTGATGAGCCATGAGGCGCTTGGTCTATGAGAGATTCTG 900  
QY 904 CTTTGGGCAAGGA 917  
DB 901 CTTTGGGCAAGGA 914

## RESULT 6

US-10-346-241-5  
; Sequence 5, Application US/10346241  
; Publication No. US20030157647A1  
; GENERAL INFORMATION:  
; APPLICANT: STORMANN, THOMAS M.  
; APPLICANT: LEVINTHAL, CYNTHIA  
; APPLICANT: STOROHANN, LAURA  
; APPLICANT: HAMMERLAND, LANCE G.  
; APPLICANT: KRAPCHO, KAREN J.  
; APPLICANT: NPS PHARMACEUTICALS, INC.  
; TITLE OF INVENTION: A NOVEL HUMAN METABOTROPIC GLUTAMATE RECEPTOR  
; FILE REFERENCE: 1094.2.6  
; CURRENT APPLICATION NUMBER: US/10/346,241







84 GGTGGCTCACATGCTGGGTGACATCATTTATGAGCTCTCTTTCTGTATCAGCAGCC 143  
DB GGTGGCTCACATGCTGGGTGACATCATTTATGAGCTCTCTTTCTGTATCAGCAGCC 405  
QY 144 TACTGTGACGAAGTTGATGAGAGAAAGTGTGGGCGAGTCCGTGAACAGTATGACATTC 203  
DB TCCGGCCGAAGAAAGTCCCGAGAGAAAGTGTGGGAGATCATGAGGAGCAGTATGACATCA 465  
QY 204 GAGAGTGAAGCCATGCTGATACCTCTGGAAGAAAGATCATTTCAAGCCCACTCTTGGC 263  
DB GAGGAGTGAAGCCATGCTGATACCTCTGGAAGAAAGATCATTTCAAGCCCACTCTTGGC 525  
QY 264 CAACATCACACTGGGCTGTGAGATTAAGGAGATTCCTGTGACATTCGGCTGTGAGCCCTAGA 323  
DB CAACATCACACTGGGCTGTGAGATTAAGGAGATTCCTGTGACATTCGGCTGTGAGCCCTAGA 585  
QY 324 GCAGAGCATTAAGTTCTAAGAGATTCCTCATTTCTTGGAGAGAGAGAGAGAGGCTTGGT 383  
DB ACAGAGCATTAAGTTCTAAGAGATTCCTCATTTCTTGGAGAGAGAGAGAGAGGCTTGGT 645  
QY 384 ATGC-----TCTGTGATGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 434  
DB CAACCGGTGTCTGCTTACGCGCCAGTCCCTCCCGCAGGAGAGAGAGAGAGAGAGAGAGAG 705  
QY 435 AGGGGTGATGGGCTGGTCTGATTCATTTAGCCATTCAGGTCAGAGATTTGCTCCAGCT 494  
DB GGGAGTATGAGTCTGGGCTGGTCTGATTCATTTAGCCATTCAGGTCAGAGATTTGCTCCAGCT 765  
QY 495 TTTCACATACCTCAGATTCCTTACTGAGCAACCATATGAGATTCAGATTCAGACTCT 554  
DB CTTCGATCATCCCGAGATTCCTTACTGAGCAACCATATGAGATTCAGATTCAGACTCT 825  
QY 555 GTTCAATATTTTCTGAGGCTTGTGCTTCTGATGCTCAGAGGAGAGAGAGAGAGAGAGAG 614  
DB GTTCAATATTTTCTGAGGCTTGTGCTTCTGATGCTCAGAGGAGAGAGAGAGAGAGAGAG 885  
QY 826 GTTCAATATTTTCTGAGGCTTGTGCTTCTGATGCTCAGAGGAGAGAGAGAGAGAGAGAG 885  
DB GTTCAATATTTTCTGAGGCTTGTGCTTCTGATGCTCAGAGGAGAGAGAGAGAGAGAGAG 945  
QY 615 CATAGTGAAGAGTGAACATGACCTATGATGACCGGTACACAGAGAGAGAGAGAGAGAGAG 674  
DB CATAGTGAAGAGTGAACATGACCTATGATGACCGGTACACAGAGAGAGAGAGAGAGAGAG 945  
QY 886 CATAGTGAAGAGTGAACATGACCTATGATGACCGGTACACAGAGAGAGAGAGAGAGAGAG 945  
DB CATAGTGAAGAGTGAACATGACCTATGATGACCGGTACACAGAGAGAGAGAGAGAGAGAG 945  
QY 675 AGAAGTGAAGTGAAGCTTCAAGATATGTCAGCGAGAGAGAGAGAGAGAGAGAGAGAGAG 734  
DB GAGAGGAGAGTGAAGCTTCAAGATATGTCAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1005  
QY 946 GAGAGGAGAGTGAAGCTTCAAGATATGTCAGCGAGAGAGAGAGAGAGAGAGAGAGAGAG 1005  
DB GAGAGGAGAGTGAAGCTTCAAGATATGTCAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1005  
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DB CTCTTAAGAAATCTACGATATGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1065  
QY 1006 TTCTGAAGAAATCTACGATATGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1065  
DB TTCTGAAGAAATCTACGATATGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1065  
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QY 1066 CCGAGAGAGGCTTCCAGAGGCTGAGTGTGCTTCTGTGAGGAGAGAGAGAGAGAGAGAGAG 1125  
DB CCGAGAGAGGCTTCCAGAGGCTGAGTGTGCTTCTGTGAGGAGAGAGAGAGAGAGAGAGAGAG 1125  
QY 855 AGGTCTGTGATGAGCCTGAGAGGCGGCTGAGTGTGAGGAGAGAGAGAGAGAGAGAGAGAG 914  
DB AGGTCTGTGATGAGCCTGAGAGGCGGCTGAGTGTGAGGAGAGAGAGAGAGAGAGAGAGAGAG 914  
QY 1126 AGGAGCTCTGAGGCGCAGTGTGAGGCGGCTGAGTGTGAGGAGAGAGAGAGAGAGAGAG 1185  
DB AGGAGCTCTGAGGCGCAGTGTGAGGCGGCTGAGTGTGAGGAGAGAGAGAGAGAGAGAGAGAG 1185  
QY 915 GGA 917  
DB 1186 TGA 1188

RESULT 10  
US-10-300-473-3  
Sequence 3, Application US/10300473  
Publication No. US20030113873A1  
GENERAL INFORMATION:  
APPLICANT: STORMANN, THOMAS M.  
APPLICANT: HAMERLAND, LAURA L.  
APPLICANT: FULLER, FOREST H.  
APPLICANT: KRAPCHO, KAREN J.  
TITLE OF INVENTION: CHIMERIC RECEPTORS AND METHODS FOR IDENTIFYING  
TITLE OF INVENTION: COMPOUNDS ACTIVE AT METABOTROPIC GLUTAMATE

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Db      419 AACCAATGCTGCTTATATGGCCAGACCCCTGCCCTTGGCAGAGACTATAGAAAGCTATTGCT 47
QY      436 GGGGTCATTGAGGCTTGCTGTTCCAGTTCTTTAGCCATTCAAGTCCAGAAATTGCTCCAGCTT 49
Db      479 GGAGTGATCGGCGCTGCTCCAGCTCTGAGCTGTGGCCATTCAAGTCCAGAAATTCTTCCAGCTG 53
QY      496 TTCAACATACCTCAAGTTGCTTACTACTAGCAACCATATAGATCTGAGTACAAAGACTCTG 55
Db      539 TTGACATATCCCAAGATGCGCTTATTTCTGCAACAGATAGACCTTAGTACAAAACTTTG 59
QY      556 TTCAAAATATTATGAGGGTGTGCTTCAGATGCTCAGCAGGCAAGTCCATGCTGAGC 61
Db      599 TACAAATACCTTCTGAGGGTGTGCTTCTTGACACTTTGACGCAAGGCGGATCTCGAC 65
QY      616 ATAGTAAAGAGTAACTGAACTGAACTTATGATACGCGGTACACACAGAAAGCAATATGGA 67
Db      659 ATAGTCAAGGTTAACTGAACTGAACTTATGATCAGCAGTCCACACAGAAAGGAATTAAGC 71
QY      676 GAAAGTGGAGTGAAGCTTCAAAAGATATGTACAGCAAGAAAGGATTGTCATCGCCAC 73
Db      719 GAAAGTGAATGATATCTTCAAAAGAACTGGCTGCCAGAAAGGCTCTGCAATCGCAC 77
QY      736 TCTTACAAATCTACAGTATGACAGGGAGCAGAGCTTGATATAGCTGTGAAGAGCTC 79
Db      779 TCGACAAATCTACAGCAATGCTGGCGAAGAAAGCTTTGACCGGCTCTTGGTAACTTC 83
QY      796 ACAAGTCACTTGGCCCAAGGCCCGGGTGTGAGCTACTTCTGTAGAGGCAATGACGTTGAA 85
Db      839 CGGAGCGGCTTCCCAAGGCGAGAGGTGTGATGTCTTCTTGAGAGGCAATGACGTCGG 89
QY      856 GGTCTGCTGATGCCCATAGAGCGGCTTGCTTACTAGTGGAGAAATTTCTGCTTGGCAGG 91
Db      899 GGGTCTACTGATGCTCATGCGCGGCTGGCGGCTGTGTTGGAGGAGGCAATGACGTCGG 95
QY      916 GA 917
Db      959 GA 960

RESULT 12
US-10-300-473-4
: Sequence 4, Application US/10300473
: Publication No. US20030113873A1
: GENERAL INFORMATION:
: APPLICANT: STORMANN, THOMAS M.
: APPLICANT: STORJOHANN, LAURA L.
: APPLICANT: HAMMERLAND, LANCE G.
: APPLICANT: FULLER, FORREST H.
: APPLICANT: KAPACHO, KAREN J.
: TITLE OF INVENTION: CHIMERIC RECEPTORS AND METHODS FOR IDENTIFYING
: TITLE OF INVENTION: COMPOUNDS ACTIVE AT METABOTROPIC GLUTAMATE
: TITLE OF INVENTION: RECEPTORS AND THE USE OF SUCH COMPOUNDS IN THE
: TITLE OF INVENTION: TREATMENT OF NEUROLOGICAL DISORDERS AND DISEASES
: FILE REFERENCE: 072827/0909
: CURRENT APPLICATION NUMBER: US/10/300,473
: CURRENT FILING DATE: 2003-02-21
: PRIOR APPLICATION NUMBER: 09/435,897
: PRIOR FILING DATE: 1999-11-08
: PRIOR APPLICATION NUMBER: 08/687,289
: PRIOR FILING DATE: 1996-07-25
: PRIOR APPLICATION NUMBER: 60/001,526
: PRIOR FILING DATE: 1995-07-26
: NUMBER OF SEQ ID NOS: 8
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 4
: LENGTH: 3219
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Synthesized human
: OTHER INFORMATION: mGluR and human calcium receptor
: US-10-300-473-4

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; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 211782
; LENGTH: 687
; TYPE: DNA
; ORGANISM: Human
; NAME/KEY: misc feature
; LOCATION: (1)...(687)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-211782
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QY 1234 CCTACAAGTTTCTTGATGAGGGGTGCTCAGACTTTCACCTCTGCAAGTATTAATCTGGAG 1293
DB 399 TCTGAATGTTTCTTCAATGAGGGGGCTGATTTTTCATCTGCAATTTTATGGAG 458
QY 1294 GTCCATGTGGGGACCTCTTGGAATTTGGCTTTGGTGTGTAATAGTCTGAAAGGG 1353
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QY 1354 AAGATCAGATGCGCATATATATGAGAGAGAGGACTCTTTAGTCTTGGGATTGTTAG 1413
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RESULT 15  
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; Sequence 211781, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
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; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 211781
; LENGTH: 687
; TYPE: DNA
; ORGANISM: Human
; NAME/KEY: misc feature
; LOCATION: (1)...(687)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-211781
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Best Local Similarity 77.5%; Pred. No. 6,4e-62;
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Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>  
 Contact: amg@bcm.tmc.edu  
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Louissege, H.,  
 Kowis, C.R., Sneed, A.J., Martin, R.G., Kuzny, D.M., Navavali,  
 A.N., Gbbs, R.A.

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/INL at: <http://image.inl.gov>  
 Series: IRAC Plate: 51 Row: a Column: 11  
 This clone was selected for full length sequencing because it  
 passed the following selection criteria: matched mRNA gi: 4504142  
 This clone has the following problem: retained intron.

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Best Local Similarity 97.8%; Pred. No. 1.2e-62; Mismatches 15; Indels 0; Gaps 0;

Matches 652; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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121 CTCTTTCTGTTCATCAACAGCTCTGTGAGAGAGAGAGAGAGAGAGAGT 180

488 CTCTTTCTGTTCATCAACAGCTCTGTGAGAGAGAGAGAGAGAGAGT 547

181 GTCCGTGAACAGTATGAGATTCAGAGAGAGAGAGAGAGAGAGAGAGT 240

548 GTCCGTGAACAGTATGAGATTCAGAGAGAGAGAGAGAGAGAGAGAGT 607

241 AATTCAAGACCCACACTCTTCCCAACATCACTGAGAGAGAGAGAGAGT 300

608 AATTCAAGACCCACACTCTTCCCAACATCACTGAGAGAGAGAGAGAGT 667

301 TGGCATTCGGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 360

668 TGGCATTCGGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 727

361 TCGAAGT 420

728 TCGAAGT 787

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481 AATTGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 540

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541 AGTGAAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 600

908 AGTGAAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 967

601 AGGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 660

968 AGGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 1027

Qy 661 GAAGCA 667  
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## RESULT 2

CA449274/c

LOCUS

DEFINITION

CA449274

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

COMMENT

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QY 1221 TATCACTGCAACACCTACAGTCTTCTTGACGGGGGCTCAGACTTTCACTTGCGCAA 1280  
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 DEFINITION IMAGE:3281166, mRNA sequence.  
 ACCESSION BX280403  
 VERSION BX280403.1 GI:28612394  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 515)  
 Ebert, L., Heil, O., Hennig, S., Neubert, P., Patrsch, E., Peters, M.,  
 Radehof, U., Schneider, D. and Korn, B.  
 Human Unigeneset - RZPD3  
 Unpublished  
 Contact: Ina Rolfe  
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
 Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany  
 RZPD; IMAGE998A078034.  
 RZPDLIB; I.M.A.G.E. cDNA Clone Collection;  
 Human Unigeneset - RZPD3 (RZPDLIB No.972)  
 http://www.rzpd.de/CloneCards/cgi-  
 bin/showlib.pl.cgi/response?libno=972 Contact: Ina Rolfe  
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
 Heubnerweg 6, D-14059 Berlin, Germany  
 Tel: +49 30 32639 101  
 Fax: +49 30 32639 111  
 www.rzpd.de  
 This clone is available royalty-free from RZPD;

contact RZPD (clone@rzpd.de) for further information. Seq primer:  
 M13r. Primer sequence: TTTCACACAGGAAACAGCATATAC.  
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 library NCI CGAP Lu24 was prepared, and as circles were  
 made in vitro. Following HAP purification, this DNA was  
 used as tracer in a subtractive hybridization reaction.  
 The driver was PCR-amplified cDNAs from a pool of 5,000  
 clones made from the same library (clonids  
 141920-141791 and 1520904-1522439). Subtraction by Bento  
 Soares and M. Fatima Bonaldo."

BASE COUNT 137 a 138 c 105 g 133 t 2 others  
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 Best Local Similarity 99.4%; Pred. No. 7.9e-48;  
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 QY 1156 CATATCTTCTGATGAGGAGATTTGAGAGACATTTGATGAGATGAGTCAACCAATGCG 1215  
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 PRECURSOR. ; mRNA sequence.  
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 VERSION BE674422.1 GI:10034963  
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 REFERENCE  
 1 (bases 1 to 519)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 AUTHORS  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL  
 Unpublished  
 COMMENT  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgaps-remail.nih.gov  
 Tissue Procurement: Christopher Moskalk, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: M. Bento Soares, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LINL, send email to:  
 info@image.llnl.gov  
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 made in vitro. Following HAP purification, this DNA was  
 used as tracer in a subtractive hybridization reaction.  
 The driver was PCR-amplified cDNAs from a pool of 5,000  
 clones made from the same library (cloneids  
 141920-1417991 and 1520904-1522439). Subtraction by Bento  
 Soares and M. Fatima Bonaldo."  
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 QY 547 AAGACTGCTTCAAAATTTTCATGAGGGTGTGCTTCAAGTGTCTGACGAGGAGGCTCC 606  
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 QY 607 ATGGTGACATAGTGAAGAGGTACACTGACCTATGATACAGCCGTACACAGAAAGC 666  
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 DEFINITION  
 h266408.x1 NCI CGAP Lu24 Homo sapiens CDNA clone IMAGE:3212943.3  
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 REFERENCE  
 1 (bases 1 to 499)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 AUTHORS  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL  
 Unpublished  
 COMMENT  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgaps-remail.nih.gov  
 Tissue Procurement: Christopher Moskalk, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: M. Bento Soares, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LINL, send email to:  
 info@image.llnl.gov  
 Seq primer: -40UP from GIBCO  
 High quality sequence stop: 493.  
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 made in vitro. Following HAP purification, this DNA was  
 used as tracer in a subtractive hybridization reaction.  
 The driver was PCR-amplified cDNAs from a pool of 5,000  
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 141920-1417991 and 1520904-1522439). Subtraction by Bento  
 Soares and M. Fatima Bonaldo."  
 BASE COUNT 141 a 107 c 138 g 113 t  
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 Best Local Similarity 100.0%; Pred. No. 1.9e-46;  
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Db 301 GTGCTTCCCAAGAGCCGCGGTGTGCTTCTGTAGAGGAGATGAGGTGAGGTG 360  
QY 860 TGTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 919  
Db 361 TGTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420  
QY 920 CAGATGCGCATCTTATTTAGATCTCAAGAGAGAGAGAGAGAGAGAGAGAGAG 979  
Db 421 CAGATGCGCATCTTATTTAGATCTCAAGAGAGAGAGAGAGAGAGAGAGAGAG 480  
QY 980 GCCAAGGTGCTTCTTCA 998  
Db 481 GCCAAGGTGCTTCTTCA 499

RESULT 6 690 bp mRNA linear EST 21-APR-2001  
Bg193349  
LOCUS Bg193349  
DEFINITION Atherys RAGE Library Homo sapiens cDNA, mRNA sequence.  
ACCESSION Bg193349  
VERSION Bg193349.1 GI:13715036  
KEYWORDS EST.  
SOURCE Homo sapiens  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R.,  
Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J.,  
Lerner, L., Costanzo, D., McElligott, K., Booser, S., Mays, R., Smith,  
J., Danzig, J., and Ducar, M.  
Creation of genome-wide protein expression libraries using random  
activation of gene expression  
Nat. Biotechnol. 19 (5), 440-445 (2001)  
11329013  
11329013  
Contact: Scott J. Cain  
Atherys, Inc.  
3201 Carnegie Ave, Cleveland, OH 44115, USA  
Tel: 216 431 9900  
Fax: 216 361 9596  
Email: scain@atherys.com

TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT  
Contact: Scott J. Cain  
Atherys, Inc.  
3201 Carnegie Ave, Cleveland, OH 44115, USA  
Tel: 216 431 9900  
Fax: 216 361 9596  
Email: scain@atherys.com

FEATURES  
source  
High quality sequence stop: 551.  
Location/Qualifiers  
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/note="See 'Creation of Genome-wide Protein Expression  
Libraries using Random Activation of Gene Expression',  
Nature Biotechnology, in press. Note that even though the  
method was used, these sequence tags are not necessarily  
expressed in HT1080 under normal circumstances."

BASE COUNT  
ORIGIN  
190 a 142 c 150 g 207 t 1 others

Query Match 26.0%; Score 473.2; DB 10; Length 690;  
Best Local Similarity 82.1%; Pred. No. 1.1e-43;  
Matches 566; Conservative 1; Mismatches 120; Indels 2; Gaps 2;  
QY 1119 AGTGATTTTCTGCTGCTTATTAATGAAGCCACAGTCATATCTTGATGTGAGATTT 1178  
Db 3 AGTGATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 61  
QY 1179 GAGAGCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1238  
Db 62 GAGAGCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 121  
QY 1239 AAGTTTCTTGCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1298  
Db 122 AAGTTTCTTGCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 181  
QY 1299 TGT-GGGGAGCTCTGGAATTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGG 1357  
Db 182 CGTGGGAGGAGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGG 241  
QY 1358 ATGAGATGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1417  
Db 242 GACAGATGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 301  
QY 1418 ACATTCAGTCAAGTCTTCTTACCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCC 1477  
Db 302 GACATTCAGTCAAGTCTTCTTACCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCC 361  
QY 1478 CCACCATGATGATTAATTTCTGATGATGATGATGATGATGATGATGATGATGAT 1537  
Db 362 CCACCATGATGATTAATTTCTGATGATGATGATGATGATGATGATGATGATGAT 421  
QY 1538 ATCAAGCTCCCTTATTAACCAATCCCTTATTTGCTCTCTCACTCTCTCACTCTCA 1597  
Db 422 ATCAAGCTCCCTTATTAACCAATCCCTTATTTGCTCTCTCACTCTCTCACTCTCA 481  
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Db 482 TCTTTTCTGATTAATCTCTGACAGAGCAATGAGAGAGAGAGAGAGAGAGAGAG 541  
QY 1658 AACCCCTTATCCCATTAAGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1717  
Db 542 AACCCCTTATCCCATTAAGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 601  
QY 1718 TGTTTTATGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 1777  
Db 602 CATTTAATGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 661  
QY 1778 AATGCTGTAATTAACCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1806  
Db 662 AATGCTGTAATTAACCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 690

RESULT 7  
EX116917  
LOCUS EX116917 494 bp mRNA linear EST 07-FEB-2003  
DEFINITION EX116917 NCI CGAP GGC Homo sapiens cDNA clone IMAGE2310813, mRNA sequence.  
ACCESSION EX116917  
VERSION EX116917.1 GI:27840301  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R.,  
Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J.,  
Lerner, L., Costanzo, D., McElligott, K., Booser, S., Mays, R., Smith,  
J., Danzig, J., and Ducar, M.  
Creation of genome-wide protein expression libraries using random  
activation of gene expression  
Nat. Biotechnol. 19 (5), 440-445 (2001)  
11329013  
11329013  
Contact: Scott J. Cain  
Atherys, Inc.  
3201 Carnegie Ave, Cleveland, OH 44115, USA  
Tel: 216 431 9900  
Fax: 216 361 9596  
Email: scain@atherys.com

BASE COUNT  
ORIGIN  
190 a 142 c 150 g 207 t 1 others

Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany  
 RZPD; IMAGP98A25727.  
 RZPDLib; I.M.A.G.E. cDNA Clone Collection;  
 Human Unigeneset - RZPD3 (RZPDLib No.972)  
 http://www.rzpd.de/Clonecards/cgi-bin/BrowseLib.pl.cgi/respone?libno=972 Contact: Ina Rolfe  
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
 Heubnerweg 6, D-14059 Berlin, Germany  
 Tel: +49 30 32639 101  
 Fax: +49 30 32639 111  
 www.rzpd.de

This clone is available royalty-free from RZPD;  
 contact RZPD (clone@rzpd.de) for further information. Seq primer:  
 M13r, Primer sequence: TTTACACAGGAAGACGATGATGAC.

## FEATURES

source

1..494  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
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 /lab\_host="DH10B"  
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 /note="Vector: pT73D-Pac (Pharmacia) with a modified  
 polylinker; Site\_1: Not I; Site\_2: Eco RI; Plasmid DNA  
 from the normalized library NCI CGAP GC4 was prepared, and  
 as circles were made in vitro. Following HAP purification,  
 this DNA was used as tracer in a subtractive hybridization  
 reaction. The driver was PCR-amplified cDNAs from a pool  
 of 5,000 clones made from the same library (cloneids  
 1257096-1258631, 1469064-1470983, and 1475592-1476743).  
 Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT  
 ORIGIN

118 a 118 c 105 g 153 t

Query Match 25.4%; Score 463.6; DB 13; Length 494;  
 Best Local Similarity 96.2%; Pred. No. 1.6e-42;  
 Matches 475; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

1242 TTTTCTGGCAGGGGCTGAGACTTCACTCGGACGATTAATACGGAGGCCATGT 1301  
 1 TTTTCTGGCAGGGGCTGAGACTTCACTCGGACGATTAATACGGAGGCCATGT 60  
 1302 GGGGGAATCTTGGATGGGCTTGGCTTGTGTAATAGTACTGAAAGGAAGATCA 1361  
 61 GGGGGAATCTTGGATGGGCTTGGCTTGTGTAATAGTACTGAAAGGAAGATCA 120  
 1362 GAATGGCAATATATATGAGAGAGAGGAGCTCTTGAATGTTAAAGACGAT 1421  
 121 GAATGGCAATATATATGAGAGAGAGGAGCTCTTGAATGTTAAAGATGACAT 180  
 1422 TCGATGAGCTCTTTTCACTCCAGTTACATGACAGATATGCCAAGACCTATCAA 1481  
 181 TCGATGAGCTCTTTTCACTCCAGTTACATGACAGATATGCCAAGACCTATCAA 240  
 1482 CCATGTAGATTAATCTCTGATTTGTGAAGCTAGAACTGAGCTCGTTGATGTTATCA 1541  
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 301 AAGCTCCCTATATACCAATCCCTAATGCTCTTCACTCTTCAAGGCTATCTT 360  
 1602 TTCTGTATCATCTCTGACACAGAGCAATATGGAATGTTATGCTGTGGAGAAC 1661  
 361 TTCTGTATCATCTCTGACACAGAGCAATATGGAATGTTATGCTGTGGAGAAC 420  
 1662 CCTTATATCCATTAAGGCTCTTCTTGTGCTTATATCAAGAGCAATAGTCTGTT 1721  
 421 CCTTATATCCATTAAGGCTCTTCTTGTGCTTATATCAAGAGCAATAGTCTGTT 480  
 1722 TTATGCTTGAATT 1735  
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Db 481 TTATGCTTGAATT 494

RESULT 8  
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 LOCUS K-EST0210877 BT694954 Homo sapiens cDNA clone BT694954-28-C09 5',  
 DEFINITION mRNA sequence.  
 ACCESSION CB153433  
 VERSION CB153433.1 GI:28138427  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,  
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and  
 Kim,Y.S.  
 21C Frontier Korean EST Project 2001

TITLE  
 JOURNAL Unpublished  
 COMMENT Contact: Kim YS

Genome Research Center  
 Korea Research Institute of Bioscience & Biotechnology  
 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea  
 Tel: +82-42-860-4470  
 Fax: +82-42-860-4409  
 Email: yongsung@mail.kribb.re.kr  
 Plate: 28 row: C column: 09  
 High quality sequence stop: 449.

## FEATURES

source

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 /note="Organ: Brain; Vector: pcnS-D2; Site\_1: EcoRI;  
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 bacterial alkaline phosphatase (BAP) and then deacapped  
 with tabacco acid pyrophosphatase (TAP). The deacapped  
 intact mRNA was ligated with DNA-RNA linker including  
 EcoRI site by treatment of T4 RNA ligase and the first  
 strand cDNA was synthesized from oligo dt-selected mRNA by  
 priming with dt-tailed vector. The dt-tailed vector was  
 adjusted to have about 60nt. The cDNA vector was  
 circularized with E. coli DNA ligase after digestion of  
 EcoRI which site is also included in vector. An RNA strand  
 converted to a DNA strand by Okayama-Berg method. The  
 obtained cDNA vectors were used for transformation of  
 competent cells E. coli Top10P by electroporation method.  
 The cDNA libraries constructed by this method are  
 full-length enriched cDNA library."

BASE COUNT  
 ORIGIN

106 a 112 c 112 g 119 t

Query Match 24.5%; Score 445.8; DB 14; Length 449;  
 Best Local Similarity 99.6%; Pred. No. 1.6e-40;  
 Matches 447; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

123 CTTTCTGTTTCATCACCAGCTTACTGTGACGAAAGTTCAATGAGAGAAAGTGGGCACT 182  
 1 CTTTCTGTTTCATCACCAGCTTACTGTGACGAAAGTTCAATGAGAGAAAGTGGGCACT 60  
 183 CCGTGAACAGTATGAGCATTCAAGAGTGAAGGCGCATGTCATACCTTGAAGATCAA 242  
 61 CCGTGAACAGTATGAGCATTCAAGAGTGAAGGCGCATGTCATACCTTGAAGATCAA 120  
 243 TTGAGACCCCACTCTTGGCCCAATCACTGGGCTGTGAGATTAAGGATTCCTGCTG 302  
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QY 303 GCATTCGGCTGTCGCTTACAGAGAGCATTTAGTTCATTAAGAGATTCCTCATTTCTTC 362
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Db 241 GGAAGAGAGAGAGAGGCTTGTATGCTCTGTGTAGATGAGCTCTCTCTCTCTCTCTCTCA 300
QY 423 GAAGCCATATGATGAGGCTCATTTGGGCTGCTTCAAGTCTTTTACCATTCAGTCCAGAA 482
Db 301 GAAGCCATATGATGAGGCTCATTTGGGCTGCTTCAAGTCTTTTACCATTCAGTCCAGAA 360
QY 483 TTTGCTCCAGCTTTTCAACATTCAGATTTGCTTCTGACCAACATCATATGATCTGAG 542
Db 361 TTTGCTCCAGCTTTTCAACATTCAGATTTGCTTCTGACCAACATCATATGATCTGAG 420
QY 543 TGACAACTCTGTTCAAAATTTTCATGA 571
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DEFINITION RST19284 Atherys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION BG199987
VERSION BG199987.1 GI:13721674
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 729)
Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.,
Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith
,E., Veloso,N., Kika,A., Hess,J., Cochren,K., Lo,K., Offenbacher
,J., Danzig,J. and Ducar,M.
Creation of genome-wide protein expression libraries using random
activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
JOURNAL 21227151
MEDLINE 21227151
PUBMED 11329013
COMMENT Contact: Scott J. Cain
Atherys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@atherys.com
High quality sequence stop: 445.
Location/Qualifiers
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/clone_lib="Atherys RAGE Library"
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Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
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expressed in HT1080 under normal circumstances."

BASE COUNT 186 a 166 c 160 g 217 t
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QY 1517 CTGTGAGCTTGTGATATGTTAATCAAAGCTCCCTATATATACCATCTTAATGCTCT 1576
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Db 480 GATGCTCTATATGCTCTGTGGAAACCTGTTATCCAGAAAGCCCTCTTTTGGCACTCA 539
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VERSION AM015382.1 GI:5864139
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 442)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Oligo-dT track not found. Not 1 site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: NCI-CGAP clone distribution
Information can be found through the I.M.A.G.E. Consortium/ILNL at:
www.bio.lnl.gov/bbrp/image/image.html
Seq primer: M13 Forward
POLYA=No.
Location/Qualifiers
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/mol_type="mRNA"
FEATURES
source

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NCI CGAP Sub1 library is a subtracted library derived from
B1. B1 constitutes a mixture of 21 normalized or
subtracted NCI CGAP libraries: NCI CGAP_Co4,
NCI CGAP_Pr22, NCI CGAP_Pr28, NCI CGAP_Co10, NCI CGAP_Co16
, NCI CGAP_Kid5, NCI CGAP_Kid12, NCI CGAP_Kid3,
NCI CGAP_Kid11, NCI CGAP_Lym2, NCI CGAP_Biz2, NCI CGAP_Co8,
NCI CGAP_CLL1, NCI CGAP_Le12, NCI CGAP_Brn3, NCI CGAP_Lu5
, NCI CGAP_Lu24, NCI CGAP_Lu19, NCI CGAP_GC4, NCI CGAP_GC6
, NCI CGAP_Brn25. These 21 libraries were pooled and a
single-stranded DNA preparation of the resulting mixture
was used as a tracer in a subtractive hybridization with a
driver whose composition is detailed below: NCI CGAP_Kid3
pool 1 L1AM 3334-3337, 3682-3683, 3798-3803 (IMAGE
Clonides 132376-132391, 145608-145675, 150055-150285
) NCI CGAP_Kid5 pool 1 L1AM 3338-3342, 3722-3725,
3776-3778 (IMAGE Clonides 1323912-132831,
1471368-1472903, 1492104-1493255) NCI CGAP_Lu5 pool 1 L1AM
3575-3582, 3851-3854 (IMAGE Clonides 141920-1417991,
1520904-1522439) NCI CGAP_GC4 pool 1 L1AM 3164-3167,
3716-3720, 3733-3735 (IMAGE Clonides 1257096-1258631,
1469064-1470983, 1475592-1476743) NCI CGAP_Pr22 pool 1
L1AM 2457-2459, 2758-2759, 3062-3068 (IMAGE Clonides
985608-986759, 1101192-1101959, 1217928-1220615)
NCI CGAP_Co10 pool 1 L1AM 2644-2653, 2871-2872 (IMAGE
Clonides 1057416-1061255, 1144584-1145351) The resulting
subtracted library contained 530,000 recombinants.
Subtraction was performed as previously described [Bonaldo
, Lemon & Soares (1996): Normalization and Subtraction:
Two Approaches To Facilitate Gene Discovery. Genome
Research 6, 791-806.
Tag LIB=NCI CGAP_Le12
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TAG_SEQ=ATCG"
BASE COUNT      118 a      97 c      127 g      100 t
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Query Match      23.3%; Score 424.4; DB 9; Length 442;
Best Local Similarity 99.5%; Pred. No. 3,7e-38;
Matches 433; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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DB      425 TCTGGGAGGAGACGAGA 442

RESULT 11
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DEFINITION AGENCOURT_7931447 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6151700
5', mRNA sequence.
ACCESSION BU154755
VERSION   BU154755.1 GI:22668287
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 888)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
plate: L1AM13488 row: f column: 21
High quality sequence stop: 570.
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Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 2 kb. Library constructed by Life
Technologies."
BASE COUNT      235 a      215 c      206 g      232 t
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Query Match      23.2%; Score 423.8; DB 13; Length 888;
Best Local Similarity 80.2%; Pred. No. 2.8e-38;
Matches 548; Conservative 0; Mismatches 127; Indels 8; Gaps 4;

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 QY 1358 ATCAATGAGCAATATATATGAGAGGAGGAGCT-CTTATGCTTGGGATTTTAAAGAC 1416  
 DB 566 ATCAATGAGCAATATATATGAGAGGAGGAGCTCTTATGCTTGGGATTTTAAAGAC 625  
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 DB 686 CTTACCAACCATGAGGATTTTCCCTGGGATTTGTAAGTGAAGTGAAGTCTTCTCT 745  
 QY 1530 TGAATTTATCAAGCTCCCTTATATACCATCTTATGCTCTTCTCTCTCTCT 1589  
 DB 746 TCCCGTTGATGTTAGTTCGAAAGCTCCCGCTTATATACCCCAATCCCTTAAAT 805  
 QY 1590 CAGGCTATCTTTTCTGATTTATCATCTCTGACGAGAGCAATCAAGAAATGTTATCT 1649  
 DB 806 TTGGGTTCTCTTCTCAAACTTTCCTTTTAAAGAAACCCCAAACTTTTCTTCT 865  
 QY 1650 GCTGTGGGAACCCCTTATCCCA 1672  
 DB 866 CCGGGGAATTTCTCTCCCA 888

RESULT 12 452 bp mRNA linear EST 08-MAR-2000  
 A1950429/w35601.x1 NCI CGAP G66 Homo sapiens CDNA clone IMAGE:2473249.3  
 LOCUS similar to SW:BUZY\_HUMAN Q13410 BUTYROPHILIN PRECURSOR ;, mRNA  
 DEFINITION sequence.

ACCESSION A1950429 GI:5742739  
 VERSION A1950429  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 452)  
 NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index

JOURNAL Unpublished  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgaaps-remail.nih.gov  
 Tissue Procurement: Christopher A. Morkaluk, M.D., Ph.D., Michael  
 R. Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
 Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CCGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 www-bio.1lm.gov/db/tp/image/image.html  
 Insert length: 607 Std Error: 0.00  
 Seg primer: -40UP from Gibco.  
 Location/Qualifiers

FEATURES  
 source 1..452

/organism="Homo sapiens"  
 /mol\_type="mRNA"  
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 /lab\_host="DH10B"  
 /clone\_1b="NCI CGAP G66"  
 /note="Vector: pT73D-Pac (Pharmacia) with a modified  
 polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA  
 from the normalized library NCI CGAP G66 was prepared, and  
 as circles were made in vitro. Following HAP purification,

Query Match 23.0%; Score 420.2; DB 9; Length 452;  
 Best Local Similarity 95.4%; Pred. No. 1.1e-37;  
 Matches 431; Conservative 1; Mismatches 20; Indels 0; Gaps 0;  
 BASE COUNT 139 a 81 c 109 g 122 t 1 others  
 ORIGIN

this DNA was used as tracer in a subtractive hybridization  
 reaction. The driver was PCR-amplified cDNAs from a pool  
 of 5,000 clones made from the same library (clones  
 1257086-1258631, 1469064-1470983, and 1473592-1476743).  
 Subtraction by Bento Soares and M. Fatima Bonaldo.

QY 1348 AAGGAGCAATGAGATGAGCAATATATATGAGAGGAGGAGCTTTAGTCTTGGAT 1407  
 DB 452 AAGGAGCAATGAGATGAGCAATATATATGAGAGGAGGAGCTTTAGTCTTGGAT 393  
 QY 1408 GTTAAAGCAATGAGATGAGCAATATATATGAGAGGAGGAGCTTTAGTCTTGGAT 1467  
 DB 392 GTTAAAGCAATGAGATGAGCAATATATATGAGAGGAGGAGCTTTAGTCTTGGAT 333  
 QY 1468 CCAAGCTTACCAACGATGAGATATTTCTGAGATTTGAGAGTGAAGTGAAGTTC 1527  
 DB 332 CCAAGCTTACCAACGATGAGATATTTCTGAGATTTGAGAGTGAAGTGAAGTTC 273  
 QY 1528 GTTATGTTATCAAGTCTCCCTATATACACCATCTTATGCTCTTCTCACTCTCT 1587  
 DB 272 GTTATGTTATCAAGTCTCCCTATATACACCATCTTATGCTCTTCTCACTCTCT 213  
 QY 1588 CTCAGGCTATCTTTTCTGATTTATCATCTCTGACGAGAGCAATGAGATGTTAT 1647  
 DB 212 CTCAGGCTATCTTTTCTGATTTATCATCTCTGACGAGAGCAATGAGATGTTAT 153  
 QY 1648 CTGCTGTGGGAACCCCTTATCCCAAAAGCCCTCTTCTGAGCTTATCAAAAGAG 1707  
 DB 152 CTGCTGTGGGAACCCCTTATCCCAAAAGCCCTCTTCTGAGCTTATCAAAAGAG 93  
 QY 1708 AATAGTCTGTTTATGCTTGAATTCATCTTATGATTTATTAACCTATTATGT 1767  
 DB 92 AATAGTCTGTTTATGCTTGAATTCATCTTATGATTTATTAACCTATTATGT 33  
 QY 1768 GTTACTATTAAATGTGTAAGCAAAAAA 1799  
 DB 32 GTTACTATTAAATGTGTAAGCAAAAAA 1

RESULT 13 667 bp DNA linear GSS 02-NOV-2001  
 AG046849 Pan troglodytes DNA, clone: PTB-026D03.F, genomic survey sequence.  
 LOCUS AG046849  
 DEFINITION AG046849.1 GI:16583741  
 ACCESSION GSS.  
 VERSION Pan troglodytes (chimpanzee)  
 KEYWORDS Pan troglodytes  
 SOURCE Pan troglodytes  
 ORGANISM Pan troglodytes

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.  
 1 (bases 1 to 667)

REFERENCE Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,  
 Totoki, Y., Watanabe, H. and Sakaki, Y.  
 BAC end sequences of library PTB  
 Unpublished

TITLE Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,  
 Totoki, Y., Watanabe, H. and Sakaki, Y.  
 JOURNAL Direct Submission  
 COMMENT Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical  
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
 1-7-22 Suenho-chu, Tsukuba, Ibaraki, Japan, Yokohama, Kanagawa 230-0045, Japan  
 (E-mail: chimpes@sc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/  
 Tel: 81-45-503-9111, Fax: 81-45-503-9170)  
 Clones are derived from the chimpanzee BAC library PTB This BAC end  
 was generated during the RDP process and may have higher chance of  
 clone tracking errors.



## PRIMERS

Sequencing: -21M13  
LIBRARY

Vector : PKS145

R.Site 1 : SacI

R.Site 2 : SacI

## FEATURES

## source

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/cell\_type="Lymphoblast"  
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BASE COUNT 156 a 142 c 158 g 210 t 1 others  
ORIGIN

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Best Local Similarity 82.6%; Pred. No. 1.7e-37;  
Matches 489; Conservative 0; Mismatches 102; Indels 1; Gaps 1;

115 GAGAGCTCTCTTCTGTCATACAGCCTAAGTGAAGGAGGAGTGT 174  
66 GAGAGCTCTCTTCTGTCATACAGCCTAAGTGAAGGAGGAGTGT 125  
175 GGGGCAATCCGTGAAGATGAGATGAGAGGAGGAGGAGGAGGAG 234  
126 GGGGCGGTCCGTGAAGATGAGATGAGAGGAGGAGGAGGAGGAG 185  
235 AGGATCAATTCAGACCCCACTCTGCCCCCACTCACTGAGGAGTGA 294  
186 AGGATCAATTCATACCCCACTCTGCCCCCACTCACTGAGGAGTGA 245  
295 TCTGCTGAGATTCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAG 354  
246 TACTGCTGAGATTCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAG 305  
355 ATTCTTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 414  
306 ATTCTTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 365  
415 CGCTCCAGAGAGCCATAGTGGAGGAGGAGGAGGAGGAGGAGGAGG 474  
366 CGCTCCAGAGAGCCATAGTGGAGGAGGAGGAGGAGGAGGAGGAGG 425  
475 GTCCAGAAATTTCTCCAGCTTTTCAACATACCTGAGTTGTTA 534  
426 GCGCAGATGTGGTGCAGTTTTCATACATCTGATGTTTACTGATGA 485  
535 GATCTGATGACAGAGATCTCTTCAATATTTCAATGAGGAGTGGCTT 594  
486 GATCTGATGACAGAGATCTCTTCAATATTTCAATGAGGAGTGGCTT 544  
595 CAGGCAAGTTCATGAGTGAATAGAGGAGTGAAGGAGTGAAGGAGTGA 654  
545 TTGTTTATGATATGAGTGAATAGAGGAGTGAAGGAGTGAAGGAGTGA 604  
655 CACACAGAGGCAATATGAGAGAGGAGTGAAGGAGTGAAGGAGTGA 706  
605 CTCACATTAAGATTTTATTTCTTGTATTAATCTGCTGTATATGTTAT 656

RESULT 14 455 bp mRNA linear EST 17-DEC-1999  
AI655261/c 455 bp mRNA linear EST 17-DEC-1999

LOCUS wb88b1.1 NCI CGAP G66 Homo sapiens cDNA clone IMAGE:2310813 3'  
DEFINITION similar to SM:BUYY\_HUMAN Q13410 BUTYROHILIN PRECURSOR ;, mRNA

ACCESSION AI655261  
VERSION AI655261.1 GI:4739240  
KEYWORDS EST.  
SOURCE Homo sapiens (human)

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

1 (bases 1 to 455)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index

## JOURNAL

## COMMENT

Contact: Robert Strausberg, Ph.D.  
Email: cgapsb@emil.nih.gov  
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael  
R. Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldi, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/ILNL at:  
[www-bio.illn.gov/dbp/image/image.html](http://www-bio.illn.gov/dbp/image/image.html)  
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Seq primer: -40UP from Glibco.

## FEATURES

## source

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/note="Vector: pTZ19-Pac (Pharmacia) with a modified  
polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA  
from the normalized library NCI CGAP G64 was prepared, and  
86 circles were made in vitro. Following HAP purification,  
this DNA was used as tracer in a subcloning hybridization  
reaction. The driver was PCR-amplified cDNAs from a pool  
of 5,000 clones made from the same library (cloneids  
1257096-1258631, 1469064-1470983, and 1475592-1476743).  
Subcloning by Bento Soares and M. Fatima Bonaldi."

## BASE COUNT

138 a 82 c 111 g 124 t

Query Match 22.7%; Score 413.8; DB 9; Length 455;  
Best Local Similarity 95.6%; Pred. No. 5.5e-37;  
Matches 435; Conservative 1; Mismatches 18; Indels 1; Gaps 1;

1346 GAAAGGAGAGATGCAATGATGCAATATATATGAGAGAGGAGGAGTGT 1405  
455 GAAAGGAGAGATGCAATGATGCAATATATATGAGAGAGGAGGAGTGT 396  
1406 TTGTTAAGAGAGATGCAATGATGCAATATATATGAGAGAGGAGTGT 1465  
395 GTGTTAAGAGAGATGCAATGATGCAATATATATGAGAGAGGAGTGT 336  
1466 TCCCAAGACTCAACCAATGATGATATATCTGAGATTGTGAAGTGAAGT 1525  
335 TCCCAAGACTCAACCAATGATGATATATCTGAGATTGTGAAGTGAAGT 276  
1526 TCGTTATGTTAATCAAGAGTCCCTATATATACCAATCCCTAATGCTCT 1585  
275 TCGTTATGTTAATCAAGAGTCCCTATATATACCAATCCCTAATGCTCT 216  
1586 CTCTCAGGCTTATCTTTGCTGATATCATCTGACAGAGAGAAATGATGTT 1645  
215 CTCTCAGGCTTATCTTTGCTGATATCATCTGACAGAGAGAAATGATGTT 156  
1646 ATCTGCTGAGAGAGCCCTTATCCATTAAGGCTCTTCTGCTGCTTATCAACAG 1705  
155 ATCTGCTGAGAGAGCCCTTATCCATTAAGGCTCTTCTGCTGCTTATCAACAG 96  
1706 ACAATATGTTCTGTTATATGTTATGTTAATGATGATTTAT -GTTATTAATCAATCAATTAT 1764  
95 ACAATATGTTCTGTTATATGTTATGTTAATGATGATTTAT -GTTATTAATCAATCAATTAT 36



QY 1765 TGGTACTATTAAATGTTGGTAAACACAAATAA 1799  
DB 35 TGTGTTACTATTAAATGTTGGTAAACACCTAAATA 1

RESULT 15  
BO277274 1400 bp mRNA linear EST 07-MAY-2002  
LOCUS AGENCOURT\_6824224 NIH\_MGC\_127 Homo sapiens cDNA clone IMAGE:5810504  
DEFINITION 5', mRNA sequence.  
ACCESSION BO277274  
VERSION BO277274.1 GI:20487482  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 1400)  
NIH-MGC http://mgi.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: cga@bbs-r@mail.nih.gov  
Tissue Procurement: NCI  
CDNA Library Preparation: Michael Brownstein Laboratory  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLCM2057 row: n column: 09  
High quality sequence stop: 410.  
Location/Qualifiers  
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/tissue\_type="mixed (pool of 40 RNAs)"  
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Site 2: SfiI (ggccgcctcgcc); Double-stranded cDNA;  
prepared from a pool of 40 cell line polyA+ RNAs (bladder  
- 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon -  
4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%,  
kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%,  
ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary  
gland - 1.3%, and skin - 2.3%). 5' and 3' adaptors were  
used in cloning as follows:  
5'-AAGCAGTGTATCAACGACGAGTGCCTATTCAGCGCGG-3' and  
5'-ATTCTAGAGCCGAGCGCGCCGACATG-dt(30)NN-3'. Full-length  
enriched library was constructed using the Clontech  
Creator SMART kit and size-selected to contain the 1-2 kb  
size fraction (other fractions present in NIH\_MGC\_126 and  
NIH\_MGC\_128). Library created in the laboratory of T.  
Usdin, M.D., Ph.D. (NIH, NIH). Note: this is a NIH\_MGC  
Library."

BASE COUNT 360 a 429 c 267 g 342 t 2 others  
ORIGIN

Query Match 22.0%; Score 401.6; DB 13; Length 1400;  
Best Local Similarity 90.7%; Pred. No. 6e-36;  
Matches 439; Conservative 0; Mismatches 44; Indels 1; Gaps 1;

QY 1253 GGGGTGCTCAGACTTACCTGCGAAGATATCTGGAGTGCATGTGGGGACTTT 1312  
DB 3 GGGGTGCTCAGACTTACCTGCGAAGATATCTGGAGTGCATGTGGGGACTTT 62

QY 1313 GGAATTGGGCTTGGTGTGTTGTAATAGTACTGAAAGGAGATCAGAAATGCAATA 1372  
DB 63 GGAATTGGGCTTGGTGTGTTGTAATAGTACTGAAAGGAGATCAGAAATGCAATA 122

QY 1373 TATATGAGAGAGAGGAGACTCTTAACTTGGATTGTTAAGACGACATTCAGTGCAGTC 1432  
DB 123 TATATGAGAGAGAGGAGACTCTTAACTTGGATTGTTAAGACGACATTCAGTGCAGTC 182

QY 1433 TCTTACGACCTCCCACTTACCTGACAGTATGTCGCAAGACCTTACCAACATGTAGAT 1492  
DB 183 CCTTACGACCTCCCACTTACCTGACAGTATGTCGCAAGACCTTACCAACATGTAGAT 242

QY 1493 TATTCCTGATGTGAGCTAGACTGAGAGCTTGTGATGTATCAAAAGTCCCTTA 1552  
DB 243 TATTCCTGATGTGAGAGCTAGAGAGCTTGTGATGTATCAAAAGTCCCTTA 302

QY 1553 TATACACCATCCCTAATGCTCTCTGACCTCCCTGAGGCTATCTTGGCTGATTC 1612  
DB 303 TATACACCATCCCTAATGCTCTCTGACCTCCCTGAGGCTATCTTGGCTGATTC 362

QY 1613 ATCTGACACGAGACCAATCAGAAATGTTATCTGCTGTGGAAACCTTTATCCGA 1672  
DB 363 ACTCTGACACGAGATTAATCAGAAATGTTATCTGCTGTGGAAACCTTTATCCGA 422

QY 1673 TAAAGCCCTTCTCTGCTTATCAGAGCAATAGTT-CTGTTTATGCTTG 1731  
DB 423 GGAAGCCCTTCTCTGCTTATCAGAGCAATAGTTCTGTTTATGCTTG 482

QY 1732 AATT 1735  
DB 483 AATT 486

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Job time : 4169.16 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: December 14, 2003, 23:45:56 ; Search time 4626 Seconds

(without alignments)  
3263.219 Million cell updates/sec

Title: US-10-027-923-2  
Perfect score: 1873  
Sequence: 1 WVLILLISLTLKEDVRGSA.....QPLNLELSSGPITGLDRRI 369

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2886711 segs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seg length: 0  
Maximum DB seg length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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-UNITS=bits -START=1 -END=-1 -MATRIX=blomsum62 -TRANS=human40.cdi -LIST=45  
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-OUTFMT=ptc -HEADSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl: \*  
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2: gb\_hcg: \*  
3: gb\_in: \*  
4: gb\_om: \*  
5: gb\_ov: \*  
6: gb\_pac: \*  
7: gb\_ph: \*  
8: gb\_pl: \*  
9: gb\_pr: \*  
10: gb\_ro: \*  
11: gb\_scs: \*  
12: gb\_sy: \*  
13: gb\_un: \*  
14: gb\_vl: \*  
15: em\_ba: \*  
16: em\_fun: \*  
17: em\_hum: \*  
18: em\_in: \*  
19: em\_mu: \*  
20: em\_ox: \*  
21: em\_or: \*  
22: em\_ov: \*  
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27: em\_scs: \*  
28: em\_un: \*

29: em\_vl: \*  
30: em\_hcg\_hum: \*  
31: em\_hcg\_inv: \*  
32: em\_hcg\_other: \*  
33: em\_hcg\_mus: \*  
34: em\_hcg\_pin: \*  
35: em\_hcg\_rtd: \*  
36: em\_hcg\_mam: \*  
37: em\_hcg\_vrt: \*  
38: em\_sy: \*  
39: em\_hcgo\_hum: \*  
40: em\_hcgo\_mus: \*  
41: em\_hcgo\_other: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1873	100.0	1110	6 AX709349	AX709349 Sequence
2	1873	100.0	1823	6 AX709347	AX709347 Sequence
3	1870	99.8	2172	6 AX068372	AX068372 Sequence
4	1830.5	97.7	2349	6 AX068368	AX068368 Sequence
5	1794	95.8	2149	6 AX068374	AX068374 Sequence
6	1780	95.0	2551	6 AX068366	AX068366 Sequence
7	1754.5	93.7	2326	6 AX068370	AX068370 Sequence
8	1648	88.0	2064	6 AX068376	AX068376 Sequence
9	1608.5	85.9	2241	6 AX068371	AX068371 Sequence
10	1484.5	79.3	4078	6 AR270570	AR270570 Sequence
11	1484.5	79.3	4207	6 AR145364	AR145364 Sequence
12	1484.5	79.3	4207	6 AR145365	AR145365 Sequence
13	1484.5	79.3	4303	6 AR145366	AR145366 Sequence
14	1484.5	79.3	4303	6 AR145367	AR145367 Sequence
15	1484.5	79.3	4518	6 AX548892	AX548892 Sequence
16	1484.5	79.3	4518	6 HUMMGGR55A	D28538 Human mRNA
17	1484.5	79.3	4614	9 HUMMGGR55B	D28539 Human mRNA
18	1470.5	78.5	3282	6 AR038828	AR038828 Sequence
19	1470.5	78.5	3282	6 AR038845	AR038845 Sequence
20	1470.5	78.5	3282	6 AR256861	AR256861 Sequence
21	1470.5	78.5	3282	6 I21438	I21438 Sequence 11
22	1470.5	78.5	4085	6 AR038826	AR038826 Sequence
23	1470.5	78.5	4085	6 AR038843	AR038843 Sequence
24	1470.5	78.5	4085	6 AR256859	AR256859 Sequence
25	1470.5	78.5	4085	6 I21436	I21436 Sequence 7
26	1470.5	78.5	4181	6 AR038827	AR038827 Sequence
27	1470.5	78.5	4181	6 AR038844	AR038844 Sequence
28	1470.5	78.5	4181	6 AR256860	AR256860 Sequence
29	1470.5	78.5	4181	6 I21437	I21437 Sequence 9
30	1460	77.9	3918	10 RATMGJLUR	D10891 Rattus norv
31	1412.5	75.4	3471	5 AF227201	AF227201 Gallus ga
32	1412.5	75.4	3567	5 AF227202	AF227202 Gallus ga
33	1412.5	75.4	3729	5 AF227203	AF227203 Gallus ga
34	1124	60.0	4326	5 AB066273	AB066273 Oncorhyn
35	1118.5	59.7	2634	6 AX280723	AX280723 Sequence
36	1118.5	59.7	3295	6 HUMMGJLUB	L76631 Homo sapien
37	1118.5	59.7	3321	6 AR038823	AR038823 Sequence
38	1118.5	59.7	3321	6 AR038827	AR038827 Sequence
39	1118.5	59.7	3321	6 AR256856	AR256856 Sequence
40	1118.5	59.7	3582	6 AR173179	AR173179 Sequence
41	1118.5	59.7	3670	6 AX658279	AX658279 Sequence
42	1118.5	59.7	3670	6 HSU31216	U31216 Human metab
43	1118.5	59.7	4074	6 AR270912	AR270912 Sequence
44	1118.5	59.7	4074	6 HSU31215	U31215 Human metab
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## ALIGNMENTS

RESULT 1

AX709349  
 LOCUS AX709349 1110 bp DNA linear PAT 04-APR-2003  
 DEFINITION Sequence 3 from Patent WO02070708.  
 ACCESSION AX709349  
 VERSION AX709349.1 GI:29564891  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE  
 1 Bates,B.G., Xie,Y., Gulukota,K. and Paulsen,J.E.  
 Glutamate receptor modulatory proteins and nucleic acids encoding them  
 JOURNAL Patent: WO 02070708-A 3 12-SEP-2002;  
 MYECH (US)  
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 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
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 ACCESSION AX709347  
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 REFERENCE  
 1 Bates,B.G., Xie,Y., Gulukota,K. and Paulsen,J.E.  
 Glutamate receptor modulatory proteins and nucleic acids encoding them  
 JOURNAL Patent: WO 02070708-A 1 12-SEP-2002;  
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LOCUS      Sequence 7 from Patent WO0102566.
DEFINITION      AX068372
ACCESSION      AX068372
VERSION      AX068372.1 GI:12578537
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE      1 Schwarz, D.A. and Maki, R.A.
AUTHORS      Metabotropic glutamate receptors and methods of use therefor
TITLES      Patent: WO 0102566-A 7 11-JAN-2001;
JOURNAL      Neurocrine Biosciences, Inc. (US)
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Percent Similarity: 100.00%      Conservative: 1
Best Local Similarity: 99.73%      Mismatches: 0
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QY      41 PheSerValHisHisGlnProThrValAspGluValHisGluArgGlySerGlyValAlaVal 60
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Db      605 TCAGACCCCACTGCTGCTCCCAACATCACTGGGCTGTGAAGATTAAGAGGATTCCTGCTGG 664
Qy      101 HisSerAlaValAlaLeuGluGlnSerIleGluPheIleArgAspSerIleSerSer 120
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Qy      121 GluGluGluGluGluLeuValCysSerValAspGlySerSerSerSerPheArgSerLys 140
Db      725 GAAGAGAAAGAGGCTTGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 784
Qy      141 LysProIleValGlyValIleGlyProGlySerSerSerSerLeuAlaIleGlnValGlnAsn 160
Db      785 AAGCCCATAGTAGGGGCTCATTTGGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 844
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Qy      201 SerMetValAspIleValIleValArgIleThrValSerAlaValAlaIleThrGlu 220
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Qy      321 GluAspArgArgLysCysGlnGlyArgPheLeuGlnGlyPheGlyLysIleLeuHisArg 340
Db      1325 GAAGAGAAAGAGGAGTGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1384
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ACCESSION      AX068368
VERSION      AX068368.1 GI:12578534
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SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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REFERENCE
1 Schwarz,D.A. and Maki,R.A.
AUTHORS      Metabotropic glutamate receptors and methods of use therefor
TITLE      Patent: WO 0102566-A 3 11-JAN-2001;
JOURNAL      Neurocrine Biosciences, Inc. (US)
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Qy      81 SerAspProThrLeuLeuProAsnIleThrLeuGlyCysGluIleArgAspSerCysTyr 100
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QY	41	PheSerValHisHisGlnProThrValAspGIuValHisGIuArgIleCysGIuAlaVal	60
Db	485	TTTTCTGTTCATCAACCAAGCTACTGTGGACGAAGTTCATGAGAGAGAGTGTGGGCACTC	54
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QY	141	IleProIleValGIuValIleGIuProGIuSerSerSerLeuAlaIleGlnValGlnAsn	160
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QY	161	LeuLeuGIuIleuPheAsnIleProGlnIleAlaIleSerIleAsnIleMetAspLeuSer	180
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QY	321	GIuAspArgArgIleCysGIuIleArgPheIleuGIuIlePheGIuAspIleLeuHisArg	340
Db	1325	GAAACACGAAGAATAATCCAAAGGTCCGTCTCTC-----AG	1360
QY	340	gSerGIuSerValIleuLeuHisMetProGlnIleProLeuAsnLeuGIuLeuSerSerGIuIle	360
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Sequence 1 from Patent WO0102566.
AX068366
VERSION  AX068366.1  GI:12578533
KEYWORDS
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ORGANISM Homo sapiens
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REFERENCE
1      Schwarz, D.A. and Maki, R.A.
      Metabotropic glutamate receptors and methods of use therefor
      Patent: WO 0102566-A 11-JAN-2001;
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Score:          1780.00      Matches:      368
Percent Similarity: 74.40%      Conservative: 1
Best Local Similarity: 74.19%      Mismatches: 0
Query Match:      95.03%      Indels:      127
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Db      725 GAAGAGGAAGAGGGCTTGTTGTGCTCTGTGTGATGCTCTCTCTCTCTCTCTCTCTCAAG 784
Qy      141 LysProIleValGlyValIleGlyProGlySerSerSerSerLeuAlaIleGlnValGlnAsn 160
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Qy      161 LeuLeuGlnLeuPheAsnIleProGlnIleAlaIleArgSerAlaThrIleMetAspLeuSer 180
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Qy      220 ----- 220
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Qy      314 rIlyAsnSerIleLeuTyrGluAspArgArgGlyCysGlnGlyArgPheLeuGlnGlyP 334
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DEFINITION
Sequence 5 from Patent WO0102566.
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VERSION  AX068370.1  GI:12578535
KEYWORDS
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
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 AUTHORS  
 TITLE  
 JOURNAL  
 Neurotropic glutamate receptors and methods of use therefor  
 Patent: WO 0102566-A 5 11-JAN-2001;  
 Neurotropic Biosciences, Inc. (US)  
 Location/Qualifiers  
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 LOCUS  
 DEFINITION Sequence 11 from Patent WO0102566.  
 ACCESSION AX068376  
 VERSION AX068376.1 GI:12578539  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
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 AUTHORS  
 TITLE  
 JOURNAL  
 Neurotropic glutamate receptors and methods of use therefor  
 Patent: WO 0102566-A 11 11-JAN-2001;  
 Neurotropic Biosciences, Inc. (US)  
 Location/Qualifiers  
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Db      425 CACTCCAGTGAAGAGGGGTGGTGGCTCACATGCTGGGTACATCATTAATTGGAGCTCTC 484
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Db      665 CATTCGGCTGTGGCCCTAGAGAGAGCATTTGAGATTCAATGAAGATTCCTCATTTCTTCG 724
Qy      121 GluGluGluGluGlyLeuValCysSerValAspGlySerSerSerSerPheArgSerLys 140
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Qy      141 LysProIleValGlyValIleGlyProGlySerSerSerLeuAlaIleGlnValGlnAsn 160
Db      785 AAGCCCATAGTAGAGGGGTCAATTGGGCTGTGCTTCAGTTCTGAGCATTTACAGTCCAGAA 844
Qy      161 LeuLeuGlnLeuPheAsnIleProGlnIleAlaTyrSerAlaThrIleMetAspLeuSer 180
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Qy      361 IleThrGlyLeuArgAspArgLeuIle 369
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LOCUS      Sequence 6 from Patent WO0102566.
DEFINITION      AX068371
ACCESSION      AX068371
VERSION      AX068371.1 GI:12578536
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE      1 Schwarz,D.A. and Maki,R.A.
AUTHORS      Metabotropic glutamate receptors and methods of use therefor
TITLE      Patent: WO 0102566-A 6 11-JAN-2001;
JOURNAL      Neurocrine Biosciences, Inc. (US)
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US-10-027-923-2 (1-369) x AX068371 (1-2241)
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Qy      141 LysProIleValGlyValIleGlyProGlySerSerSerLeuAlaIleGlnValGlnAsn 160
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Qy      161 LeuLeuGlnLeuPheAsnIleProGlnIleAlaTyrSerAlaThrIleMetAspLeuSer 180
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 DEFINITION Sequence 1133 from patent US 6500938.  
 ACCESSION AR270570  
 VERSION AR270570.1 GI:29701804  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE  
 1 (bases 1 to 4078)  
 AUTHORS Au-Young,J. and Seilhamer,J.J.  
 TITLE Composition for the detection of signaling pathway gene expression  
 JOURNAL Patent: US 6500938-A 1133 31-DEC-2002;  
 FEATURES  
 Location/Qualifiers  
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 BASE COUNT 994 a 1074 c 1076 g 934 t  
 ORIGIN

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 Best Local Similarity: 85.00% IdMatches: 22  
 Query Match: 79.26% Indels: 24  
 DB: 6 Gaps: 2

US-10-027-923-2 (1-369) x AR270570 (1-4078)

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 QY 121 GluGluGlnGluGlyLeuValCysSerValAspGlySerSerSerPheArgSerIys 140  
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 QY 141 LysProIleValGlyValIleGlyProGlySerSerSerLeuAlaIleGlnValGlnAsn 160  
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 Db 1051 CTTCGTGGCAGTATGAGC-----TGG 1071

QY 321 GluAspArgArgIysCys-GlnGlyArgPheLeuGlnGlyPheGlyAspIleLeuHisar 340  
 DB 1072 GCTGACGGATGATGATGACAG-----ATGATAT 1101  
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 LOCUS Sequence 1 from patent US 6211353.  
 DEFINITION ARI45364  
 VERSION ARI45364.1 GI:15107231  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 4207)  
 AUTHORS Burnett,J.Paul, Jr., Mayne,N.Gail., Sharp,R.Leon. and Snyder,Y.Marie.  
 TITLE Isolated nucleic acid encoding a human mgluR5  
 JOURNAL Patent: US 6211353-A 1 03-APR-2001;  
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 /organism="unknown"  
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 Score: 1484.50 Matches: 306  
 Percent Similarity: 87.22% Conservative: 8  
 Best Local Similarity: 85.00% Mismatches: 22  
 Query Match: 79.26% Indels: 24  
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 QY 21 GlnSerSergluArgValAlaHisMetLeuGlyAspIleIleGlyAlaLeu 40  
 DB 520 CAGTCCAGTGAAGAGAGGTGGTGGCTCACATGCCGGGTGACATCATTTATGGAGCTTC 579  
 QY 41 PheSerValHisIleGlnProThrValAspGluValHisGluArgIysCysGlyAlaVal 60  
 DB 580 TTTTCTTTCATCCAGCCTTCTGTCGACAAATTCATAGAGAGATGTGGGCGGTC 639  
 QY 61 ArgGluGlnTyrGlyIleGlnArgValAlaMetLeuHisThrLeuGluArgIleAsn 80  
 DB 640 CGGGAACAGATGGCATTGAGAGGTGAGGCCATGCTGCATACCTCGAAAGATCAAT 699  
 QY 81 SerAspProThrLeuLeuProAsnIleThrLeuGlyCysGluIleArgAspSerCysTyr 100  
 DB 700 TCAGACCCCACTCTTCCCAACATCACATGGGCTGTGAGATGAAGAGACTCCTGCTGG 759  
 QY 101 HisSerAlaValAlaLeuGluGlnSerIleGluPheIleArgAspSerLeuIleSerSer 120  
 DB 760 CATTGGCTGTGGCTTGAAGCAGAGCATTTGATTAAGAGATTCCTCATTTCTTCA 819  
 QY 121 GluGluGluGluGluLeuValCysSerValAspGlySerSerSerPheArgSerIys 140  
 DB 820 GAAGAGGAAGAAGCTTGTGACGCTGTGTGATGCTCTCTCTTCCGCTCCAG 879  
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DB 940 TTGCTCAGCTTTTCAACATACCTGATGCTTACTGACAGAACGACATGATCTGAGT 999  
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 QY 201 SerMetValAspIleValIleValAspArgTyrAsnIlePheTyrValSerAlaValHisThrGlu 220  
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 DB 1411 CACGAGAGAGCTTGTGTGGCATCACATCAAGCTCCATCTCCCATGTCAGTGGT 1468  
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 ARI45365 4207 bp DNA linear PAT 08-AUG-2001  
 LOCUS Sequence 3 from patent US 6211353.  
 DEFINITION ARI45365  
 VERSION ARI45365.1 GI:15107232  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 4207)  
 AUTHORS Burnett,J.Paul, Jr., Mayne,N.Gail., Sharp,R.Leon. and Snyder,Y.Marie.  
 TITLE Isolated nucleic acid encoding a human mgluR5  
 JOURNAL Patent: US 6211353-A 3 03-APR-2001;  
 FEATURES location/Qualifiers  
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 BASE COUNT 1010 a 1121 c 1112 g 964 t  
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 Alignment Scores:  
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 Best Local Similarity: 85.00% Mismatches: 22  
 Query Match: 79.26% Indels: 24  
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 QY 321 GluAspArgArgIleCys-GlnGlyArgPheLeuGlnGlyPheGlyAspIleLeuHisArg 340  
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## RESULT 14

AR145367

LOCUS AR145367 4303 bp DNA linear PAT 08-AUG-2001  
 DEFINITION Sequence 6 from patent US 6211353.  
 ACCESSION AR145367  
 VERSION AR145367.1 GI:15107234

## KEYWORDS

SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 4303)  
 AUTHORS Burnett, J. Paul, Jr., Mayne, N. Gall., Sharp, R. Leon. and Snyder, Y. Marie.

## TITLE

Isolated nucleic acid encoding a human mGluR5

Patent: US 6211353-A 6 03-APR-2001;  
Location/Qualifiers

## JOURNAL

FEATURES  
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## ORIGIN

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## RESULT 15

AX548892

LOCUS AX548892 4518 bp DNA linear PAT 26-NOV-2002  
 DEFINITION Sequence 177 from Patent WO02061087.  
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 VERSION AX548892.1 GI:25813755

## KEYWORDS

SOURCE Homo sapiens (human)

## ORGANISM

Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

1 Burner, G.C., Roush, C.L. and Brown, J.P.  
 Antigenic peptides, such as for G protein-coupled receptors  
 (GPCRs), antibodies thereto, and systems for identifying such  
 antigenic peptides  
 Patent: WO 02061087-A 177 08-AUG-2002;

## JOURNAL

LifeSpan BioSciences, Inc. (US)  
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 QY 340 gSerGluSerValLeuLeuHisMetProGlnProLeuAsnLeuGluLeuSerSerGly 359  
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Title: US-10-027-923-2

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#### SUMMARIES

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4	1484.5	79.3	4207	3	US-08-660-148-1
5	1484.5	79.3	4207	3	US-08-660-148-3
6	1484.5	79.3	4303	3	US-08-660-148-4
7	1484.5	79.3	4303	3	US-08-660-148-6
8	1470.5	78.5	3282	1	US-08-072-574-11
9	1470.5	78.5	3282	1	US-08-486-270-11
10	1470.5	78.5	3282	3	US-08-367-264-11
11	1470.5	78.5	3282	4	US-09-153-757-11
12	1470.5	78.5	3282	4	US-09-459-715-11

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29	1117.5	59.7	3219	2	US-08-687-289A-3	Sequence 3, Appl1
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#### ALIGNMENTS

RESULT 1  
US-09-695-481-1  
/ Sequence 1, Application US/09695481  
/ Patent No. 6534287  
/ GENERAL INFORMATION:  
/ APPLICANT: STORMAN, THOMAS M.  
/ APPLICANT: LEVINTHAL, CYNTHIA  
/ APPLICANT: STOROHANN, LAURA  
/ APPLICANT: HAMMERLAND, LANCE G.  
/ APPLICANT: KRAPCHO, KAREN J.  
/ APPLICANT: NPS PHARMACEUTICALS, INC.  
/ TITLE OF INVENTION: A NOVEL HUMAN METABOTROPIC GLUTAMATE RECEPTOR  
/ FILE REFERENCE: 1094.2.6  
/ CURRENT APPLICATION NUMBER: US/09/695,481  
/ PRIOR FILING DATE: 2000-10-24  
/ PRIOR APPLICATION NUMBER: 60/161,481  
/ PRIOR FILING DATE: 1999-10-25  
/ NUMBER OF SEQ ID NOS: 7  
/ SOFTWARE: PatentIn Ver. 2.1  
/ SEQ ID NO 1  
/ LENGTH: 2826  
/ TYPE: DNA  
/ ORGANISM: Homo sapiens  
/ FEATURE:  
/ NAME/KEY: CDS  
/ LOCATION: (1)..(2826)  
/ US-09-695-481-1

#### Alignment Scores:

Pred. No.: 5,35e-175  
Score: 1484.50  
Percent Similarity: 87.22%  
Best Local Similarity: 85.00%  
Query Match: 79.26%  
DB: 4  
Length: 2826  
Matches: 306  
Conservative: 8  
Mismatch: 22  
Indels: 24  
Gaps: 2



QY 161 LeuLeuGlnLeuPheAsnIleProGlnIleAlaTyrSerAlaThrIleMetAspLeuSer 180  
 Db 481 TTGCTCAGCTTTTCAACATCTCAAGATTGCTTACTCAAGCAACGACGATGATCTGAGT 540  
 QY 181 AspLysThrLeuPheLysTyrPheMetArgValAlaProSerAspAlaGlnGlnAlaArg 200  
 Db 541 GACAAAGACTCTGTTCAAAATATTTTCATGAGGGTGTGCTTCAATGATGTACGAGGCAAG 600  
 QY 201 SerMetValAspIleValLysArgTyrAsnTyrThrTyrValSerAlaValHISThrGlu 220  
 Db 601 GCCATGTGACATATGAGAGAGTACCACTGACCTATGATACAGCCGTGCACACAGAA 660  
 QY 221 GlyAsnTyrGlyLysSerGlyMetGluAlaPheLysAspMetSerAlaLysGlnGlyIle 240  
 Db 661 GGCACATATGAGAAAGTGGAGATGAGAGCTTCAAGATATGTACGAGAAAGAGGATT 720  
 QY 241 CysIleAlaHisSerTyrLysIleTyrSerAsnAlaGlyGlnGlnSerPheAspLysLeu 260  
 Db 721 TGCATGCCCACTCTTACAAATCTACAGTATGACAGGAGGAGAGCTTGTATAGCTG 780  
 QY 261 LeuLysLysLeuThrSerHisLeuProLysAlaArgValAlaAlaTyrPheCysGlyGly 280  
 Db 781 CTGAAGAAGCTCAAGTCACTGCCCAAGCCCGGGTGGCTGCTCTGTGAGGGC 840  
 QY 281 MetThrValArgGlyLeuLeuMetAlaMetArgArgLeuGlyLeuValGlyGlnPheLeu 300  
 Db 841 ATACAGGTGAGAGTCTGCTGATGAGCCATAGCGCTGAGCTTACGCGAGAAATTTCTG 900  
 QY 301 LeuLeuGlyArgGlnProAspAlaIlePheIleGlnLysSerLysAsnSerIleLeuTyr 320  
 Db 901 CTTCTGGGCACTGATGCG-----TGG 921  
 QY 321 GluAspArgArgLysCys-GlnGlyArgPheLeuGlnGlyPheGlyAspIleLeuHisArg 340  
 Db 922 GCTGACAGGATGATGATGACAG-----ATGATAT 951  
 QY 340 GSerGlySerValLeuLeuHisMetProGlnProLeuAsnLeuGlnLeuSerGly 359  
 Db 952 CACCGAAGAGCTGTGTGGCATCAACATCAAGCTCCCAATCTCCGATGCAAGTGT 1009  
 Db  
 RESULT 3  
 US-09-016-434-1133  
 ; Sequence 1133 Application US/09016434  
 ; Patent No. 6500938  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Janice Au-Young  
 ; APPLICANT: Jeffrey J. Sellhammer  
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
 ; TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
 ; NUMBER OF SEQUENCES: 1490  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
 ; STREET: 3174 PORTER DRIVE  
 ; CITY: PALO ALTO  
 ; STATE: CALIFORNIA  
 ; COUNTRY: USA  
 ; ZIP: 94304  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/016.434  
 ; FILING DATE: HEREWITH  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Zeller, Karen J.

; REGISTRATION NUMBER: 37,071  
 ; REFERENCE/DOCKET NUMBER: PA-0002 US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (650) 855-0555  
 ; TELEFAX: (650) 845-4166  
 ; INFORMATION FOR SEQ ID NO: 1133:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 4078 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; IMMEDIATE SOURCE:  
 ; LIBRARY: GENBANK  
 ; CLONE: 91408051  
 ; US-09-016-434-1133  
 ;  
 ; Alignment Scores:  
 ; Pred. No.: 9,8e-175 Length: 4078  
 ; Score: 1484.50 Matches: 306  
 ; Percent Similarity: 87.22% Conservative: 8  
 ; Best Local Similarity: 85.00% Mismatches: 22  
 ; Query Match: 79.26% Indels: 24  
 ; DB: 4 Gaps: 2  
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 ; US-10-027-923-2 (1-369) x US-09-016-434-1133 (1-4078)  
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 QY 1 MetValLeuLeuLeuLeuLeuSerValLeuLeuLeuLysGlnAspValArgGlySerAla 20  
 Db 151 ATGTGCTTCTGTGTATCTGTGATCTGATCACTTTTGAAGAAATATCCGTGGAGTGC 210  
 QY 21 GlnSerSerGluArgArgValAlaAlaHisMetLeuGlyAspIleIleIleGlyAlaLeu 40  
 Db 211 CAGTCAATGAGAGAGGGTGTGGCTCAATCCGGGTGACATCTTATGAGCTCTC 270  
 QY 41 PheSerValHisIleGlnProThrValAspGluValHisGlnLysCysGlyAlaVal 60  
 Db 271 TTTTCTGTTCAATCAGCAGCTTACTGTGGAAGAGTTCAATGAGAGAGAGTGGCGGTC 330  
 QY 61 ArgGlnGlnTyrGlyLysIleGlnArgValGlnAlaMetLeuHisThrLeuGlnLysIleAsn 80  
 Db 331 CGTGAACAGTATGACATTCAGAGAGTGAAGGCCATCTGCATCCCTGGAAAGATCAAT 390  
 QY 81 SerAspProThrLeuLeuProAsnIleThrLeuGlyCysGlnLysLeuArgAspSerCysTyr 100  
 Db 391 TCAAGCCCACTCTTCCCAATCAATCACTGGCTGTGAGATTAAGGACTCTGCTGG 450  
 QY 101 HisSerAlaValAlaLeuGlnGlnSerIleGlnPheIleArgAspSerLeuIleSerSer 120  
 Db 451 CATTGGCTGTGGCCCTTAGAGGAGAGCATTTGATTAAGAGATTCCTCATTTCTTCA 510  
 QY 121 GlnGlnGlnGlnGlyLeuValCysSerValAspGlySerSerSerSerPheArgSerLys 140  
 Db 511 GAAGAGAAAGAGGCTTGATGACCTGTGTGAAGGCTCTCTCTCTCTCTCTCCCTCCAG 570  
 QY 141 LysProIleValGlyValIleGlyProGlySerSerSerSerLeuAlaIleGlnValAsn 160  
 Db 571 AAGCCCATGATAGGGGTCATTTGGCTTGGCTTCAGATTCGTACCAATTCAGGTCAGAA 630  
 QY 161 LeuLeuGlnLeuPheAsnIleProGlnIleAlaTyrSerAlaThrIleMetAspLeuSer 180  
 Db 631 TTGCTCAGCTTTTCAACATCTCAAGATTGCTTACTCAAGCAACGACGATGATCTGAGT 690  
 QY 181 AspLysThrLeuPheLysTyrPheMetArgValAlaProSerAspAlaGlnGlnAlaArg 200  
 Db 691 GACAAAGACTCTGTTCAAAATATTTTCATGAGGGTGTGCTTCAATGATGTACGAGGCAAG 750  
 QY 201 SerMetValAspIleValLysArgTyrAsnTyrThrTyrValSerAlaValHISThrGlu 220  
 Db 751 GCCATGTGACATATGAGAGAGTACCACTGACCTATGATACAGCCGTGCACACAGAA 810  
 QY 221 GlyAsnTyrGlyLysSerGlyMetGluAlaPheLysAspMetSerAlaLysGlnGlyIle 240  
 Db 811 GGCACATATGAGAAAGTGGAGATGAGAGCTTCAAGATATGTACAGAAAGAGGAGATT 870

QY 241 CyeIleAlaHisSerTyrIleValIleTyrSerAspAlaGlyGluGlnSerPheAspLeu 260.  
 Db 871 TGCATGCCCACTTTCACAAATCTACAGTATCAGGAGGACCTTTGATACCTG 930  
 QY 261 LeuValysLeuThrSerHisLeuProlysaAlaArgValAlaIleTyrPheCysGluGly 280  
 Db 931 CTGAAGAAGCTCAACAATCTACCTTCCCAAGGCCGGGGTGGCTGCTCTGTGAGGCGC 990  
 QY 281 MetThrValArgGlyLeuLeuMetAlaMetArgArgLeuGlyLeuValGlyGluPheLeu 300  
 Db 991 ATGACGGTGAAGGCTCTGCTGATGCGCATGAGGCGCTGGCTCAGGAGGAGAAATTTCTG 1050  
 QY 301 LeuLeuGlyArgGluProAspAlaIlePheIleGluIleSerLysAsnSerIleLeuTyr 320  
 Db 1051 CTTCTGGGCACTATGAGC-----TGG 1071  
 QY 321 GluAspArgArgLysCys-GlnGlyArgPheLeuGlnGlyPheGlyAspIleLeuHisAr 340  
 Db 1072 GCTGACAGTATGATGTGACAG-----ATGATAT 1101  
 QY 340 gSergIuSerValLeuLeuHisMetProGlnProLeuAsnLeuGluLeuSerSerGly 359  
 Db 1102 CAGGAGAGAGCTGTGGTGGCATCAACAATCAAGCTCCCAATCTCCGATGTCAAGTGTG 1159  
 RESULT 4  
 / Sequence 1, Application US/08660148  
 / Patent No. 6211353  
 / GENERAL INFORMATION:  
 / APPLICANT: Burnette, J. P.  
 / APPLICANT: Mayne, Nancy G.  
 / APPLICANT: Sharp, Robert L.  
 / APPLICANT: Snyder, Yvonne M.  
 / TITLE OF INVENTION: EXCITATORY AMINO RECEPTOR PROTEIN AND  
 / NUMBER OF SEQUENCES: 6  
 / CORRESPONDENCE ADDRES:  
 / ADDRESS: Eli Lilly and Company  
 / STREET: Lilly Corporate Center  
 / CITY: Indianapolis  
 / STATE: Indiana  
 / COUNTRY: United States of America  
 / ZIP: 46285  
 / COMPUTER READABLE FORM:  
 / MEDIUM TYPE: Floppy disk  
 / COMPUTER: IBM PC compatible  
 / OPERATING SYSTEM: PC-DOS/MS-DOS  
 / SOFTWARE: Patent In Release #1.0, Version #1.25  
 / CURRENT APPLICATION DATA:  
 / APPLICATION NUMBER: US/08/660,148  
 / FILING DATE:  
 / CLASSIFICATION:  
 / PRIOR APPLICATION DATA:  
 / APPLICATION NUMBER: US/08/282,853  
 / FILING DATE:  
 / ATTORNEY/AGENT INFORMATION:  
 / NAME: Gaylo, Paul J.  
 / REGISTRATION NUMBER: 36,808  
 / REFERENCE/DOCKET NUMBER: X-9419  
 / TELECOMMUNICATION INFORMATION:  
 / TELEPHONE: (317) 276-0756  
 / TELEFAX: (317) 276-3861  
 / INFORMATION FOR SEQ ID NO: 1:  
 / SEQUENCE CHARACTERISTICS:  
 / LENGTH: 4207 base pairs  
 / TYPE: nucleic acid  
 / STRANDEDNESS: single  
 / TOPOLOGY: linear  
 / FEATURE:  
 / NAME/KEY: CDS  
 / LOCATION: 460..3999

US-08-660-148-1  
 Alignment Scores:  
 Pred. No.: 1,03e-174 Length: 4207  
 Score: 1484.50 Matches: 306  
 Percent Similarity: 87.22% Conservative: 8  
 Best Local Similarity: 85.00% Mismatches: 22  
 Query Match: 79.26% Indels: 24  
 DB: 3 Gaps: 2  
 US-10-027-923-2 (1-369) x US-08-660-148-1 (1-4207)  
 QY 1 MetValLeuLeuLeuIleLeuSerValIleLeuLeuGlyGluAspValArgLysSerAla 20  
 Db 460 ATGGTCTTCTGTGTTGATTCCTGTACGCTTACTTTTGAAGAAGATTCCTGGAGATGCA 519  
 QY 21 GlnSerSerGluArgArgValAlaHisMetLeuGlyAspIleIleIleGlyAlaLeu 40  
 Db 520 CAGTCCAGTGAAGAGAGGAGGTGGCTGCATGCCCGGTGACATCATTAATGAGCTCTC 579  
 QY 41 PheSerValHisHisGlnProThrValAspGluValHisGluArgLysCysGlyAlaVal 60  
 Db 580 TTTTCTGTTCATCACCAAGCTTACTGTGCAAAATTCATGAGAGAGAGTGTGGGGGCTC 639  
 QY 61 ArgGluGlnTyrGlyIleGlnArgValGluAlaMetLeuHisThrLeuGluArgLysLeu 80  
 Db 640 CGTGAACAGTATGGCATTCAGAGAGTGAAGGCCATCTGCATACCTCGAAGAGATCAAT 699  
 QY 81 SerAspProThrLeuLeuProAsnIleThrLeuGlyCysGluIleArgAspSerCysTyr 100  
 Db 700 TCAGACCCCACTCTTGGCCCAACATCACATCGGGCTGAGATGAGGAGCATCTCTCTG 759  
 QY 101 HisSerAlaValAlaLeuGlnGlnSerIleGluPheIleArgAspSerLeuIleSer 120  
 Db 760 CATTGCGCTGTGGCCCTTAAGCAGACATTTGATTATAGATTCCTCATTTCTTCA 819  
 QY 121 GluGluGluGluGlyLeuValCysSerValAspGlySerSerSerPheArgSerLys 140  
 Db 820 GAAGAGAGAGAGAGCTTGGTACGCTGTGTGATGCTCTCTCTCTCTCTCTCTCTCAAG 879  
 QY 141 LysProIleValIleGlyValIleGlyProGlySerSerSerLeuAlaIleGlnValGln 160  
 Db 880 AAGCCCATGATGAGGGGTCAATGGGCTGCTCAGTTCTGTGACCATTCAGGCTCCAGAT 939  
 QY 161 LeuLeuGlnLeuPheAsnIleProGlnIleAlaTyrSerAlaThrIleLeuAspLeuSar 180  
 Db 940 TTGCTCAGCTTTTCAACATACCTCAATGCTTACTACGAAACGACGATGATCTGAGT 999  
 QY 181 AspLysThrLeuPheLysTyrPheMetArgValAlaProSerAspAlaGlnGlnAlaArg 200  
 Db 1000 GACAAAGCTCTGTCAATATTTTCAATGAGGATTTGCTTCAAGATGCTCAGCAGCGCAAG 1059  
 QY 201 SerMetValAspIleValIleValysArgTyrAsnTyrThrTyrValSerAlaValHisThr 220  
 Db 1060 GCCATGTGACATGATGAGAGGATGACATGACCTTAATGTATGACCTGACACAGAA 1119  
 QY 221 GlyAsnTyrGlyGlnSerGlyMetGluAlaPheLysAspMetSerAlaLysGluGlyIle 240  
 Db 1120 GGCACCTATGAGAAAGTGGAGTGAAGGCTTCAAGATATGTACGCAAGAGAGGAGATT 1179  
 QY 241 CyeIleAlaHisSerTyrIleValIleTyrSerAsnAlaGlyGluGlnSerPheAspLysLeu 260  
 Db 1180 TGCATGCCCACTTTCACAAATCTACAGTATGACAGGAGACAGACTTATATAGCTG 1239  
 QY 261 LeuValysLeuThrSerHisLeuProlysaAlaArgValAlaIleTyrPheCysGluGly 280  
 Db 1240 CTGAAGAAGCTCAACAATCTACCTTCCCAAGGCCGGGGTGGCTGCTGTGAGGCGC 1299  
 QY 281 MetThrValArgGlyLeuLeuMetAlaMetArgArgLeuGlyLeuValGlyGluPheLeu 300  
 Db 1300 ATGACGGTGAAGGCTCTGCTGATGCGCATGAGGCGCTGGCTGTGACGGGAGAAATTTCTG 1359  
 QY 301 LeuLeuGlyArgGluProAspAlaIlePheIleGluIleSerLysAsnSerIleLeuTyr 320

Db 1360 CTTCTGGGCGATGATGCG-----TGG 1380  
 Qy 321 GUAAPARGArglycys-GlnGlyArgPheLeuGlnGlyPheGlyAspIleuHsAr 340  
 Db 1381 GCTGACAGGTATGATGATGACAG-----ATGGATAT 1410  
 Qy 340 gSerGluSerValIleuLeuHsMetProGlnProLeuAsnLeuGluLeuSerGly 359  
 Db 1411 CAGCGAAGAGCGTGTGTGTGATCATCATCAAGCTCCATCTCCGATGTCAAGTGT 1468  
 RESULT 5  
 US-08-660-148-3  
 / Sequence 3, Application US/08660148  
 / Patent No. 6211353  
 / GENERAL INFORMATION:  
 / APPLICANT: Burnett, J. P.  
 / APPLICANT: Mayne, Nancy G.  
 / APPLICANT: Sharp, Robert L.  
 / APPLICANT: Snyder, Yvonne M.  
 / TITLE OF INVENTION: EXCITATORY AMINO RECEPTOR PROTEIN AND  
 / NUMBER OF SEQUENCES: 6  
 / CORRESPONDENCE ADDRESS:  
 / ADDRESS: Eli Lilly and Company  
 / STREET: Lilly Corporate Center  
 / CITY: Indianapolis  
 / STATE: Indiana  
 / COUNTRY: United States of America  
 / ZIP: 46285  
 / COMPUTER READABLE FORM:  
 / MEDIUM TYPE: Floppy disk  
 / COMPUTER: IBM PC compatible  
 / OPERATING SYSTEM: PC-DOS/MS-DOS  
 / SOFTWARE: Patent Release #1.0, Version #1.25  
 / CURRENT APPLICATION DATA:  
 / APPLICATION NUMBER: US/08/660,148  
 / FILING DATE:  
 / CLASSIFICATION:  
 / PRIOR APPLICATION DATA:  
 / APPLICATION NUMBER: US/08/282,853  
 / FILING DATE:  
 / ATTORNEY/AGENT INFORMATION:  
 / NAME: Gaylo, Paul J.  
 / REGISTRATION NUMBER: 36,808  
 / REFERENCE/DOCKET NUMBER: X-9419  
 / TELECOMMUNICATION INFORMATION:  
 / TELEPHONE: (317) 276-0756  
 / TELEFAX: (317) 276-3861  
 / INFORMATION FOR SEQ ID NO: 3:  
 / SEQUENCE CHARACTERISTICS:  
 / LENGTH: 4207 base pairs  
 / TYPE: nucleic acid  
 / STRANDEDNESS: single  
 / TOPOLOGY: linear  
 / MOLECULE TYPE: mRNA  
 / US-08-660-148-3  
 Alignment Scores:  
 Pred. No.: 1.03e-174 Length: 4207  
 Score: 1484.50 Matches: 306  
 Percent Similarity: 87.224 Conservative: 8  
 Best Local Similarity: 85.004 Mismatches: 22  
 Query Match: 79.264 Indels: 24  
 Gaps: 2  
 US-10-027-923-2 (1-369) x US-08-660-148-3 (1-4207)  
 Qy 1 MetValIleuLeuLeuIleLeuSerValIleuLeuLeuLeuLeuLeuValArgGlySerAla 20  
 Db 460 AUGGUCUUCUGUUGUUAUCCUUCUUCUUCUUCUUCUUCUUCUUCUUCUUCUUCUUCUUCU 519  
 Qy 21 GlnSerSerGluArgValValAlaHsMetLeuGlyAspIleIleIleGlyAlaLeu 40

Db 520 CAGUCCAGUGAGAGAGGUGUGGUCUACAUCCGGGUGACAUCAUUAUUGAGUCUC 579  
 Qy 41 PheSerValHsHsIleGlnProThrValAspGluValHsIleGlyArgGlySerGlyAlaVal 60  
 Db 580 UUUUCUGUCUACUACACACACUUGGAGCAAAUUCUUAUGAGAGAAUGUGGGGCGUC 639  
 Qy 61 ArgGluGlnIleGlyIleGlnArgValGlnHsMetLeuHsIleGlnLeuGlnArgIleAsn 80  
 Db 640 CGUGAACGUAUUGGUAUUCAGAGAGUGGAGGCCAUUGUCUACCCUGAAGAAUUAU 699  
 Qy 81 SerAspProThrIleuLeuProAsnIleThrLeuGlyCysGlnIleArgAspSerCysTrp 100  
 Db 700 UCAGACCCCAACUUCUGCCCAUACUACUGGCGUGAGAUUAAGGACUUCUGCG 759  
 Qy 101 HisSerAlaValAlaLeuGlnGlnSerIleGluPheIleArgAspSerIleuLeuSer 120  
 Db 760 CAUCCGCGUGGCGCCUAGAGCAGACAUUGAGUUCUUAAGAAUUCUUCUUCUCCG 819  
 Qy 121 GluGluGluGluGlyLeuValCysSerValAspGlySerSerSerPheArgSerIle 140  
 Db 820 GAAGAGGAGAGAGGCTUGGUACCGUGUGGUGGUGGUGGUGGUGGUGGUGGUGG 879  
 Qy 141 LysProIleValGlyValIleGlyProGlySerSerSerIleAlaIleGlnValAsn 160  
 Db 880 AAGCCCAUAGAGGAGGUGUUGGCGUGGUGGUGGUGGUGGUGGUGGUGGUGG 939  
 Qy 161 LeuLeuGlnLeuPheAsnIleProGlnIleAlaIleSerIleThrIleMetAspLeuSer 180  
 Db 940 UUGCUCACGUCUUCUACAUACUUCUACUUCUUCUACUACUACUACUACUACU 999  
 Qy 181 AspLysThrLeuPheLeuPheLeuPheMetArgValProSerAspAlaGlnGlnAlaArg 200  
 Db 1000 GACAGACUUCUGUCAAUUAUUAUGAGGUGUGGUGGUGGUGGUGGUGGUGGUGG 1059  
 Qy 201 SerMetValAspIleValIleValArgTyrAsnTrpThrTyrValSerAlaValHsThrGlu 220  
 Db 1060 GCCAUGUGUAGACUAGUGAGAGAGUACUUGACCUUAUGUUCAGCGGUCACACAGAA 1119  
 Qy 221 GlyAsnTyrGlyGluSerGlyMetGluAlaPheLysAspMetSerAlaLysGlnGlyIle 240  
 Db 1120 GGCACUUAUGAGAAAGUGGAGUAGAGCCUUCAAAGAUUAUGUACGAGAGAGAGGAAU 1179  
 Qy 241 CysIleAlaHsSerTyrIleIleTyrSerAsnIleGlyGlnGlnSerPheAspLysLeu 260  
 Db 1180 UGCACUGCCCAUUCUACAAUUCUACGUAUUCAGAGGAGAGAGAGAGAGAGAG 1239  
 Qy 261 LeuLysIleLeuThrSerHsIleuProLysAlaArgValAlaTyrPheCysGlnGly 280  
 Db 1240 CUGAAGAGUUCACAGUACUUGCCCAAGGCGCGGUGGUGGUGGUGGUGGUGG 1299  
 Qy 281 MetThrValArgGlyLeuLeuMetAlaMetArgArgLeuGlyLeuValGlyLeuPheLeu 300  
 Db 1300 AUGACGUGUAGAGUGUGUGGUGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1359  
 Qy 301 LeuLeuGlyArgGluProAspAlaIlePheIleGlnIleSerLysAsnSerIleLeuTrp 320  
 Db 1360 CUUCUGGCGAGUGUUGCC-----UGG 1380  
 Qy 321 GlnAspArgArgIleCys-GlnGlyArgPheLeuGlnGlyPheGlyAspIleLeuHsAr 340  
 Db 1381 GCTGACAGUUAUGUACUAGCAG-----AUGAAU 1410  
 Qy 340 gSerGluSerValIleuLeuHsMetProGlnProLeuAsnLeuGluLeuSerGly 359  
 Db 1411 CAGCGAAGAGCGUGUGGUGGACUACAUCAAGUCUCCAGUUCUCCGAGUGUGU 1468  
 RESULT 6  
 US-08-660-148-4  
 / Sequence 4, Application US/08660148  
 / Patent No. 6211353  
 / GENERAL INFORMATION:  
 / APPLICANT: Burnett, J. P.

APPLICANT: Mayne, Nancy G.  
 APPLICANT: Sharp, Robert L.  
 APPLICANT: Snyder, Yvonne M.  
 TITLE OF INVENTION: EXCITATORY AMINO RECEPTOR PROTEIN AND  
 TITLE OF INVENTION: RELATED NUCLEIC ACID COMPOUNDS  
 NUMBER OF SEQUENCES: 6  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Eli Lilly and Company  
 STREET: Lilly Corporate Center  
 CITY: Indianapolis  
 STATE: Indiana  
 COUNTRY: United States of America  
 ZIP: 46285  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/660,148  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/282,853  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Gaylo, Paul J.  
 REGISTRATION NUMBER: 36,808  
 REFERENCE/DOCKET NUMBER: X-9419  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (317) 276-0756  
 TELEFAX: (317) 276-3861  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 4303 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 460..4095  
 US-08-660-148-4  
 Alignment Scores:  
 Pred. No.: 1.07e-174 Length: 4303  
 Score: 1484.50 Matches: 306  
 Percent Similarity: 87.22% Conservative: 8  
 Best Local Similarity: 85.00% Mismatches: 22  
 Query Match: 79.26% Indels: 24  
 DB: 3 Gaps: 2  
 US-10-027-923-2 (1-369) x US-08-660-148-4 (1-4303)

101 HisSerAlaValAlaLeuGlnSerIleGluPheIleArgAspSerIleSerSer 120  
 760 CATTGGCTGTGGCTTGAAGCAGAGCATTGATTGATTAAGATTCCTCATTTCTTCA 819  
 121 GluGlnGluGlnGlyLeuValCysSerValAspGlySerSerSerPheArgSerLys 140  
 820 GAAGAGAAAGAGCTTGGTGAACCTGGTGGTGAAGCTGCTCTTCTCCCTCCAG 879  
 141 LysProIleValIleValIleGlyProGlySerSerSerSerIleuAlaIleGlnValGlnAsn 160  
 880 AACCCCATAGTAGGGGTCATTTGGCCCTGGCTCCAGTTCTGATCCATCAGTCCAGAAAT 939  
 161 LeuLeuGlnLeuPheAsnIleProGlnIleAlaTyrSerAlaThrIleMetAspLeuSer 180  
 940 TTGCTCAGCTTTTCAACATCACTGATGCTTACTGACGAAACGACGATGATGAGT 999  
 181 AspLysThrLeuPheLysTyrPheMetArgValAlaProSerAspAlaGlnIleAlaArg 200  
 1000 GACAAAGCTCTGTCAAATATTTCAAGAGGCTTGCTCCATGATGCTCAGACAGCAGAG 1059  
 201 SerMetValAspIleValIleValIleValIleValIleValIleValIleValIleVal 220  
 1060 GCCATGCTGACATAGTGAAGAGGTACCACTGATGATATGATGATGATGATGATGAT 1119  
 221 GlyAsnTyrGlyGlnSerGlyMetGluAlaPheLysAspMetSerAlaLysGlnGlyIle 240  
 1120 GGCACATAGAGAAAGTGGATGGAAGCTTCAAGATATGTCACGGAAGAGGATTT 1179  
 241 CysIleAlaHisSerTyrIleTyrSerAsnAlaGlyGlnSerPheAspLysLeu 260  
 1180 TGCATGCGCCACTTACAAATCTACATGATGACAGGAGCAGAGCTTGTGATGAGCTG 1239  
 261 LeuLysLysLeuPheSerHisLeuProLysAlaArgValAlaIleTyrPheCysGlnGly 280  
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 1300 ATGACGCTGAGAGGTCTGCTGATGCGCATGAGCCGCTGGGTCTTACCGGAGAAATTTCTG 1359  
 301 LeuLeuGlyArgGlnProAspAlaIlePheIleGluIleSerLysAsnSerIleLeuTyr 320  
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 321 GluAspArgArgLysCysGlnGlyArgPheLeuGlnGlyPheGlyAspIleLeuHisArg 340  
 1381 GCTGACAGGTATGATGTGACAG-----ATGATAT 1410  
 340 GSerGlnSerValLeuLeuHisMetProGlnProLeuAsnLeuGlnLeuSerSerGly 359  
 1411 CAGCGAAGCTGTGTGTGATCAATCAATCAAGCTCCATCTCCGATGCAAGTGT 1468  
 RESULT 7  
 US-08-660-148-6  
 ; Sequence 6, Application US/08660148  
 ; Patent No. 6211353  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Burnette, J. P.  
 ; APPLICANT: Mayne, Nancy G.  
 ; APPLICANT: Sharp, Robert L.  
 ; APPLICANT: Snyder, Yvonne M.  
 ; TITLE OF INVENTION: EXCITATORY AMINO RECEPTOR PROTEIN AND  
 ; TITLE OF INVENTION: RELATED NUCLEIC ACID COMPOUNDS  
 ; NUMBER OF SEQUENCES: 6  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Eli Lilly and Company  
 ; STREET: Lilly Corporate Center  
 ; CITY: Indianapolis  
 ; STATE: Indiana  
 ; COUNTRY: United States of America  
 ; ZIP: 46285  
 ; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/660,148  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/282,853  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Gaylo, Paul J.  
 REGISTRATION NUMBER: 36,808  
 REFERENCE/DOCKET NUMBER: X-9419  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (317) 276-0756  
 TELEFAX: (317) 276-3861  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 4303 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: mRNA  
 US-08-660-148-6

Alignment Scores:  
 Pred. No.: 1.07e-174 Length: 4303  
 Score: 1484.50 Matches: 306  
 Percent Similarity: 87.22% Conservative: 8  
 Best Local Similarity: 85.00% Mismatches: 22  
 Query Match: 79.26% Indels: 24  
 DB: 3 Gaps: 2

US-10-027-923-2 (1-369) x US-08-660-148-6 (1-4303)

QY 1 MetValLeuLeuLeuLeuSerValLeuLeuLeuGluAspValArgIysSerAla 20  
 DB 460 AUGGUCUUCUGUGUAGUCCUGUCAGUCUUCUUAAGAAAGUAGUCCUGGAGUACA 519  
 QY 21 GlnSerSerGluArgValAlaAlaHisMetLeuGlyAspIleIleIleGlyAlaLeu 40  
 DB 520 CAGUCAGAGAGAGAGAGGUGUGUGUCUACAUCCCGGUGACUACUUAUUGAGUCUCUC 579  
 QY 41 PheSerValHisIleGlnProThrValAspGluValHisGluArgIysCysGlyAlaVal 60  
 DB 580 UUUUCUGUACUACAGCAGCCUACUGGAGCAAGUUCUACUAGAGAGAGUUGUGGCGGUC 639  
 QY 61 ArgGluGlnIleGlyIleGlnArgValGluAlaMetLeuHisThrLeuGluArgIleAsn 80  
 DB 640 CGUGAACAGUAGUAGUUCAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 699  
 QY 81 SerAspProThrLeuLeuProAsnIleThrLeuGlyCysGluIleArgAspSerCysTrp 100  
 DB 700 UCGAGACCCACACUUCUGCCCAUACUACUGGCGUGAGUAGAGGAGCUCUCUGUG 759  
 QY 101 HisSerAlaValAlaLeuGlnIleGlnIleGluPheIleArgAspSerLeuIleSerSer 120  
 DB 760 CAUUCGCGUGGCGCCUAG 819  
 QY 121 GluGluGluGluGluLeuValCysSerValAspGlySerSerSerSerPheArgSerIys 140  
 DB 820 GAAGAGAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 879  
 QY 141 LysProIleValGlyValIleGlyProGlySerSerSerSerLeuAlaIleGlnValGlnAsn 160  
 DB 880 AACCCCAUAGUAGGAGUACUUGGCGUGGAGUACUUGGCGUGGAGUACUUGGCGUGGAGU 939  
 QY 161 LeuLeuGlnLeuPheAsnIleProGlnIleAlaIleTyrSerAlaThrIleMetAspLeuSer 180  
 DB 940 UUGCUCAGGCUUUUCAAUACCUCAAGAUUGCUUACUACAGCAACAGCAAGAUUGAUUGAGU 999

QY 181 AspIleThrLeuPheIleTyrPheMetArgValProSerAspAlaGlnIleAlaArg 200  
 DB 1000 GACAGACUUCUUCUCAAUAUUCUAGAGGUGUGGUCUUCAGAUUCUACAGCAGCAGAG 1059  
 QY 201 SerMetValAspIleValIleValArgTyrAsnTrpThrTyrValSerAlaValHisThrGlu 220  
 DB 1060 GCCAUGUGAGACUAGUAGAGUACAACUGAGCCUAGUAGUAGAGCCUGGACACAGAA 1119  
 QY 221 GlyAsnTrpGlyGluSerGlyMetGluAlaPheIleAspMetSerAlaIleGluGlyIle 240  
 DB 1120 GGCACUAGAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1179  
 QY 241 CysIleAlaHisSerTyrIleTyrSerAsnAlaGlyGluGlnSerPheAspIleLeu 260  
 DB 1180 UGCAUGCCCAUUCUACAAUUCUACAGUAGUAGAGGAGGAGGAGGAGGAGGAGGAGGAG 1239  
 QY 261 LeuIleValLeuThrSerHisLeuProIleValAlaArgValAlaIleTyrPheCysGluGly 280  
 DB 1240 CUGAAGAGCUCACAAAGUACUUGCCCAAGGCCCGGUGUGGCGUCUUCUGAGAGGC 1299  
 QY 281 MetThrValArgGlyLeuLeuMetAlaMetArgArgLeuGlyLeuValGlyGluPheLeu 300  
 DB 1300 AUGACGUGAGAGGUCUUGGAGUAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1359  
 QY 301 LeuLeuGlyArgGluProAspAlaIlePheIleGluIleSerIleAsnSerIleLeuTrp 320  
 DB 1360 CUUCUGGAGAGUAGUAGC-----UGG 1380  
 QY 321 GluAspArgArgIleCysGlnGlyArgPheLeuGlnIlePheGlyAspIleLeuHisArg 340  
 DB 1381 GCUGACAGUAGUAGUAGUAGCAG-----AUGAUU 1410  
 QY 340 gSerGluSerValLeuLeuHisMetProGlnProLeuAsnLeuGluLeuSerSerIys 359  
 DB 1411 CAGCGAGAGCUGUGUGGAGUACAUCAAGCUCUCCAGUAGUAGUAGUAGUAGUAGU 1468

# RESULT 8

US-08-072-574-11  
 Sequence 11, Application US/08072574  
 Patent No. 5521297  
 GENERAL INFORMATION:  
 APPLICANT: Daggett, Lorrie  
 APPLICANT: Ellis, Steven B.  
 APPLICANT: Liaw, Chen  
 APPLICANT: Postler, Aaron  
 TITLE OF INVENTION: HUMAN MATABOTROPIC GLUTAMATE RECEPTORS,  
 NUMBER OF SEQUENCES: 13  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
 STREET: 444 South Flower Street, Suite 2000  
 CITY: Los Angeles  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 00719  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/072,574  
 FILING DATE: 19930604  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Reiter, Stephen B.  
 REGISTRATION NUMBER: 31,192  
 REFERENCE/DOCKET NUMBER: P41 9383  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 213-622-7700  
 TELEFAX: 213-489-4210  
 INFORMATION FOR SEQ ID NO: 11:  
 SEQUENCE CHARACTERISTICS:









DB 430 CAGTCCAGTGAAGAGGGTGTGGCTCAGATGCCGGGTGACATCATTTATGAGGCTTC 489  
QY 41 PheservAlHihieGlnProthrValaspGluValHieGluArgLysCysGlyAlaVal 60  
DB 490 TTTTCTGTCATCACAGGCTACTGTGAGCAAGTTTCATAGAGGAGTGTGGGGGGCTC 549  
QY 61 ArgGluGluTyrGlyIleGlnArgValGluAlaMetLeuHieThrLeuGluValGlyIleAsn 80  
DB 550 CGTGAACAGTATGAGCATTCAGAGAGTGGAGGCCATGCTGATACCTCTGGAAGAGATCAT 609  
QY 81 SeraspProThrLeuLeuProAsnIleThrLeuGlyCysGluIleArgAspSerCysTrp 100  
DB 610 TCAGACCCCACTCTTGGCCCAATCAGACTGGGGGTGATGATTAAGGAGCTCTGCTGG 669  
QY 101 HiaservAlaValAlaLeuGluGlnSerIleGluPheIleArgAspSerLeuIleSerSer 120  
DB 670 CATTCGGCTGTGGCCCTTACGAGAGCATTTGAGTTTCATAGAGATTCCTCATTTCTTCA 729  
QY 121 GlnGluGluGluGlyLeuValCysSerValaspGlySerSerSerSerPheArgSerLys 140  
DB 730 GAAGAGAGAGAGGCTTGGTACGCTGTGTGATGGCTCTCTCTCTCTCTCTCTCTCCAG 789  
QY 141 LysProIleValGlyValIleGlyProGlySerSerSerSerLeuAlaIleGlnValGlnAsn 160  
DB 790 AAGCCATGATGAGGGGTCATTTGGGCTGGCTCCAGTTCTGTACCATTCAGTCCAGAAAT 849  
QY 161 LeuLeuGlnLeuPheAsnIleProGlnIleAlaIleThrSerAlaThrIleMetAspLeuSer 180  
DB 850 TTGCTCAGCTTTTCAACATCTCAGATTGCTTACTCAGCAACAGCATGATGATCTGAGT 909  
QY 181 AspLeuThrLeuPheIleThrPheMetArgValValProSerAspAlaGlnGlnAlaArg 200  
DB 910 GACAGAGCTCTGTTCAAAATTTTCAAGAGGGTGTGTCTTCAAGATGCTCAGAGGAGG 969  
QY 201 SerMetValaspIleValLysArgTyrAsnTrpThrTyrValSerAlaValHieThrGlu 220  
DB 970 GCATGTGTGACATATGAGAGAGTCACTGACCTATATCAGCCGTCAGACAGAA 1029  
QY 221 GlyAsnTyrGlyGluSerGlyMetGluAlaPheLysAspMetSerAlaLysGluGlyIle 240  
DB 1030 GGCACATATGAGAAAGTGGAGTGAAGAGCTCCAAAGATGTGTACAGCAAGAGGAGATT 1089  
QY 241 CysIleAlaHieSerTyrIleTyrIleTyrSerAspAlaGlyGluGlnSerPheAspLeu 260  
DB 1090 TGCATGCCACCTTACAAATCTTCAAGTATGACAGGAGAGAGAGCTTTGATTAAGCTG 1149  
QY 261 LeuLysLeuLeuThrSerHieLeuProLysAlaArgValAlaIleTyrPheCysGluGly 280  
DB 1150 CTGAAGAGCTCAGAGTCACTTGGCCCAAGGCCGGGTGTGGCTTCTGTGTAGGGC 1209  
QY 281 MetThrValArgGlyLeuLeuMetAlaMetArgArgLeuGlyLeuValGlyGluPheLeu 300  
DB 1210 ATGACGCGTGAAGAGTGTGCTGATGAGCATGAGCGCTGGGTCTAGCGGAGAAATTTCTG 1269  
QY 301 LeuLeuGlyArgGluProAspAlaIlePheIleGluIleSerLysAsnSerIleLeuTrp 320  
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DB 1291 GCGAGAGAGTATGATGACAG-----ATGATAT 1320  
QY 340 gSerGluSerValLeuLeuHieMetProGlnProLeuAsnLeuGluLeuSerSerGly 359  
DB 1321 CAGCGAGAGAGTGTGTGGCATCACAATCAAGCTCAATCTCCGATGCAAGTGGT 1378

RESULT 12  
US-09-459-715-11  
Sequence 11, Application US/09459715  
Patent No. 6485919  
GENERAL INFORMATION:  
APPLICANT: Daggett, Lorrie

Ellis, Steven B.  
Liaw, Chen  
Pontstler, Aaron  
Johnson, Edwin C.  
Hees, Stephen D.  
TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,  
NUCLEIC ACIDS ENCODING SAME AND USES THEREOF  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSES: Pretty, Schroeder, Brueggemann & Clark  
STREET: 444 South Flower Street, Suite 2000  
CITY: Los Angeles  
STATE: CA  
COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/459, 715  
FILING DATE: 13-Dec-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/367,264  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen B.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: PP41 9772  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-546-4737  
TELEFAX: 619-546-9392  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3282 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 370..3003  
OTHER INFORMATION: /product= "HUMAN MGLUR5C"  
/note= "variant of MGLUR5A with truncated 3' end."  
SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-09-459-715-11  
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Pred. No.: 3,85e-173 Length: 3282  
Score: 1470.50 Matches: 304  
Percent Similarity: 86.67% Conservative: 8  
Best Local Similarity: 84.44% Mismatches: 24  
Query Match: 78.51% Indels: 24  
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US-10-027-923-2 (1-369) x US-09-459-715-11 (1-3282)  
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QY 21 GlnSerSerGluArgArgValAlaAlaHieMetLeuGlyAspIleIleIleGlyAlaLeu 40  
DB 430 CAGTCAGAGAGAGAGGGTGTGGCTCAGTCCGGGTGACATCATTTATGAGGCTTC 489  
QY 41 PheservAlHihieGlnProthrValaspGluValHieGluArgLysCysGlyAlaVal 60  
DB 490 TTTTCTGTCATCACAGGCTACTGTGAGCAAGTTTCATAGAGGAGTGTGGGGGGCTC 549  
QY 61 ArgGluGluTyrGlyIleGlnArgValGluAlaMetLeuHieThrLeuGluValGlyIleAsn 80

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Qy      121 GluGluGluGluGlyLeuValCysSerValAspGlySerSerSerSerPheArgSerLys 140
Db      730 GAAGAGAGAAAGAGCTTGTGTAACGCTGTGTGATGCTCTCTCTCTCTCTCTCTCTCTCAAG 789
Qy      141 LysProIleValGlyValIleGlyProGlySerSerSerSerLeuAlaIleGlnValAsn 160
Db      790 AAGGCCATAGTGGGGATTTGGCTGGCTGGCTGCCATTTCTGAGCATTCAGATCAAGT 849
Qy      161 LeuLeuGlnLeuPheAsnIleProGlnIleAlaTyrSerAlaThrIleMetAspLeuSer 180
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Qy      181 AspLysThrLeuPheLysTyrPheMetArgValAlaProSerAspAlaGlnGlnAlaArg 200
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Qy      241 CysIleAlaHisSerTyrLysIleTyrSerAsnAlaGlyGluGlnSerPheAspLeu 260
Db      1090 TGCATCCGCCCACTCTTCAAAATCTCAAGTATGACAGGGAGCAGACCTTGTATTAAGCTG 1149
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Db      1210 ATGACGCTGAGAGGCTCTGCTGATGCGCATGAGGCGCTGCTAGGGGAGATTTCTG 1269
Qy      301 LeuLeuGlyArgGluProAspAlaIlePheIleGluIleSerLysAsnSerIleLeuTrp 320
Db      1270 CTTCTGGGCACTGATGCG-----TGG 1290
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: CITY: Los Angeles
: STATE: CA
: COUNTRY: USA
: ZIP: 00719
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/072,574
: FILING DATE: 19930604
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Reiter, Stephen E.
: REGISTRATION NUMBER: 31,192
: REFERENCE/DOCKET NUMBER: P41 9383
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 213-622-7700
: TELEFAX: 213-489-4210
: INFORMATION FOR SEQ ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4085 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: both
: TOPOLOGY: both
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 370..3912
: OTHER INFORMATION: /product= "HUMAN MGUR5A"
:
: US-08-072-574-7
:
: Alignment Scores:
: Pred. No.: 5,53e-173 Length: 4085
: Score: 1470.50 Matches: 304
: Percent Similarity: 86.67% Conservative: 8
: Best Local Similarity: 84.44% Mismatches: 24
: Query Match: 78.51% Indels: 24
: DB: 1 Gaps: 2
:
: US-10-027-923-2 (1-369) x US-08-072-574-7 (1-4085)
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: Qy      1 MetValLeuLeuLeuLeuLeuSerValLeuLeuLeuLysGluAspValArgGlySerAla 20
: Db      370 ATGCTCTTCTGTGATCCTGTCACTTACTTGTGAAAGAAATGCTCCGTGGAGTGC 429
: Qy      21 GlnSerSerGluArgArgValAlaAlaHisMetLeuGlyAspIleIleIleGlyAlaLeu 40
: Db      430 CAGTCCAGTGAAGAGAGGTGTGGCTCATGCCCCGGGTGACATCATTTATGAGCTCTC 489
: Qy      41 PheSerValHisIleGlnProThrValAspGluValHisGluArgLysCysGlyAlaVal 60
: Db      490 TTTTCTGTTATACACAGCCCTACTGTGACAAAGTTCATGAGAGAGTGTGGGCGGTC 549
: Qy      61 ArgGluGlnTyrGlyIleGlnArgValAlaAlaMetLeuHisThrLeuGluArgIleAsn 80
: Db      550 CGTGAACAGTATGCGATTTCAGAGAGTGGAGCCATGCTGATACCTCGGAAAGATCAAT 609
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: Db      610 TCAGACCCCACTCTTGGCCCAACATCACTGGGCTGTGATGAAGAGACTCTGCTGG 669
: Qy      101 HisSerAlaValAlaLeuGluGlnSerIleGluPheIleArgAspSerLeuIleSerSer 120
: Db      670 CATTGGCTGTGGCCCTTAGAGCAGACATTGAGTTCAATTAAGAGATTCCTCATTTCTTCA 729
: Qy      121 GluGluGluGluGlyLeuValCysSerValAspGlySerSerSerSerPheArgSerLys 140
: Db      730 GAAGAGAGAAAGAGCTTGTGTAACGCTGTGTGATGCTCTCTCTCTCTCTCTCTCTCAAG 789
: Qy      141 LysProIleValGlyValIleGlyProGlySerSerSerSerLeuAlaIleGlnValAsn 160

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Db 790 AMGCCATAGTAGGGGTCATTGGGCTGCTCCAGTTCTGTAGCAATTCAGTCCAGAAAT 849  
Qy 161 LeuLeuGlnLeuPheAsnIleProGlnIleAlaTySerAlaThrIleMetAspLeuSer 180  
Db 850 TTGCTCAGGCTTTTCAACATACCTCAGATTGCTTACTACACCAACAGCATGAGATCTGAGT 909  
Qy 181 AspLysThrLeuPheLysTyrPheMetArgValAlaProSerAspAlaGlnAlaArg 200  
Db 910 GACAAAGCTCTGTCAAAATTTTCAATGAGGTTGTGCTTCAGATGCTCAGCAGGCAAG 969  
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Db 970 GCCATGTGACATGAGTGAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1029  
Qy 221 GlyAsnTyrGlyGluSerGlyMetGluAlaPheLysAspMetSerAlaLysGluGlyIle 240  
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Qy 241 CyeIleAlaHisSerTyrLysIleTyrSerAsnAlaGlyGluGlnSerPheAspLysLeu 260  
Db 1090 TGATGCGCCCACTCTTACAAATCTACAGTAATGCAAGGAGGAGGAGGAGGAGGAGGAG 1149  
Qy 261 LeuLysLysLeuThrSerHisLeuProLysAlaArgValAlaAlaTyrPheCysGluGly 280  
Db 1150 CTGAAAGAGCTCAACAGTCACTTGCACCAAGCCCGGCTGCTGCTTCTGTAGAGGC 1209  
Qy 281 MetThrValArgGlyLeuLeuMetAlaMetArgArgLeuGlyLeuValGlyIlePheLeu 300  
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Db 1270 CTTCTGGGCGAGTATGCG-----TGG 1290  
Qy 321 GluAspArgArgLysCys-GlnGlyArgPheLeuGlnGlyPheGlyAspIleLeuHisArg 340  
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RESULT 14  
US-08-486-270-7  
; Sequence 7, Application US/08486270  
; Patent No. 5807689  
; GENERAL INFORMATION:  
; APPLICANT: Daggett, Lorrie  
; APPLICANT: Ellis, Steven B.  
; APPLICANT: Liaw, Chen  
; APPLICANT: Pontbier, Aaron  
; APPLICANT: Johnson, Edwin C.  
; TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,  
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME AND USES THEREOF  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: Pretty, Schroeder, Brueggemann & Clark  
; STREET: 444 South Flower Street, Suite 2000  
; CITY: Los Angeles  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/486,270  
; FILING DATE: 02-JUN-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/072,574  
; FILING DATE: 04-JUN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Reiter, Stephen E.  
; REGISTRATION NUMBER: 31,192  
; REFERENCE/DOCKET NUMBER: FP41 9772  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-546-4737  
; TELEFAX: 619-546-9392  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4085 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 370..3912  
; OTHER INFORMATION: /product= "HUMAN MGLUR5A"  
US-08-486-270-7  
Alignment Scores:  
Pred. No.: 5,53e-173 Length: 4085  
Score: 1470.50 Matches: 304  
Percent Similarity: 86.67% Conservative: 8  
Best Local Similarity: 84.44% Mismatches: 24  
Query Match: 78.51% Indels: 24  
DB: 1 Gaps: 2  
US-10-027-923-2 (1-369) x US-08-486-270-7 (1-4085)  
Qy 1 MetValLeuLeuLeuLeuLeuSerValLeuLeuLeuGlyGluAspValArgGlySerAla 20  
Db 370 ATGCTCTTCTGTATGATCTGTCACTTATCTTGAAGAAAGATATCCGTGGAGTGA 429  
Qy 21 GlnSerSerGluArgArgValAlaHisMetLeuGlyAspIleIleIleGlyAlaLeu 40  
Db 430 CAGTCCAGTGAAGAGAGGCTGTGCTCAGATCCCGGTGACATCTTATGGAGCTTC 469  
Qy 41 PheSerValHisIleGlnProThrValAspGluValHisGluArgLysCysGlyAlaVal 60  
Db 490 TTTTCTGTTCAATCAGCAGCTACTGTGGAAGAAAGTTCATGAGAGGAAGTGGGGGCTC 549  
Qy 61 ArgGluGlnTyrGlyIleGlnArgValGluAlaMetLeuHisThrLeuGluArgIleAsn 80  
Db 550 CGTGAACAGTATGCAATTCAGAGAGTGAAGGCCATCTCATCTCCGAAAGATCAAT 609  
Qy 81 SerAspProThrLeuLeuProAsnIleThrLeuGlyCysGluIleArgAspSerCysTrp 100  
Db 610 TCAGACCCCACTCTTGGCCCAATCAATCACTGGGCTGTGAGATTAAGGACTCTGCTGG 669  
Qy 101 HisSerAlaValAlaLeuGlnSerIleGluPheIleArgAspSerLeuIleSerSer 120  
Db 670 CATTGGCTGTGGCCCTTAAGACAGAGCATTTGATTAAGATATCCCATTTCTTCA 729  
Qy 121 GluGluGluGluGlyLeuValCysSerValAspGlySerSerSerSerPheArgSerLys 140  
Db 730 GAAGAGAGAGAGGCTGTGATCCCTGTGTGAGATGGCTCTCTCTCTCTCTCTCTCAAG 789  
Qy 141 LysProIleValGlyValIleGlyProGlySerSerSerLeuAlaIleGlnValAsn 160  
Db 790 AMGCCATAGTAGGGGTCATTGGGCTGCTCCAGTTCTGTAGCAATTCAGTCCAGAAAT 849  
Qy 161 LeuLeuGlnLeuPheAsnIleProGlnIleAlaTySerAlaThrIleMetAspLeuSer 180  
Db 850 TTGCTCAGGCTTTTCAACATACCTCAGATTGCTTACTACACCAACAGCATGAGATCTGAGT 909  
Qy 181 AspLysThrLeuPheLysTyrPheMetArgValAlaProSerAspAlaGlnAlaArg 200  
Db 910 GACAAAGCTCTGTCAAAATTTTCAATGAGGTTGTGCTTCAGATGCTCAGCAGGCAAG 969  
Qy 201 SerMetValAspIleValIleValIleValIleValIleValIleValIleValIleVal 220



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Qy 261 LeuLysLeuThrSerHisLeuProlyAlaArgValAlaTyrPheCysGluGly 280
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Db 1150 CTGAAGAGCTCAACAAGTCACTTGCCCAAGCCCGGCTGGCTTGGCTTCTGTGAAGGC 1209
    |||||
Qy 281 MetThrValArgGlyLeuLeuMetAlaMetArgArgLeuGlyLeuValGlyIupheLeu 300
    |||||
Db 1210 ATGACGGGTGAGAGCTGTGCTGATGAGCGCGCTGGGTCTAGCGGAGAAATTCTG 1269
    |||||
Qy 301 LeuLeuGlyArgGluProAspAlaIlePheIleGluIleSerLysAsnSerIleLeuTrp 320
    |||||
Db 1270 CTTCTGGGCACTGATGGC-----TGG 1290
    |||||
Qy 321 GluAspArgArgLysCys-GlnGlyArgPheLeuGlnGlyPheGlyAspIleLeuHisar 340
    |||||
Db 1291 GCTGACACGGATGATGACAG-----ATGCATAT 1320
    |||||
Qy 340 gSerGluSerValLeuLeuHisMetProGluProLeuAsnLeuGluLeuSerSerGly 359
    |||||
Db 1321 CAGCGAGAGCTGTGTGGCATCACAATCAAGCTCCCATCTCCGATGTCAAGTGGT 1378
    |||||
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Search completed: December 14, 2003, 23:45:46  
Job time : 124 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_p2n model

Run on: December 15, 2003, 00:48:41 / Search time 2622 seconds

(without alignments)  
3420.424 Million cell updates/sec

Title: US-10-027-923-2  
Perfect score: 1873  
Sequence: 1 MVLLILSLVLLKEDVKGSA.....QPLNLELSGPITGLRRLI 369

Scoring table:  
BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 22781392 segs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ p2n.model -DEV=xjh  
-Q=/cg2\_1/USPRO.spool/US10027923/runat\_12122003\_122927\_25571/app\_query.faeta\_1.519  
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-UNITS=bits -START=1 -END=1 -MATRIX=blowsum62 -TRANS=human40.cdi -LIST=45  
-DOCLIGN=200 -THR SCORE=500 -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pro -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USPR=US10027923 @CGN\_1\_1\_2810 @runat\_12122003\_122927\_25571 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :  
EST:  
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3: em\_escba:\*  
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8: em\_escba:\*  
9: gb\_esc1:\*  
10: gb\_esc2:\*  
11: gb\_esc3:\*  
12: gb\_esc4:\*  
13: gb\_esc5:\*  
14: gb\_esc6:\*  
15: em\_escba:\*  
16: em\_escba:\*  
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19: em\_escba:\*  
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22: em\_escba:\*  
23: em\_escba:\*  
24: em\_escba:\*  
25: em\_escba:\*  
26: em\_escba:\*  
27: em\_escba:\*  
28: gb\_esc1:\*

29: gb\_gsa2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1065	56.9	1297	11 BC031602	BC031602 Homo sapi
2	872	46.6	519	10 BE674422	BE674422 7601a04.x
3	851	45.4	499	10 BB467477	BB467477 h266d08.x
4	750	40.0	449	14 CB153433	CB153433 K-EST0210
5	735.5	39.3	3879	11 AK032422	AK032422 Mus muscu
6	727	38.8	442	9 AW015382	AW015382 UT-H-B10-
7	718.5	38.4	657	13 BU351729	BU351729 603527561
8	718.5	38.4	669	13 BU393781	BU393781 603803380
9	693	37.0	414	10 BG150163	BG150163 nad46b03.
10	671	35.8	673	13 BU390603	BU390603 603801605
11	637	34.0	667	29 AG046849	AG046849 Pan trogl
12	612.5	32.7	471	14 CB730684	CB730684 AMGNDC:N
13	592	31.6	682	10 BG695213	BG695213 NISC_1v13
14	586.5	31.3	837	28 B2181748	B2181748 CH230-388
15	567.5	30.3	439	14 CB750802	CB750802 AMGNDC:N
16	547	29.2	3693	11 BC051384	BC051384 Mus muscu
17	541.5	28.9	1430	11 AK047733	AK047733 Mus muscu
18	535	28.6	3675	11 AK038395	AK038395 Mus muscu
19	507	27.1	763	14 CA318495	CA318495 UT-M-FW0-
20	505	27.0	4209	11 AK053447	AK053447 Mus muscu
21	499	26.6	1065	29 CNG058U4	AL352309 Tetradon
22	499	26.6	1238	11 AK020953	AK020953 Mus muscu
23	491	26.2	722	28 AZ815421	AZ815421 ZMO083H07
24	480.5	25.7	744	29 CNG03KCA	AL247981 Tetradon
25	475	25.4	664	12 B1862324	B1862324 603075928
26	433.5	23.1	392	14 T78107	T78107 YC98a01.r1
27	429	22.9	515	13 BX280403	BX280403 BX280403
28	426.5	22.8	664	14 CD355039	CD355039 UT-M-GMO-
29	391	20.9	916	13 BX410048	BX410048 BX410048
30	390	20.8	657	28 B2164680	B2164680 CH230-388
31	372.5	19.9	485	9 AL134272	AL134272 DKF2P547H
32	362	19.3	681	29 CNG0300B	AL221636 Tetradon
33	360	19.2	770	13 BU283975	BU283975 603864890
34	352	18.8	532	29 BZ930457	BZ930457 CH240_36M
35	340.5	18.6	600	14 CA526444	CA526444 8012-19 M
36	336	17.9	673	28 B2101647	AL221635 Tetradon
37	336	17.8	589	29 BX191055	B2101647 CH230-236
38	333	17.4	608	12 BM701852	BX191055 Danio rer
39	325.5	17.4	455	12 B1514260	BM701852 UT-E-CQ1-
40	318.5	17.0	2299	11 AK030224	B1514260 B160014B
41	317.5	16.7	2262	11 AK029734	AK030224 Mus muscu
42	312	16.6	703	10 BB357072	AK029734 Mus muscu
43	311	16.1	902	29 CNG04KXY	BB357072 BB357072
44	301.5	15.8	934	13 BU912251	AL295243 Tetradon
45	295	15.8	934	13 BU912251	BU912251 AGENCOURT

#### ALIGNMENTS

RESULT 1  
LOCUS BC031602 1297 bp mRNA linear HTC 04-MAR-2003  
DEFINITION Homo sapiens, clone IMAGE:5167902, mRNA.  
ACCESSION BC031602  
VERSION BC031602.1 GI:21594893  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 (bases 1 to 1297)  
Straussberg, R.



## ORIGIN

## Alignment Scores:

Pred. No.:	1,52e-91	Length:	519
Score:	872.00	Matches:	169
Percent Similarity:	99.41%	Conservative:	0
Best Local Similarity:	99.41%	Mismatches:	1
Query Match:	46.56%	Indels:	0
DB:	10	Gaps:	0

US-10-027-923-2 (1-369) x BE674422 (1-519)

QY 163 GlnLeuPheAsnIleProGlnIleAlaTySerAlaThrIleMetAspLeuSerAspLys 182  
 DB 10 CAGCTTTCAACCTACTCTATCTGCTTACTGACCAACATCATGATCTGATGACAG 69  
 QY 183 ThrLeuPheLysTyRheMetArgValIalProSerAspAlaGlnGlnAlaArgSerMet 202  
 DB 70 ACTCTGTCAAATATATTTCAATGAGGCTTGCTTCAGATCTCAGCAGGCAAGCTCCATG 129  
 QY 203 ValAspIleValIleValArgTyRantPThrTyValSerAlaValHisThrGluGluAan 222  
 DB 130 GGGAGACATAGTGAAGAGTACCACTGACCTATGTATCAGCCCTACACACAGAAAGCCAC 189  
 QY 223 TYRGLYGLuSerGlyMetGluAlaPheLysAspMetSerAlaLysGluGluIleCysIle 242  
 DB 190 TATGGAGAAAGTGGATGGAGAGCTTCAGAGATATGTCAACCAAGAGAGGATTTGCATC 249  
 QY 243 AlaHisSerTyRlyIleTyRSerAsnAlaGlyGluGlnSerPheAspLysLeuLeuLys 262  
 DB 250 GCCCACTCTTACAAATATCTACAGTAATGACGGAGAGAGAGCTTGTATAGCTGCTGAAG 309  
 QY 263 LysLeuThrSerHisLeuProLysAlaArgValIalAlaTyRheCysGluGluMetThr 282  
 DB 310 AAGCTCAACAGTCACTTCCCAAGGCCCGGCTGTGCTTCTGTGAGGGCATGACG 369  
 QY 283 ValArgGlyLeuLeuMetAlaMetArgArgLysGlyLeuValGlyGluPheLeuLeu 302  
 DB 370 GTGAGAGGCTGCTGATATGCGCATGAGAGCCCTTGCTTACTGAGAGATTTCTGCTTCG 429  
 QY 303 GlyArgGluProAspAlaIlePheIleGluIleSerLysAsnSerIleLeuTrpGluAsp 322  
 DB 430 GGGAGGAGAACAGATGCCATCTTTATTTGAGATCTCAAGAAAGACGATCCATGGAGAAC 489  
 QY 323 ArgArgLysCysGlnGlyArgPheLeuGln 332  
 DB 490 AGAAGAAATGCGAAGTCCCTTCCTTCAG 519

RESULT 3  
 BE467477 499 bp mRNA linear EST 27-JUL-2000  
 LOCUS h26608.x1 NCI CGAP Lu24 Homo sapiens CDNA IMAGE:3212943 3'  
 DEFINITION similar to SW-MGR5 HUMAN P41594 METABOTROPIC GLUTAMATE RECEPTOR 5  
 PRECURSOR ; mRNA sequence.  
 ACCESSION BE467477 GI:9513252  
 VERSION BE467477  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapdb-remail.nih.gov  
 Tissue Procurement: Christopher Moskajuk, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: M. Bento Soares, Ph.D.  
 CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNU, send email to:  
 info@image.llnl.gov  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 493.  
 Location/Qualifiers  
 1. 499  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3212943"  
 /issue\_type="Carcinoid"  
 /lab\_host="DH10B"  
 /clone\_idb="NCI CGAP Lu24"  
 /note="Organ: lung; Vector: pTZ19-Pac (Pharmacia) with a  
 modified polylinker; Plasmid DNA from the normalized  
 library NCI CGAP Lu5 was prepared, and 88 circles were  
 made in vitro. Following HAP purification, this DNA was  
 used as tracer in a subtractive hybridization reaction.  
 The driver was PCR-amplified cDNAs from a pool of 5,000  
 clones made from the same library (clones  
 1414920-1417991 and 1520904-1522439). Subtraction by Bento  
 Soares and M. Fatima Bonaldo."

BASE COUNT 141 a 107 c 138 g 113 t  
 ORIGIN

## Alignment Scores:

Pred. No.:	4.11e-89	Length:	499
Score:	851.00	Matches:	165
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	45.44%	Indels:	0
DB:	10	Gaps:	0

US-10-027-923-2 (1-369) x BE467477 (1-499)

QY 167 IleProGlnIleAlaTySerAlaThrIleMetAspLeuSerAspLysThrLeuPheLys 186  
 DB 3 ATACCTCAATGCTTACTACAGCAACATCATGATCTGATGACAAAGCTTGTCCAA 62  
 QY 187 TYRPhMetArgValIalProSerAspAlaGlnGlnAlaArgSerMetValAspIleVal 206  
 DB 63 TATTTTCATAGAGGTTGTGCTTCAAGATGCTCAGACGAGCAAGGTCATGGTGGACATAGTG 122  
 QY 207 LysArgTyRantPThrTyRValSerAlaValHisThrGluGlyAsnTyRgluSer 226  
 DB 123 AAGAGGTACACCTGACCTATGTATCAGCCGTTACACAGAAAGCAACTATGGAGAAAGT 182  
 QY 227 GlyMetGluAlaPheLysAspMetSerAlaLysGluGlyIleCysIleAlaHisSerTyR 246  
 DB 183 GGGATGGAAGCCCTTCAAGATATGTACAGCAAGAGGAGATTTGCATCGCCCATCTTTAC 242  
 QY 247 LysIleTySerAsnAlaGlyGluGlnSerPheAspLysLeuLeuLysLeuThrSer 266  
 DB 243 AAAATCTACAGTATGACAGGAGACGAGACTTTGATTAAGCTGTGAAGAGCTCACAACT 302  
 QY 267 HisLeuProLysAlaArgValIalAlaTyRheCysGluGlyMetThrValArgGlyLeu 286  
 DB 303 CACTTCCCAAGGCCCGGTGTGGCTTCTGTGAGGGCATGACGGTGAAGAGGTCG 362  
 QY 287 LeuMetAlaMetArgArgLysGlyLeuValGlyGluPheLeuLeuLeuGluArgGluPro 306  
 DB 363 CTGATGGCCATAGAGGGCTGTGAGTGAAGAAATTTCTGTTTGGGAGGAGCAACCA 422  
 QY 307 AspAlaIlePheIleGluIleSerLysAsnSerIleLeuTrpGluAspArgArgLys 326  
 DB 423 GATGCCATCTTTATGATGATCTCAAGAAACAGCATCTTATGGAGACACAGAAATATGC 482  
 QY 327 GlnGlyArgPheLeu 331  
 DB 483 CAAGGTCGCTTCCTT 497

RESULT 4

CB153433 449 bp mRNA linear EST 29-JAN-2003  
 LOCUS K-EST0210877 BT694954 Homo sapiens cDNA clone BT694954-28-C09 5',  
 DEFINITION mRNA sequence.  
 ACCESSION CB153433  
 VERSION CB153433.1 GI:28138427  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 449)  
 AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,  
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and  
 Kim,Y.S.  
 TITLE 21C Frontier Korean EST Project 2001  
 JOURNAL Unpublished  
 COMMENT Contact: Kim YS  
 Genome Research Center  
 Korea Research Institute of Bioscience & Biotechnology  
 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea  
 Tel: +82-42-860-4470  
 Fax: +82-42-860-4409  
 Email: yongjung@mail.kribb.re.kr  
 Plate: 28 row: C column: 09  
 High quality sequence stop: 449.  
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 1..449  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="BT694954-28-C09"  
 /sex="M"  
 /lab\_host="Top10F"  
 /clone\_id="BT694954"  
 /note="Organ: Brain; Vector: PCNS-D2; Site: 1: EcoRI;  
 Site 2: NotI; The poly (A)+ RNA was dephosphorylated with  
 bacterial alkaline phosphatase (BAP) and then deapped  
 with tobacco acid pyrophosphatase (TAP). The deapped  
 intact mRNA was ligated with DNA-RNA linker including  
 EcoRI site by treatment of T4 RNA ligase and the first  
 strand cDNA was synthesized from oligo dt-selected mRNA by  
 priming with dt-tailed vector. The dt-tailed vector was  
 adjusted to have about 60nt. The cDNA vector was  
 circularized with E. coli DNA ligase after digestion of  
 EcoRI which site is also included in vector. An RNA strand  
 converted to a DNA strand by Okayama-Berg method. The  
 obtained cDNA vectors were used for transformation of  
 competent cells E. coli Top10F by electroporation method.  
 The cDNA libraries constructed by this method are  
 full-length enriched cDNA library."  
 BASE COUNT 106 a 112 c 112 g 119 t  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 2,32e-77 Length: 449  
 Score: 750.00 Matches: 147  
 Percent Similarity: 99.33% Conservative: 1  
 Best Local Similarity: 98.66% Mismatches: 1  
 Query Match: 40.04% Indels: 0  
 Gaps: 0  
 US-10-027-923-2 (1-369) x CB153433 (1-449)  
 QY 41 PheserValHshIsgInProThValAspGluValHsgIuArgLySvGlyAlaVal 60  
 Db 2 TTTTCTGTCATCCACGACCTACTGTGACGACAGTTCATGAGAGAGTGCGGCAGTC 61  
 QY 61 ArgGluGlnTyrGlyIleGlnArgValAlaMetLeuHshIsthLeuGluArgTlleasn 80  
 Db 62 CGTGAAAGATATGCAATTCAGAGAGTGAAGGCCATGTGCGTACCCCTGGAAGATCAAT 121  
 QY 81 SerAspProThrLeuLeuProAsnIleThrLeuGlyCysGluIleArgAspSerCysTirp 100

Db 122 TCAGACCCCACTTGGCCCACTACACTGGCTGTGAGATGAGGATTCCTCTGG 181  
 QY 101 HtSerAlaValAlaLeuGluGlnSerIleGluPhaIleArgAspSerLeuIleSerSer 120  
 Db 182 CATTCGGCTGTGGCCCTTACGAGACGACATTCATGATTCATTAAGATTCCTCATTTCTTCG 241  
 QY 121 GluGluGluGluGluValCysSerValAspGlySerSerSerSerPheArgSerLyS 140  
 Db 242 GAAGAGAGAGAGGCGCTTGGATTCCTCTGTGAGATGCTCTCTCTTCTCTCCCTCCAG 301  
 QY 141 LysProIleValGlyValIleGlyProGlySerSerSerSerLeuAlaIleGlnValGlnAsn 160  
 Db 302 AACCCCATGATGAGGGGTCATTGGGCTGGTTCAGATTCTGTAGCCATTCAGATTCAGATCAGAAT 361  
 QY 161 LeuLeuGlnLeuPheAsnIleProGlnIleAlaTyrSerAlaThrIleMetAspLeuSer 180  
 Db 362 TTGCTCCAGCTTTTCAACATCTCAGATTGCTTACTCAGCAACCATCATGATCTGAGT 421  
 QY 181 AspLysThrLeuPheLysTyrPheMet 189  
 Db 422 GACAGACTCTGTTCAAAATTTTCATG 448  
 RESULT 5  
 AK032422  
 LOCUS  
 DEFINITION Mus musculus adult male olfactory brain cDNA. RIKEN full-length  
 enriched library, clone:6430542K11 product:METABOTROPIC GLUTAMATE  
 RECEPTOR MGLUR5 PRECURSOR homolog [Rattus norvegicus], full insert  
 sequence.  
 ACCESSION AK032422  
 VERSION AK032422.1 GI:26082838  
 KEYWORDS HTC, CAP trapper.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1  
 AUTHORS Carninci,P. and Hayashizaki,Y.  
 TITLE High-efficiency full-length cDNA cloning  
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
 MEDLINE 99279253  
 PUBMED 10349636  
 REFERENCE 2  
 AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,  
 Itoh,M., Komno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new genes  
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
 MEDLINE 20499374  
 PUBMED 11042159  
 REFERENCE 3  
 AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,  
 Komno,H., Akiyama,J., Nishi,K., Kitsuai,T., Taishiro,H., Itoh,M.,  
 Sumi,N., Ieshi,Y., Nakamura,S., Hazama,M., Nishino,T., Harada,A.,  
 Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Keshwagi,K.,  
 Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,K., Tanaka,T., Ohara,E., Matsuki,M.,  
 Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuyama,S., Kawai,J.,  
 Okazaki,Y., Muramatsu,M., Inoue,Y., Kita,A. and Hayashizaki,Y.  
 TITLE RIKEN integrated sequence analysis (RISA) system-384-format  
 sequencing pipeline with 384 multicapillary sequencer  
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)  
 MEDLINE 20530913  
 PUBMED 11076861  
 REFERENCE 4  
 AUTHORS Kawai,J., Shingawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,  
 Arakawa,T., Hara,A., Fukunishi,Y., Komno,H., Adachi,J., Fukuda,S.,  
 Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamana,I.,  
 Saito,T., Okazaki,Y., Gojodori,T., Bono,H., Kasukawa,T., Saito,R.,  
 Kadoya,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,C.,  
 Fleischmann,M., Gaasterland,T., Glessl,C., King,B., Kochiwa,H.,  
 Kuehl,P., Lewis,S., Matsuo,Y., Nikido,I., Pesole,G.,  
 Quackenbush,J., Schirral,L.M., Staabli,F., Suzuki,R., Tomita,M.,

Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, G., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bull, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustinich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombauts, P., Nordone, P., Ring, B., Ritzwald, M., Rodriguez, I., Sakamoto, N., Saeki, H., Sato, K., Schonbach, C., Seta, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyooka, K., Wang, K.H., Weitz, C., Whitaker, C., Wilmink, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohseuk, S. and Hayashizaki, Y.

**TITLE**  
Functional annotation of a full-length mouse cDNA collection

**JOURNAL**  
Nature 409 (6821), 685-690 (2001)

**MEDLINE**  
21085660

**PUBMED**  
11217851

**REFERENCE**  
5

**AUTHORS**  
The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

**TITLE**  
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

**JOURNAL**  
Nature 420 563-573 (2002)

**REFERENCE**  
6 (bases 1 to 3879)

**AUTHORS**  
Maachi, U., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imetani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Komori, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohnato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Yamanaka, M. and Hayashizaki, Y.

**TITLE**  
Direct Submission

**JOURNAL**  
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Chemical Research, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gscc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

**COMMENT**  
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

**FEATURES**  
Please visit our web site for further details.  
URL: http://genome.gsc.riken.go.jp/  
URL: http://fantom.gsc.riken.go.jp/.  
Location/Qualifiers

**source**  
1..3879  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="FANTOM:DB:6430542K11"  
/db\_xref="taxon:10090"  
/clone="6430542K11"  
/sex="male"  
/tissue\_type="olfactory brain"  
/clone\_lib="RIKEN full-length enriched mouse cDNA library"  
/dev\_stage="adult"  
1..3063  
/note="METABOTROPIC GLUTAMATE RECEPTOR MGLUR5 PRECURSOR homolog [Rattus norvegicus] (SPT|BAA01711, evidence: FASTV, 98.5%ID, 87%length, match=3058) putative"

**BASE COUNT**  
1026 a 975 c 954 g 924 t

**ORIGIN**

**Alignment Scores:**  
Pred. No.: 3.57e-74 Length: 3879  
Score: 735.50 Matches: 147

Percent Similarity: 88.24% Conservative: 3  
Best Local Similarity: 86.47% Mismatches: 7  
Query Match: 39.27% Indels: 13  
DB: 11 Gaps: 1

US-10-027-923-2 (1-369) x AK032422 (1-3879)

Qy 154 LeuAl11glnAlaGlnAenLeuGlnInLeuPheAenIleProGlnIleAlaTyrSer 173  
Db 3 GTGGCATTCAAGTTCAGAACTTCTCCAGCTTTCACACTTCTCAGTCTGCTTACTCT 62

Qy 174 AlaThr11eMetAspLeuSerAspLysThrLeuPheLysTyrPheMetArgValPro 193  
Db 63 GCACACTGACATGATTTGAGTGAACAAGCTCTTCAAGTACTTCAAGTGGTGTACT 122

Qy 194 SerAspAlaGlnAlaArgSerMetValAspIleValaArgTyrAenTPThrTyr 213  
Db 123 TCCGATGCCACAGAACCCGACCATGTGTGACATGTGAAAGATCAACTGCACTTAT 182

Qy 214 ValSerAlaValHisThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 233  
Db 183 GTCTCAGCTGTGACACAGAGGCACTATGAGAAAGTGAGTGAAGGCTTCAAGAT 242

Qy 234 MetSerAlaLysGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 253  
Db 243 ATCTCAGCAGAGAGAGATTTGATTCATCCGCACTTCAAAATCTACAGCAATGCTGG 302

Qy 254 GlnGlnSerPheAspLysLeuLysLysLysLysLysLysLysLysLysLysLysLys 273  
Db 303 GAACAGAGCTTTGACAGAGCTTTGAAAGAGCTCAGAAATCATTTACTTAAAGCCGGTG 362

Qy 274 ValAlaTyrPheGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 293  
Db 363 GTAGCTGCTTCTGTAAAGCAGACAGTTCAGGCTGCTCAGGCAAGACAGCCTTG 422

Qy 294 GlnLeuValGlnGlnPheLeuLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 313  
Db 423 GGTCTGACAGAGAGATTTCTACTTCTGGCAGAGATGCG----- 461

Qy 314 SerLysAsnSerIleLeuTyrGlnAparG 323  
Db 462 -----TGGGCTGACAGG 473

**RESULT 6**  
AW015382 442 bp mRNA linear EST 10-SEP-1999  
LOCUS  
DEFINITION  
UI-H-B10-aat-d-06-0-UI-g1 NCI CGAP\_Sub1 Homo sapiens cDNA clone  
IMAGE:2710331 3', mRNA sequence.  
AW015382  
AW015382.1 GI:5864139  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 442)  
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Oligo-dT track not found. Not 1 site shown in beginning of sequence  
is likely internal to the message. cDNA library preparation: M.B.  
Soares Lab Clone distribution: NCI-CCAP clone distribution  
Information can be found through the I.M.A.G.E. Consortium/LNL at:  
www.bio.lnl.gov/btrp/image/image.html  
Seq primer: M13 Forward  
POLYA=No.

**FEATURES**  
Location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="mRNA"

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/db_xref="taxon:9606"
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/clone_lib="NCI CGAP Sub1"
/Note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not 1; Site 2: Eco RI; The
NCI CGAP Sub1 library is a subtracted library derived from
BI - BI constitutes a mixture of 21 normalised or
subtracted NCI CGAP libraries: NCI CGAP C04,
NCI CGAP Pr22, NCI CGAP Pr28, NCI CGAP C010, NCI CGAP C016
, NCI CGAP Kid5, NCI CGAP Kid2, NCI CGAP Kid3,
NCI CGAP Kid1, NCI CGAP Lym2, NCI CGAP Br2, NCI CGAP C08,
NCI CGAP CUL1, NCI CGAP Lel2, NCI CGAP Brn23, NCI CGAP Lm5
, NCI CGAP Lm24, NCI CGAP Lm19, NCI CGAP GC4, NCI CGAP GC6
, NCI CGAP Brn25. These 21 libraries were pooled and a
single-stranded DNA preparation of the resulting mixture
was used as a tracer in a subtractive hybridization with a
driver whose composition is detailed below: NCI CGAP Kid3
pool 1 LmM 3334-3337, 3682-3683, 3798-3803 (IMAGE_
Cloneids 1322376-1323911, 1456008-1456775, 1500552-1502855
) NCI CGAP Kid5 pool 1 LmM 3338-3342, 3722-3725,
3776-3778 (IMAGE Cloneids 1323912-1325831,
1471368-1472903, 1492104-1493255) NCI CGAP Lm5 pool 1 LmM
3575-3582, 3851-3854 (IMAGE Cloneids 1414920-1417991,
1520904-1522439) NCI CGAP GC4 pool 1 LmM 3164-3167,
3716-3720, 3733-3735 (IMAGE Cloneids 1257096-1258631,
1469064-1470983, 1475592-1476743) NCI CGAP Pr22 pool 1
LmM 2457-2459, 2758-2759, 3062-3068 (IMAGE Cloneids
985608-986759, 1101192-1101959, 1217928-1220615)
NCI CGAP C010 pool 1 LmM 2644-2653, 2871-2872 (IMAGE
Cloneids 1057416-1061255, 1144584-1145351) The resulting
subtracted library contained 530,000 recombinants.
Subtraction was performed as previously described [Bonaldo
, Lemon & Soares (1996): Normalization and Subtraction:
Two Approaches to Facilitate Gene Discovery. Genome
Research 6, 791-806.
TAG LIB=NCI CGAP Lel2
TAG TISSUE=leiomysarcoma
TAG_SEQ=ATCG"

```

```

BASE COUNT      118 a      127 g      100 t
ORIGIN
Alignment Scores:
Pred. No.:      1,11e-74      Length:      442
Score:          727.00      Matches:      144
Percent Similarity: 99.31%      Conservative: 0
Best Local Similarity: 99.31%      Mismatches: 0
Query Match:     38.81%      Indels:      1
DB:              9      Gaps:      0

```

```

US-10-027-923-2 (1-369) x AM015382 (1-442)
QY 163 Glnleupheanilleproglinlealatyrsenalathrlleemetspleusezasplys 182
DB 8 CAGCTTTTCAACATACCTCAGATGCTTACTCAGAACATCATCATGATCTGATGACAG 67
QY 183 ThrleuphelelytyrphemecaryvalaProserapalaglnlnalargsermet 202
DB 68 ACTCGTTCAAATATTTTCATGAGGGTTCGCTTCAGATGCTTCAGACAGGAGGTCATG 127
QY 203 ValaspllevallyarGtyrasntrphtyrvalaserlaValaIleThGlnlglvsn 222
DB 128 GTGACATAGAGAGAGGTACACCTGACCTTATGATACGCCGTACACACAGAGGCAAC 187
QY 223 TyrglgluserGlymetGlnalaphelyaspmetserralalygluglylyleCyrlle 242
DB 188 TATGAGAAAGTGGGATGGAAGCTTCAAGTATAGTCAGAGGAAGAGGATTTGCATC 247
QY 243 AlaHisserlytyrlyleTyrsenalaglygluglnserpheasplyleuleuly 262
DB 248 GCCCACTTTCACAAATCTACAGTATGACAGGGAGCAGAGCTTGATTAAGCTCTGAAG 307
QY 263 LysleuThrserHleuProlysalargValaIaTyrrPheCygluglymetthr 282

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```

DB 308 AAGTCACAAAGTCACTTGCCCAAGGCCGGGTGGCTCACTTCTGTGAGGGCATACG 367
QY 283 ValArglyleuleuMetalaMetArgArgleuGlyleuValGlyglu-Pheleule 302
DB 368 GTGAGAGGTCTGCTGAGAGGCGCATAGGCGCTTGCTGATGAGGAATTTCTGCTTCT 427
QY 302 UGlyArgGluPro 306
DB 428 GGGCAGGGAACCA 440
RESULT 7
BU351729 657 bp mRNA linear EST 28-NOV-2002
603527561F1 CSEBCHN69 Gallus gallus CDNA clone CHEST47616 5', mRNA
sequence.
ACCESSION BU351729
VERSION BU351729.1 GI:25859730
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Bukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 657)
Boardman, P.E., Sanz-Eguerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken CDNA
Curr. Biol. 12 (22), 1965-1969 (2002)
22335534
JOURNAL MEDLINE
PUBMED 12445392
COMMENT Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology (UMIST)
)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
FEATURES
Source
location/Qualifiers
1..657
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Compton Line 151"
/db_xref="taxon:9031"
/clone="CHEST47616"
/sex="Female"
/tissue_type="cerebellum"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="CSEBCHN69"
/Note="Organ: brain; Vector: pBluescript II KS(+); Site_1:
EcoRI; Site_2: NotI; This normalized library was
constructed from 1 million independent clones. CDNA
synthesis was initiated using an oligo(dT) primer, using
methyated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded CDNA
was blunted, ligated to NotI adapters, digested with EcoRI
, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."

```

```

BASE COUNT      161 a      168 c      178 g      150 t
ORIGIN
Alignment Scores:
Pred. No.:      2.07e-73      Length:      657
Score:          718.50      Matches:      141
Percent Similarity: 78.90%      Conservative: 31
Best Local Similarity: 64.68%      Mismatches: 29

```

Query Match: 38.36% Indels: 17  
 DB: 13 Gaps: 2  
 US-10-027-923-2 (1-369) x BU351729 (1-657)

QY 138 ArgSerlyblybProIleValIleGlyValIleGlyProGlySerSerSerLeuAlaIleGln 157  
 DB 11 CGCTGAGGAAGCCATTGGCGGAGTCAATGGCCCTGCTCCAGCTCAGTGGCATTGAG 70  
 QY 158 ValGlnAsnLeuLeuGlnLeuPheAsnIleProGlnIleAlaIleValSerAlaIleMet 177  
 DB 71 GTCCAGAACTCTGCGACCTCTTGACATCCCAAAATTCCTACTGTCACACAGATC 130  
 QY 178 AspLeuSerAspIleThrLeuPheIleThrPheMetArgValIleProSerAspAlaGln 197  
 DB 131 GACTGAGTACAGAACTCTCTACAAATTTCTCCGTGTGCTCCCTGACACATC 190  
 QY 198 GlnAlaArgSerMetValAspIleValIleValArgTyrAsnThrTyrValIleSerAlaVal 217  
 DB 191 CAAAGCCCGCCATGCTCGATATTGTCAAGCGTTACAACTGACTTACGTGCTCCGCTG 250  
 QY 218 HisThrGlnGlyAsnTyrGlyGlySerGlyMetGlnAlaPheIleAspMetSerAlaIle 237  
 DB 251 CACACTGAAGAAATTAACGGGGAAGTGAATGAGCGCTTCAAAAGAGCTGCGCCCAA 310  
 QY 238 GlnGlyIleCysIleAlaHisSerTyrIleValIleTyrSerAsnAlaGlyGlnSerPhe 257  
 DB 311 GAGGCGCTCTGCACTTCTCATCTTGCACAAATCTATGCAATGCTGGGGAAGAAAGCTT 370  
 QY 258 AspIleLeuLeuIleValIleThrSerHisLeuProIleValIleValIleValIleValIle 277  
 DB 371 GATCGCTGCTCCGCAAGCTCGCGAAGAAATTAACCAAGCTGAGCGTGTGCTTC 430  
 QY 278 CysGlnGlyMetThrValAlaArgGlyLeuLeuMetAlaMetArgIleGlyLeuValIle 297  
 DB 431 TGTGAGGCGATGACGCTGAGGAGGATCTCTATGCTATGACAGCTGCGAGTGGCTGGG 490  
 QY 298 GlnPheLeuLeuLeuGlnIleValArgGlnProAspAlaIlePheIleGlnIleSerIle 317  
 DB 491 GAGTTCCTGCTAATGGAAGTGAACGGT----- 517  
 QY 318 IleLeuTrpGlnAspArgArgIleValGlnGlyArgPheLeuGlnIlePheGlyAspIle 337  
 DB 518 -----TGGGCAGACAG-----GATGAATCATTTGAGGTTTGAACAGAA 559  
 QY 338 LeuHisArgSerIleValIleLeuHisMetProGlnIleLeuLeuLeuGlnIle 355  
 DB 560 GCAAAATGAGGATCATCTATCAATGCAATGCAAGAGTCTTGATTTGAT 613

RESULT 8  
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 LOCUS 603803380F1 CSEBCHN57 Gallus gallus cDNA clone CHEST778020 5', mRNA  
 DEFINITION  
 ACCESSION BU393781  
 VERSION BU393781.1 GI:25762820  
 KEYWORDS EST.  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.  
 1 (bases 1 to 669)  
 Boardman, P.E., Sanz-Esguero, J., Overton, I.M., Burt, D.W., Bosch, E.,  
 Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.,  
 A Comprehensive Collection of Chicken CDNAS  
 Curr. Biol. 12 (22), 1965-1969 (2002)  
 22335534  
 12445392  
 COMMENT  
 Contact: Simon Hubbard  
 Department of Biomolecular Sciences  
 University of Manchester Institute of Science and Technology (UMIST)

PO Box 88, Manchester, M60 1QD, UK  
 Tel: 01612008930  
 Fax: 01612360409  
 Email: Simon.Hubbard@umist.ac.uk.  
 Location/Qualifiers  
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 /mol\_type="mRNA"  
 /strain="White Leghorn, Hissx"  
 /db\_xref="taxon:9031"  
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 /note="Organ: Brain; Vector: pBluescript II KS(+); Site: 1:  
 EcoRI; Site: 2: NotI; This normalized library was  
 constructed from 1 million independent clones. cDNA  
 synthesis was initiated using an oligo(dT) primer, using  
 methylated C in the first strand synthesis reaction.  
 Following this first strand reaction, double-stranded cDNA  
 was blunted, ligated to NotI adapters, digested with EcoRI  
 , size-selected, and cloned into the NotI and EcoRI  
 compatible sites of a custom modified MCS of the  
 pBluescript (KS+) vector. The library was normalized in 2  
 rounds using conditions adapted from Soares et al., PNAS  
 (1996): 791, except that a significantly longer  
 reannealing hybridization was used."

BASE COUNT 165 a 174 c 179 g 151 t  
 ORIGIN

Alignment Scores:  
 Pred. No.: 2.13e-73 Length: 669  
 Score: 718.50 Matches: 141  
 Percent Similarity: 78.90% Conservative: 31  
 Best Local Similarity: 64.68% Mismatches: 29  
 Query Match: 38.36% Indels: 17  
 DB: 13 Gaps: 2

US-10-027-923-2 (1-369) x BU393781 (1-669)

QY 138 ArgSerlyblybProIleValIleGlyValIleGlyProGlySerSerSerLeuAlaIleGln 157  
 DB 23 CGCTGAGGAAGCCATTGGCGGAGTCAATGGCCCTGCTCCAGCTCAGTGGCATTGAG 82  
 QY 158 ValGlnAsnLeuLeuGlnLeuPheAsnIleProGlnIleAlaIleValSerAlaIleMet 177  
 DB 83 GTCCAGAACTCTGCGACCTCTTGACATCCCAAAATTCCTACTGTCACACAGATC 142  
 QY 178 AspLeuSerAspIleThrLeuPheIleThrPheMetArgValIleProSerAspAlaGln 197  
 DB 143 GACTGAGTACAGAACTCTCTACAAATTTCTCCGTGTGCTCCCTGACACATC 202  
 QY 198 GlnAlaArgSerMetValAspIleValIleValArgTyrAsnThrTyrValIleSerAlaVal 217  
 DB 203 CAAAGCCCGCCATGCTCGATATTGTCAAGCGTTACAACTGACTTACGTGCTCCGCTG 262  
 QY 218 HisThrGlnGlyAsnTyrGlyGlySerGlyMetGlnAlaPheIleAspMetSerAlaIle 237  
 DB 263 CACACTGAAGAAATTAACGGGGAAGTGAATGAGCGCTTCAAAAGAGCTGCGCCCAA 322  
 QY 238 GlnGlyIleCysIleAlaHisSerTyrIleValIleTyrSerAsnAlaGlyGlnSerPhe 257  
 DB 323 GAGGCGCTCTGCACTTCTCATCTTGCACAAATCTATGCAATGCTGGGGAAGAAAGCTT 382  
 QY 258 AspIleLeuLeuIleValIleThrSerHisLeuProIleValIleValIleValIleValIle 277  
 DB 383 GATCGCTGCTCCGCAAGCTCGCGAAGAAATTAACCAAGCTGAGCGTGTGCTTC 442  
 QY 278 CysGlnGlyMetThrValAlaArgGlyLeuLeuMetAlaMetArgIleGlyLeuValIle 297  
 DB 443 TGTGAGGCGATGACGCTGAGGAGGATCTCTATGCTATGACAGCTGCGAGTGGCTGGG 502

Qy 298 GluPheLeuLeuLeuGluArgGluProAspAlaIlePheIleGluIleSerLyAsnSer 317  
 Db 503 GAGTCTCTGCTAATTGAGAGTACCGT-----529  
 Qy 318 TleLeuTrpGluAspArgLyGysGlnGlyArgPheLeuGlnGlyPheGlyAspIle 337  
 Db 530 -----TGGGACAGACAG-----GATGAGTCATTGAAGTTATGAAACAGGAA 571  
 Qy 338 LeuHisArgSerGluSerValLeuLeuHisMetProGlnProLeuAsnLeuGlu 355  
 Db 572 GCAAATGAGAGCATCACTATCAACTGCATCTTCAGAGGCTTGTCAATTGAT 625

RESULT 9  
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 LOCUS 414 bp mRNA linear EST 05-FEB-2001  
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 similar to SW:NMRS\_HUMAN P41594 METABOTROPIC GLUTAMATE RECEPTOR 5  
 PRECURSOR. [1] ;, mRNA sequence.  
 BG150163  
 ACCESSION BG150163.1 GI:12662193  
 VERSION EST.  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 414)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: M. Bento Soares, Ph.D.  
 DNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LMW, send email to:  
 info@image.llnl.gov  
 Seq primer: -40UP from Glibco  
 High quality sequence stop: 354.  
 Location/Qualifiers  
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 /lab\_host="DH10B"  
 /clone\_lib="NCI-CGAP Lu24"  
 /note="Organ: Lung; Vector: p77TD-Pac (Pharmacia) with a  
 modified polylinker; Plasmid DNA from the normalized  
 library NCI CGAP Lu5 was prepared, and ss clones were  
 made in vitro. Following HAP purification, this DNA was  
 used as tracer in a subtractive hybridization reaction.  
 The driver was PCR-amplified cDNAs from a pool of 5,000  
 clones made from the same library (cloneIDs  
 1414920-1417991 and 1520904-1522439). Subtraction by Bento  
 Soares and M. Fatima Bonaldo."  
 BASE COUNT 110 a 91 c 118 g 95 t  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 9.59e-71 Length: 414  
 Score: 693.00 Matches: 134  
 Percent Similarity: 100.00% Conservative: 1  
 Best Local Similarity: 99.26% Mismatches: 0  
 Query Match: 37.00% Indels: 0  
 DB: 10 Gaps: 0  
 US-10-027-923-2 (1-369) x BG150163 (1-414)

Qy 163 GluPheAsnIleProGlnIleAlaIlySerAlaThrIleMetAspLeuSerAspLyS 182  
 Db 10 CACCTTTCAACATTCCTCAGATTGCTTACTGACGACATCATGATTCGATGACGAC 69  
 Qy 183 ThrLeuPheIleYrPheMetArgValValProSerAspAlaGlnGlnAlaArgSerMet 202  
 Db 70 ACTCTGTCMAATATTTCAATGAGGCTTGCCCTTCGATGCTCAGACGACGACGCTCATG 129  
 Qy 203 ValAspIleValIleValArgTrpAsnTrpThrIlyValSerAlaValHisThrGlnIlyAsn 222  
 Db 130 GTGACCATGTGAGAGGTGACACCTGACCTATGTAATTCACCCCTACACAGAGGAC 189  
 Qy 223 TyrGlyIleSerGlyMetGlnAlaPheLyAspMetSerAlaIlyGlnIlyIleCysIle 242  
 Db 190 TATGAGAAAGTGGATGAGAGGCTTCMAAGATATATGACGAGGAGGAGGATTCATC 249  
 Qy 243 AlHisSerTrpIlyIleTrpSerAlaAlaGlyGlnGlnSerPheAspLyLeuLeuLyS 262  
 Db 250 GCCCAGCTTACAAATCTACACTAATGCGAGGACAGAGCTTTGATTAAGCTGCTGAG 309  
 Qy 263 LysLeuThrSerHisLeuProIlyAlaArgValIlyAlaIlyPheCysGlnIlyMetThr 282  
 Db 310 AACCTCAAGATCACTTGCCCAAGCCCGGTGTGCTTCTTCTGTGAGGCAATGACG 369  
 Qy 283 ValArgGlyLeuLeuMetAlaMetArgLyLeuValGly 297  
 Db 370 GTGAGAGTCTGCTGATGCGCATGAGGCGCTGCTGATATTGGG 414

RESULT 10  
 BU390603  
 LOCUS 673 bp mRNA linear EST 27-NOV-2002  
 DEFINITION 603801605F1 CSEQCHN57 Gallus gallus CDNA clone CHEST77411 5', mRNA  
 sequence.  
 BU390603  
 ACCESSION BU390603.1 GI:25759641  
 VERSION EST.  
 KEYWORDS Gallus gallus (chicken)  
 SOURCE Gallus gallus  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.  
 REFERENCE 1 (bases 1 to 673)  
 Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,  
 Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.  
 A Comprehensive Collection of Chicken cDNAs  
 Curr. Biol. 12 (22), 1965-1969 (2002)  
 22335534  
 JOURNAL MEDLINE  
 PUBMED 12445392  
 COMMENT Contact: Simon Hubbard  
 Department of Biomolecular Sciences  
 University of Manchester Institute of Science and Technology (UMIST)  
 PO Box 88, Manchester, M60 1QD, UK  
 Tel: 01612008930  
 Fax: 01612360409  
 Email: Simon.Hubbard@umist.ac.uk.  
 Location/Qualifiers  
 1. 673  
 /organism="Gallus gallus"  
 /mol\_type="mRNA"  
 /strain="White Leghorn, Hisex"  
 /db\_xref="taxon:9031"  
 /clone="CHEST77411"  
 /dev\_stage="16 day embryo"  
 /lab\_host="DH10B"  
 /clone\_lib="CSEQCHN57"  
 /note="Organ: brain; Vector: pBluescript II KS(+); Site\_1:  
 EcoRI; Site\_2: NotI; This normalized library was  
 constructed from 1 million independent clones. cDNA  
 synthesis was initiated using an oligo(dT) primer. using  
 methylated C in the first strand synthesis reaction.  
 Following this first strand reaction, double-stranded cDNA  
 was blunted, ligated to NotI adapters, digested with EcoRI



, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

BASE COUNT 165 a 173 c 180 g 155 t

ORIGIN

Alignment Scores:

Pred. No.: 7.82e-68 Length: 673  
Score: 671.00 Matches: 144  
Percent Similarity: 76.09% Conservative: 31  
Best Local Similarity: 62.61% Mismatches: 30  
Query Match: 35.82% Indels: 25  
DB: 13 Gaps: 3

US-10-027-923-2 (1-369) x BU930603 (1-673)

Qy 138 ArgSerLysProlLeuVal-GlyValIle-GlyProGlySerSerLeuAlaIleG 157  
Db 23 GGCTGAGAGAGCCATTGTCGAGATTCATTCCTCGCTCCAGCTCAGTCCATCC 82  
Qy 157 InValGln-AsnLeuLeuGlnLeuPheAsnIleProGlnIleAlaTySerAlaThrIle 176  
Db 83 AGGTGCTAGAACTCTCCGAGCTCTTGACATCCCAATTCCTCTGCTCCACAGC 142  
Qy 177 MetAspLeuSerAspLysThrLeuPheLysTyThrMetArgValValProSerAspAla 186  
Db 143 ATCGACCTGAGTGCAGAACTCTCTACAGATTTCTCCGTGTCCTCCCTCGACACA 202  
Qy 197 GlnGlnAlaArgSerMetValAspIleValLysArgTyThrAspThrTyValSerAla 216  
Db 203 CTCACAGCCCGCGCATGCTCATGATTCAGAGGTACCACTGAGCTTACGTCGCC 262  
Qy 217 ValHisThrGlnGlnAsnTyArgLysGlyLysGlyLysGlyLysGlyLysGlyLysGly 236  
Db 263 GTGCACACTAGAGAAATTACGGGAAAGTGAATGAGAGCTTCAAGAGCTGCTGCC 322  
Qy 237 LysGlnGlyTLeuCyAlaLeuHisSerTyLysIleTySerAsnAlaGlyLysGlnSer 256  
Db 323 CAGAGAGGCTCTGCTCATTCATTCATGACAAATCATGATGCTGCGGAGAAAGC 382  
Qy 257 PheAspLysLeuLeuLysLysLysLeuThrSerHisLeuProLysAlaArgValAlaTy 276  
Db 383 TTGTATGCTGCTGCTCCGCAAGCTGCGAAGAAATTACCAAGGCTAGAGTGTGCTTGC 442  
Qy 277 PheCyGlnGlnGlyMetThrValArgGlyLeuLeuMetAlaMetArgArgLeuGlyLeuVal 296  
Db 443 TTCTGTAGAGGCAATGACGCTGAGGGGAGATCTCTCTCTGATGACGCTGCGAGTCTT 502  
Qy 297 GlyLysLeuLeuLeuGlyArgGlyProAspAlaIlePheIleGlnLysSerLysAsn 316  
Db 503 GGGAGAGTCTCTGTAATTGGAAGTACGCT----- 532  
Qy 317 SerIleLeuThrGlnLysAspArgLysCyGlnGlnLysArgPheLeuGlnLysPheGlyAsp 336  
Db 533 -----TGGGACAGACAG-----GATGAGTCAATGAGGCTTATGAAACAG 571  
Qy 337 IleLeuHisArgSerGlnSerValLeuLeuHisMetProGlnProLeuAsn----- 353  
Db 572 GAAGCAATGAGAGCATCATCAATGCAATCTCAAGAGCTTGTCTTTGATGAC 631  
Qy 354 -----LeuGlnLeuSerSerGly 359  
Db 632 TACTATCTGAGAGCTGCTTCTGA 655

RESULT 11

LOCUS AG046849 667 bp DNA linear GSS 02-NOV-2001  
DEFINITION Pan troglodytes DNA, clone: PTB-026D03.F, genomic survey sequence.  
ACCESSION AG046849

VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AG046849.1 GI:16583741  
GSS.  
Pan troglodytes (chimpanzee)  
Pan troglodytes

REFERENCE

1 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.  
BAC end sequences of library PTB

TITLE  
JOURNAL  
AUTHORS

Unpublished  
2 (bases 1 to 667)  
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.

TITLE  
JOURNAL

Submitted (02-AUG-2001) Aaso Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC), 1-7-22 Suenro-chou, Tsukuba, Ibaraki, Japan, 305-8565, Japan (E-mail: chimbase@gs.c.riken.go.jp, URL: http://hsp.gsc.riken.go.jp/, Tel: 81-45-503-9111, Fax: 81-45-503-9170)

COMMENT

Clones are derived from the chimpanzee BAC library PTB. This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.

PRIMERS

Sequencing: -21M13  
LIBRARY

FEATURES  
source

Vector : PKS145  
R.Site 1 : SacI  
R.Site 2 : SacI  
Location/Qualifiers  
1..667  
/organism="Pan troglodytes"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9598"  
/clone="PTB-026D03.F"  
/sex="male"  
/cell\_type="lymphoblast"  
/clone\_11b="PTB Chimpanzee Male BAC library"

BASE COUNT  
ORIGIN

156 a 142 c 158 g 210 t  
1 others

Alignment Scores:

Pred. No.: 7.37e-64 Length: 667  
Score: 637.00 Matches: 132  
Percent Similarity: 81.25% Conservative: 11  
Best Local Similarity: 75.00% Mismatches: 33  
Query Match: 34.01% Indels: 1  
DB: 29 Gaps: 0

US-10-027-923-2 (1-369) x AG046849 (1-667)

Qy 38 GlyAlaLeuPheSerValHisGlnProThrValAspGlnValHisGlnArgLysCys 57  
Db 66 GAGAGCTCTCTTTCTGTTATCAACAGCTACTGTGAGCAAAATTCATGAGAGAGTGT 125  
Qy 58 GlyAlaValArgGlnGlnTyArgLysIleGlnArgValGlnAlaMetLeuHisThrLeuGln 77  
Db 126 GGGGCGGTCGTTGAAAGATGCAATGCAAGAGTGAAGGCTGCTGCTACCTCGAA 185  
Qy 78 ArgIleAsnSerAspProThrLeuLeuProAsnIleThrLeuGlyCysGlnLysLeuArgAsp 97  
Db 186 AGATCAATTCATCAACCCACACTCTTGGCCCAATCACTAGGAGCTGTGAGATGAGGAC 245  
Qy 98 SerCysThrHisSerAlaValAlaLeuGlnGlnSerIleGlnLeuHisLeuArgAspSerLeu 117  
Db 246 TACTGCTGGCATTCGGTTGGTCTTGAAGCATAGCATTCATGTTCTTAAAGATTCCTT 305  
Qy 118 IleSerSerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 137  
Db 306 ATTCTTTTAAAGAGAAAGGCTGTGACCTGTGTGTGATGAGCTCTGCTTCTTCTT 365  
Qy 138 ArgSerLysProlLeuValGlyValIleGlyProGlySerSerSerLeuAlaIleGln 157

Db 366 CGGTCAAGAGCCTATTATGAGGTTATGATCTGATTCAGTTCGCTCATTCAG 425  
 Qy 158 ValGlnAenLeuInleuPheAsnIleProGlnIleAlaIYSerAlaThrIleMet 177  
 Db 426 GCGCAGATGCTGCGAGTTTTCACATCCTCACTGTTTCTATGATGACACCATG 485  
 Qy 178 AspLeuSerAlyThrIleuPheIleTyPheMetArgValProSerAapAlaGln 197  
 Db 486 GATTCGATGACCAAGACTCTGTTCAAAATTATCAATAGATGAGTTCCTTAATT-GCTTAA 544  
 Qy 198 GlnAlaArgSerMetValAspIleValIleArgTyPheAsnTrpThrTy 213  
 Db 545 TTGTTTATGATTATGCGGACATPCTGTATGCTCATTTGCTCTAT 592  
 RESULT 12  
 CB730684 471 bp mRNA linear EST 11-APR-2003  
 LOCUS AMGNNUC:NRHY7-00025-C6-A nrhy7 (10850) Rattus norvegicus cDNA clone  
 DEFINITION nrhy7-00025-c6 5', mRNA sequence.  
 ACCESSION CB730684  
 VERSION CB730684.1 GI:29797818  
 KEYWORDS EST.  
 SOURCE Rattus norvegicus (Norway rat)  
 ORGANISM Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 REFERENCE 1 (bases 1 to 471)  
 AUTHORS Angen Est Program.  
 TITLE Angen Rat EST Program  
 JOURNAL Unpublished  
 COMMENT Contact: Dan Fitzpatrick  
 Angen, Inc  
 One Angen Center Drive, Thousand Oaks, CA 91320-1799, USA  
 Tel: 805 447-4881  
 Plate: 00025 row: c column: 6.  
 FEATURES  
 source location/Qualifiers  
 1..471  
 /organism="Rattus norvegicus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:10116"  
 /clone="nrhy7-00025-c6"  
 /clone\_lib="nrhy7 (10850)"  
 /note="vector: pSPORT1, Site\_1: SalI, Site\_2: NotI; W Rat  
 hypothalamus adult female Wistar rat avg. Insert size 2.3  
 kb fraction 6 and 7"  
 BASE COUNT 113 a 134 c 120 g 104 t  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 3,13e-61 Length: 471  
 Score: 612.50 Matches: 123  
 Percent Similarity: 89.10% Conservative: 16  
 Best Local Similarity: 78.85% Mismatches: 14  
 Query Match: 32.70% Indels: 3  
 Gaps: 3  
 DB: 14  
 US-10-027-923-2 (1-369) x CB730684 (1-471)  
 Qy 82 AspProThrLeuLeuProAsnIleThrLeuGlyCysGlnIleArgAspSerCysTrpHis 101  
 Db 3 GACCGGCTGCTCTGCGCCACATCATCTTGCGGACGTAGATCCGGGACTCCTGCTGCAC 62  
 Qy 102 SerAlaValAlaLeuGlnSerIleGlnPheIleArgAspSerLeuIleSer---Ser 120  
 Db 63 TCTTCAGTGGCTCTCGAAGACATTCATTCATCAGAGACTCCCTGATTTCCATCCGA 122  
 Qy 121 GlnGlnGlnGlnGlnGln---ValCysSerValAspGlySerSer---SerSerPheArg 138  
 Db 123 GATGAGAGAGATGAGCTGACCCGATGCTGCTGATGCGCAGCCCTGCGGCGG 182  
 Qy 139 SerIleValPheProIleValIleGlyProGlySerSerSerSerLeuAlaIleGlnVal 158

Db 183 ACTAAGAGCCTATTATGAGGTTATGATCTGATTCAGTTCGCTCATTCAGTTC 242  
 Qy 159 GlnAenLeuInleuPheAsnIleProGlnIleAlaIYSerAlaThrIleMetAsp 178  
 Db 243 CAGATCTTCTCAGCTGCTGCGACATCCACAGATGCTTATTCGACAGCATGAC 302  
 Qy 179 LeuSerAlyThrIleuPheIleTyPheMetArgValProSerAapAlaGln 198  
 Db 303 CTGATGACAAACTTTGTCAAATCTTCTGAGGTCCTCCCTTGCACATTCGAC 362  
 Qy 199 AlaArgSerMetValAspIleValIleArgTyPheAsnTrpThrTyPheValSerAlaValHis 218  
 Db 363 GCAAGGCGATGCTCGACATGATCAAGCGTTACAACTGACCTATGCTCAGCAGTCCAC 422  
 Qy 219 ThrGlnIleValSerTyGlyGlySerGlyMetGlnAlaPheIleAspMet 234  
 Db 423 ACAGAGGAAATTACGCGGAGATGAGATGATGCTTCAAGAACTG 470  
 RESULT 13  
 BG695213 682 bp mRNA linear EST 04-MAY-2001  
 LOCUS NISC\_IV13909.w1 Soares NMBP2 pituitary Mus musculus cDNA clone  
 DEFINITION IMAGE:4317880 5', mRNA sequence.  
 ACCESSION BG695213  
 VERSION BG695213.1 GI:13954900  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 682)  
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute, Cancer Genome Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgaabs-r@mail.nih.gov  
 CDNA Library Preparation: M. Bento Soares Laboratory  
 CDNA Sequencing Arrayed by: The I.M.A.G.E. Consortium/LINL  
 DNA Sequencing Center (NISC)  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LINL at:  
 info@image.lnl.gov  
 MGI:1598648  
 Plate: LHM9922 row: M column: 17  
 Seq primer: T7 primer.  
 FEATURES  
 source location/Qualifiers  
 1..682  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:4317880"  
 /clone\_lib="pituitary gland"  
 /issue\_type="pituitary gland"  
 /dev\_stage="embryo, 14 dpc"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="Soares NMBP2 pituitary"  
 /note="Organ: brain; Vector: pTR73D-Pac; Site\_1: NotI;  
 Site\_2: EcoRI; 1st strand cDNA was primed with a NotI -  
 oligo(dT) primer  
 5'-ACTGGAAGAATTGCGCGCGCGCTTTTCTTTTCTTTTCTTTT-3';  
 double-stranded cDNA was ligated to EcoRI adaptors  
 5'-ATTTCGACAGAG-3' AND 5'-CTCTGCGCG-3' (pharmacia),  
 digested with NotI and cloned into the NotI and EcoRI  
 sites of the pTR73D-Pac vector. Library went through one  
 round of normalization, and was constructed in the  
 laboratory of M. Bento Soares (University of Iowa)."  
 BASE COUNT 190 a 121 c 162 g 209 t  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 1,42e-58 Length: 682  
 Score: 592.00 Matches: 115

Percent Similarity: 97.48%  
 Best Local Similarity: 96.64%  
 Query Match: 31.61%  
 DB: 10  
 Gaps: 0

US-10-027-923-2 (1-369) x BG695213 (1-682)

QY 186 LysTyrPheMetArgValAlaProSerAspAlaGlnAlaArgSerMetValAspIle 205  
 Db 7 AAGTACTTCAATGAGCGTTTACCTTCGGATGCCAGACGCCAGCATGTGACATA 66  
 QY 206 ValIleAspGlyArgTyrPheTyrValSerAlaValHisThrGluGluGlu 225  
 Db 67 GTGAGAGATACACACTGACTTATGTCTCAAGCTGTGACACAGAGCAACTATAGAGAA 126  
 QY 226 SerGlyMetGluAlaPheIleAspMetSerAlaIleGluGlyIleCysGlyLeuHisSer 245  
 Db 127 AGTGGAGATGAGGGCTTTCAGAAATATGTCAAGCAAGAGGATTTGCATCGCCACTCT 186  
 QY 246 TyrIleValTyrSerAspAlaGlyGlnSerPheAspIleLeuLeuValLeuThr 265  
 Db 187 TACAAATCTACACCAATGCTGGGGAACAGACTTTGACAGCTGTGAAAACTCAGA 246  
 QY 266 SerHisLeuProIleValIleValAlaTyrPheCysGluGluMetThrValArgGly 285  
 Db 247 AGTCATTACTTAAAGCCCGGTGTGAGCTGCTTCTGTGAAGCATGACAGTTCCAGGT 306  
 QY 286 LeuLeuMetIleMetArgValArgLeuValGlyIlePheLeuLeuGlyArg 304  
 Db 307 CTGCTCATGGCCATGAGACCGCTTGGGTCTGACAGAGGGAATTTCTACTTGGGCGAGA 363

RESULT 14  
 BZ181748 837 bp DNA linear GSS 11-OCT-2002  
 DEFINITION CH230-388J12.TU CHORI-230 Segment 2 Rattus norvegicus genomic clone  
 BZ181748  
 BZ181748.1 GI:23827927  
 GSS.  
 Rattus norvegicus (Norway rat)  
 Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 1 (bases 1 to 837)  
 Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn  
 'A., Gebregeorgis,B., Overton,L., Russell,D., Chen,D., Riggs,P., de  
 Jong,P. and Fraser,C.M.  
 Rat BAC End Sequences from Library CHORI-230 MboI segment  
 Unpublished  
 Contact: Shaying Zhao  
 Department of Eukaryotic Genomics  
 The Institute for Genomic Research  
 9712 Medical Center Dr., Rockville, MD 20850, USA  
 Tel: 301 838 0208  
 Fax: 301 838 0208  
 Email: szhao@tigr.org  
 Clones are derived from the rat BAC library CHORI-230  
 (http://www.chori.org/bacpac/rat230.htm). For BAC library  
 availability, please contact Pieter de Jong (pdejong@mail.cho.org).  
 Clones may be purchased from BACPAC Resources  
 (http://www.chori.org/bacpac/or\_eirng\_information.htm). BAC end  
 page: http://www.tigr.org/tdb/bac\_ends/rat/bac\_end\_intro.html  
 Plate: 388 row: J column: 12  
 Seq primer: SP6  
 Class: BAC ends.

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

## FEATURES

source  
 1. 837  
 location/Qualifiers  
 /organism="Rattus norvegicus"  
 /mol\_type="genomic DNA"  
 /strain="BN/SENHed/MCW"  
 /db\_xref="taxon:10116"  
 /clone="CH230-388J12"

/sex="Female"  
 /cell\_type="Brain"  
 /clone\_1lb="CHORI-230 Segment 2"  
 /note="Vector: PTARPA1.3; Site 1: MboI; Site 2: MboI;  
 CHORI-230 Rat (BN/SENHed/MCW) BAC library produced by  
 Pieter de Jong"

BASE COUNT 186 a 224 c 256 g 171 t  
 ORIGIN

## Alignment Scores:

Pred. No.: 8,64e-58 Length: 837  
 Score: 586.50 Matches: 121  
 Percent Similarity: 83.73% Conservative: 18  
 Best Local Similarity: 72.89% Mismatches: 24  
 Query Match: 31.31% Indels: 3  
 DB: 28 Gaps: 3

US-10-027-923-2 (1-369) x BZ181748 (1-837)

QY 20 AlaGlnSerSerGluArgValAlaAlaHisMetLeuGluAspIleIleGlyAla 39  
 Db 336 GCAAGTGCCTGTCGCCAGCCCTCGTGGCGAAGTGAACGAGATGATCATCATGAGCC 395  
 QY 40 LeuPheSerValHisHisGlnProThrValAspGluValHisGluArgLysCysGlyAla 59  
 Db 396 CTCTTCAGTCCATACACAGCCTCCAGCGGAGAGAGTACCAGAAAGAGTGTGGGAG 455  
 QY 60 ValArgGluGlnTyrGlyIleGlnArgValGluAlaMetLeuHisThrLeuGluArgIle 79  
 Db 456 ATCAGGAGAACAGATGATGATCCAGAGGGTGAAGGCCATGTTCCACACGTTGATTAAGATT 515  
 QY 80 AsnSerAspProThrLeuLeuProAsnIleThrLeuGlyCysGluIleArgAspSerCys 99  
 Db 516 AACGGGACCCGGGTGCTCCGCCAACATCACTGTGGCGAGTATCCGGGACTCTGC 575  
 QY 100 TrpHisSerAlaValAlaLeuGluGlnSerIleGluPheIleArgAspSerLeuIleSer 119  
 Db 576 TGGCAGCTTCATGAGCTCTCGAAGAGATGGAATTCATCAGAGCTCCCTGATTCC 635  
 QY 120 --SerGluGluGluGluGluLeu--ValCysSerValAspGlySerSer--SerSer 136  
 Db 636 ATCCGAGATGAGAAGATGGGCTGAACCCAGATGCTGCTGATGAGCCAGACCTGCCCT 695  
 QY 137 PheArgSerIleValProIleValIleGlyValIleGlyProGlySerSerSerLeuAlaIle 156  
 Db 696 GGCAGAGACTAAGAGCTATGTCTGAGTGTATGGCCCTGCTGCAGCTGTGGCCATT 755  
 QY 157 GlnValGlnAsnLeuGluLeuPheAsnIleProGlnIleAlaTyrSerAlaThrIle 176  
 Db 756 TCACTCAGAAATTTTCTTCAGCTGTGTCAGATCCACAGATCCGCTTATCTGCCACCAGC 815  
 QY 177 MetAspLeuSerAspIle 182  
 Db 816 ATAGACCTGAGTACAAA 833

RESULT 15  
 CB750802 439 bp mRNA linear EST 11-APR-2003  
 LOCUS AMGNNUC.NRHYS-00030-G10-A W Rat hypothalamus (10471) Rattus  
 norvegicus cDNA clone nrhys-00030-g10 5', mRNA sequence.  
 CB750802  
 CB750802.1 GI:29818104  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

Rattus norvegicus (Norway rat)  
 Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 1 (bases 1 to 439)  
 Amgen EST Program.  
 TITLE  
 JOURNAL  
 COMMENT

Amgen, Inc  
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA

Tel: 805 447-4881  
Plate: 00030 row: 9 column: 10.

FEATURES  
source  
1..439  
Location/Qualifiers  
/organism="Rattus norvegicus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10116"  
/clone="nrh5-00030-910"  
/note="Vector: PSPORI; Site 1: SalI; Site 2: NotI; W Rat  
hypothalmus adult female Wistar rat avg. insert size 2.3  
kb fraction 6 and 7"

BASE COUNT 104 a 127 c 110 g 98 t  
ORIGIN

## Alignment Scores:

Pred. No.:	5,19e-56	Length:	439
Score:	567.50	Matches:	116
Percent Similarity:	88.97%	Conservative:	13
Best Local Similarity:	80.00%	Mismatches:	13
Query Match:	30.30%	Indels:	3
DB:	14	Gaps:	3

US-10-027-923-2 (1-369) x CB750802 (1-439)

```
QY      85  LeuLeuProaenlllethleuGlyCySGluileAargapSerCySTPHISerAlaVal 104
DB      4  CTCTCGCCACACATCACTCTGGGCGATGATCCGGGACTCTGCTGGCACTCTTCAGTG 63
QY      105 AlaLeuGluGlnSerileGluPheileAargapSerleuileSer---SerGluGluGlu 123
DB      64  GCTCTCGAACAGAGATGAAATTCATCAAGACTCTGATTTCCATCCGAGATGAGAG 123
QY      124 GluGlyLeu---ValCySerValaspGlySerSer---SerSerPheArgSerLySlys 141
DB      124  GATGGGCTGAACCGATGCTGCTGATGCGCAGACCCCTCGCGAGAGACTTAAAGAG 183
QY      142 ProileValGlyValileGlyProGlySerSerSerleuAlaileGlnValGlnasnleu 161
DB      184  CCTATTGCTGAGATGATGGCCCTGGCTCCAGCTCTGTGGCCATTCAAGTCCAGATCTT 243
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DB      424  AATTACGGCGAGAGT 438
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Search completed: December 15, 2003, 03:10:07  
Job time : 2639 secs

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OM nucleic - nucleic search, using sw model

Run on: December 14, 2003, 15:19:23 / Search time 4194.38 seconds  
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10826.305 Million cell updates/sec

Title: US-10-027-923-3

Perfect score: 1110

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Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Database :

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- 41: em\_hgt\_other:\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1110	100.0	1110	6 AX709349	AX709349 Sequence
2	1110	100.0	1823	6 AX709347	AX709347 Sequence
3	1008	90.8	2172	6 AX068372	AX068372 Sequence
4	894	80.5	2149	6 AX068374	AX068374 Sequence
5	809	72.9	2064	6 AX068376	AX068376 Sequence
6	560	50.5	2241	6 AX068371	AX068371 Sequence
7	560	50.5	2326	6 AX068370	AX068370 Sequence
8	560	50.5	2349	6 AX068368	AX068368 Sequence
9	559	50.4	2551	6 AX068366	AX068366 Sequence
10	507	45.7	152269	9 AC136759	AC136759 Homo sapi
11	378	34.1	182701	2 AC026078	AC026078 Homo sapi
12	253	22.8	58560	2 AC131048	AC131048 Homo sapi
13	253	22.8	146921	2 AC130357	AC130357 Homo sapi
14	253	22.8	173032	9 AC130364	AC130364 Homo sapi
15	253	22.8	173795	2 AC130356	AC130356 Homo sapi
16	222	20.0	4078	6 AR270570	AR270570 Sequence
17	222	20.0	4207	6 AR145364	AR145364 Sequence
18	222	20.0	4207	6 AR145365	AR145365 Sequence
19	222	20.0	4303	6 AR145366	AR145366 Sequence
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23	222	20.0	4614	9 HUMMGR85B	D28539 Human mRNA
24	176	15.9	133278	2 AC034188	AC034188 Homo sapi
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36	171	15.4	4085	6 AR256859	AR256859 Sequence
37	171	15.4	4085	6 I21436	I21436 Sequence 7
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39	171	15.4	4181	6 AR038844	AR038844 Sequence
40	171	15.4	4181	6 AR256860	AR256860 Sequence
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#### ALIGNMENTS

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AX709349 LOCUS 1110 bp DNA linear PAT 04-APR-2003  
Sequence 3 from Patent WO02070708.  
AX709349 AX709349  
VERSION AX709349.1 GI:29564891  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE  
AUTHORS Bates,B.G., Xie,Y., Gulukota,K. and Paulsen,J.E.  
TITLE Glutamate receptor modulatory proteins and nucleic acids encoding them

Pred. No. is the number of results predicted by chance to have a

JOURNAL Patent: WO 02070708-A 3 12-SEP-2002;  
Myeth (US)  
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LOCUS  
DEFINITION Sequence 1 from Patent WO2070708.  
ACCESSION AX709347  
VERSION AX709347.1 GI:29564889  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Cranial; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1  
AUTHORS Bates, B.G., Xie, Y., Gulukota, K. and Paulsen, J.E.  
TITLE Glutamate receptor modulatory proteins and nucleic acids encoding  
them  
JOURNAL Patent: WO 02070708-A 1 12-SEP-2002;  
Myeth (US)  
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 ACCESSION  
 VERSION AX068372.1 GI:12578537  
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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 AUTHORS  
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 JOURNAL  
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RESULT 4  
LOCUS AX068374 2149 bp DNA linear PAT 25-JAN-2001  
DEFINITION Sequence 9 from Patent WO0102566.  
ACCESSION AX068374  
VERSION AX068374.1 GI:12578538  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE  
AUTHORS Schwarz, D.A. and Maki, R.A.  
TITLE Metabotropic glutamate receptors and methods of use therefor  
JOURNAL Patent: WO 0102566-A 9 11-JAN-2001;  
Neurocrine Biosciences, Inc. (US)  
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RESULT 5  
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DEFINITION Sequence 11 from Patent WO0102566.  
ACCESSION AX068376  
VERSION AX068376.1 GI:12578539  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE  
AUTHORS Schwarz, D.A. and Maki, R.A.  
TITLE Metabotropic glutamate receptors and methods of use therefor  
JOURNAL Patent: WO 0102566-A 11 11-JAN-2001;





Query 601 TCATGTTGACATATGTAAGAGGATCAACTGACCTATGATGAGCCGTACACAGAA 660  
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Qy 661 GG 662  
Db 1025 GG 1026

RESULT 7  
AX068370 2326 bp DNA linear PAT 25-JAN-2001  
LOCUS AX068370  
DEFINITION Sequence 5 from Patent WO0102566.  
ACCESSION AX068370  
VERSION AX068370.1 GI:12578535  
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SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1  
AUTHORS Schwartz, D.A. and Maki, R.A.  
TITLE Metabotropic glutamate receptors and methods of use therefor  
JOURNAL Patent: WO 0102566-A 5 11-JAN-2001;  
Neurocrine Biosciences, Inc. (US)  
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source location/Qualifiers  
1.2326  
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BASE COUNT 581 a 535 c 580 g 630 t  
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Matches 660; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 661 GG 662  
Db 1025 GG 1026

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LOCUS AX068368  
DEFINITION Sequence 3 from Patent WO0102566.  
ACCESSION AX068368  
VERSION AX068368.1 GI:12578534  
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SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1  
AUTHORS Schwartz, D.A. and Maki, R.A.  
TITLE Metabotropic glutamate receptors and methods of use therefor  
JOURNAL Patent: WO 0102566-A 3 11-JAN-2001;  
Neurocrine Biosciences, Inc. (US)  
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source location/Qualifiers  
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BASE COUNT 588 a 538 c 586 g 637 t  
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Best Local Similarity 99.7%; Pred. No. 4.6e-312;  
Matches 660; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGGTCCTCTGTTGATCCTGTCAGTCTTACTTTTGAAGAAGATGTCGAGAGTGA 60  
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 DB 1025 GG 1026  
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 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE  
 AUTHORS Schwarz, D.A. and Maki, R.A.  
 TITLE Metabotropic glutamate receptors and methods of use therefor  
 JOURNAL Patent: WO 0102586-A 1 11-JAN-2001;  
 Neurocrine Biosciences, Inc. (US)  
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 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE  
 AUTHORS Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,  
 Barrera, N., Bastien, V., Bloom, T., Boguslavsky, L., Bouckhalter, B.,  
 Camarata, J., Chang, J., Chazaro, B., Choquet, Y., Collymore, A.,  
 Cook, A., Cooke, P., DeArillano, K., Dewar, K., Diaz, J.S., Dodge, S.,  
 Fero, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J.,  
 Gardyna, S., Gird, S., Graham, L., Grand-Pierre, N., Hafez, N.,  
 Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,  
 Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R.,  
 Lindblad-Toh, K., Liu, G., Maclean, C., MacDonald, P., Major, J.,  
 Matthews, C., McCarthy, M., Meldrum, J., Menus, L., Minova, T.,  
 Menga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C.,  
 Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J.,  
 Peterson, K., Phunhang, P., Pierre, N., Raymond, C., Retta, R.,  
 Risse, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schnupack, R.,  
 Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, K.,  
 Stojanovic, N., Talama, J., Tesfaye, S., Theodore, J., Topham, K.,  
 Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X.,  
 Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.  
 Direct Submission  
 Submitted (07-NOV-2002) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 3 (bases 1 to 152269)  
 Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,  
 Barrera, N., Bastien, V., Bloom, T., Boguslavsky, L., Bouckhalter, B.,  
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TITLE
JOURNAL
REFERENCE
AUTHORS
Seaman, S., Severy, P., Smith, C., Spencer, B., Strange-Thomann, N.,
Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K.,
Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X.,
Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (17-DEC-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
4 (bases 1 to 152269)
Blitten, B., Nussbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,
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Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J.,
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Peterson, K., Phunhkhang, P., Piere, N., Raymond, C., Retta, R.,
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Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K.,
Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X.,
Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (17-JAN-2003) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jan 17, 2003 this sequence version replaced gi:27151430.
All repeats were identified using RepeatMasker:
Smit, A.P.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIRB
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L28531
Center clone name: 114_J_20
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Only the first 152.3 kilobases of this clone are being submitted.
The remainder overlaps accession number AC130364 [WIGR project
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ACCESSION AC026078
VERSION AC026078.3 GI:9958231
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SOURCE Homo sapiens
ORGANISM Homo sapiens (human)
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AUTHORS Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
JOURNAL The sequence of Homo sapiens clone
REFERENCE 2. (bases 1 to 182701)
AUTHORS Mattern, R.H.
TITLE Direct Submission

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## JOURNAL COMMENT

Submitted (19-MAR-2000) Genome Sequencing Center, Washington University School of Medicine, 444 Forest Park Parkway, St. Louis, MO 63108, USA  
 On Sep 1, 2000 this sequence version replaced gi:7534279.

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----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
Center project name: H NH035L17
----- Summary Statistics -----
Sequencing vector: plasmid; 10%
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 172513 bases at least Q40
Consensus quality: 175496 bases at least Q30
Insert size: 181000; agarose-fp
Insert size: 180101; sum-of-contigs
Quality coverage: 3.98 in Q20 bases; agarose-fp
Quality coverage: 4.04 in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 27 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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38084 44601: contig of 6518 bp in length
44602 44701: gap of unknown length
44702 52335: contig of 7634 bp in length
52336 52436: gap of unknown length
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58513 58613: gap of unknown length
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67871 74319: contig of 6349 bp in length
74320 74419: gap of unknown length
74420 85531: contig of 11112 bp in length
85532 85631: gap of unknown length
85632 97530: contig of 11899 bp in length
97531 97630: gap of unknown length
97631 108267: contig of 10657 bp in length
108268 108368: gap of unknown length
108369 120275: gap of 11908 bp in length
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JOURNAL  
REFERENCE  
AUTHORS

Submitted (16-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
3 (bases 1 to 58560)  
Barren, B., Nussbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Dearrell, K., Dewar, K., Diaz, J. S., Dodge, S., Fato, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Maclean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrum, J., Menus, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Pihunkang, P., Pierre, N., Raymond, C., Retra, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schuppback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE  
JOURNAL  
COMMENT

Submitted (04-SEP-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Sep 4, 2002 this sequence version replaced g1:22267776.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence.submissions@genome.wi.mit.edu](mailto:sequence.submissions@genome.wi.mit.edu)  
Project Information  
Center project name: L27942  
Center clone name: 995\_C\_20

\* NOTE: This record contains 74 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

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\* 679 779  
\* 1480: contig of 702 bp in length  
\* 1481 1580  
\* gap of 100 bp  
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\* contig of 658 bp in length  
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\* gap of 100 bp  
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\* contig of 668 bp in length  
\* 3784 3883  
\* gap of 100 bp  
\* 3884 4565  
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\* 5370 5469  
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\* 9282 9381  
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\* 11657 11756: gap of 100 bp  
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\* 21190 21290: contig of 688 bp in length  
\* 21291 21980: gap of 100 bp  
\* 21981 22080: contig of 690 bp in length  
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\* 27563 27662: gap of 100 bp  
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\* 28373 28472: gap of 100 bp  
\* 28473 29170: contig of 698 bp in length  
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\* 29271 29949: contig of 679 bp in length  
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\* 30751 30850: gap of 100 bp  
\* 30851 31531: contig of 681 bp in length  
\* 31532 31631: gap of 100 bp  
\* 31632 32395: contig of 764 bp in length  
\* 32396 32495: gap of 100 bp  
\* 32496 33183: contig of 688 bp in length  
\* 33184 33283: gap of 100 bp  
\* 33284 33985: contig of 702 bp in length  
\* 33986 34085: gap of 100 bp  
\* 34086 34761: contig of 676 bp in length  
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* 38836 39519: contig of 684 bp in length
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Query Match 22.8%; Score 253; DB 2; Length 58560;
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Db 53279 AGGCAATATGAGGAAGTGGAGTGGAGGCTTCAAGATATGTCAGCGAAGAGGAT 53338
Qy 720 TTGCATGCGCCACTCTTCAAAATCTACAGTATGACAGGAGACAGCTTTGATTAAGCT 779
Db 53339 TTGCATGCGCCACTCTTCAAAATCTACAGTATGACAGGAGACAGCTTTGATTAAGCT 53398
Qy 780 GCTGAGAGAGCTCAAGATCACTTGGCCCAAGCCCGGCTGCTCTTCTGTGAGGG 839
Db 53399 GCTGAGAGAGCTCAAGATCACTTGGCCCAAGCCCGGCTGCTCTTCTGTGAGGG 53458
Qy 840 CATTGACGCTGAGAGCTTGTGCTGATGCGCATGAGGCGCTGCTGATGCGGAGATTCT 899
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Qy 900 GCTTCTGGGAGG 912
Db 53519 GCTTCTGGGAGG 53531

RESULT 13
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LOCUS Homo sapiens chromosome 11 clone RP11-208A14 map 11, WORKING DRAFT
DEFINITION
SEQUENCE, 3 unordered pieces.
AC130357
AC130357.2 GI:22857687
VERSION HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 146921)
Birten,B., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 11, clone RP11-208A14
Unpublished
2 (bases 1 to 146921)
Birten,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
Barra,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukhgalter,B.,
Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J.,
Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B.,
Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,
Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,
Liu,G., Maclean,C., Macdonald,P., Major,J., Matthews,C.,
McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,

```

```

TITLE
JOURNAL
REFERENCE
AUTHORS
Birten,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
Barra,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukhgalter,B.,
Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
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Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,
O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K.,
Phunhthang,P., Pierre,N., Raymont,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Roy,A., Schauer,S., Schnupack,R., Seaman,S., Severy,P.,
Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,
Tefaye,S., Theodore,J., Topham,K., Travers,M., Vasilev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (09-AUG-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 146921)
Birten,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
Barra,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukhgalter,B.,
Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J.,
Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B.,
Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,
Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,
Liu,G., Maclean,C., Macdonald,P., Major,J., Matthews,C.,
McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,
O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K.,
Phunhthang,P., Pierre,N., Raymont,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Roy,A., Schauer,S., Schnupack,R., Seaman,S., Severy,P.,
Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,
Tefaye,S., Theodore,J., Topham,K., Travers,M., Vasilev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (14-SEP-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Sep 14, 2002 this sequence version replaced gl:22165292.
All repeats were identified using RepeatMasker:
Smit,A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center Project name: L27963
Center clone name: 208 A.14
----- Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 145664 bases at least Q40
Consensus quality: 145764 bases at least Q20
Insert size: 151000; agarose-ftp
Insert size: 146721; sum-of-ctnigs
Quality coverage: 18.2 in Q20 bases; agarose-ftp
Quality coverage: 18.7 in Q20 bases; sum-of-ctnigs
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NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preceeded.
1 11413: contig of 11413 bp in length
* 11414 11513: gap of 100 bp
* 11514 12216: contig of 703 bp in length
* 12217 12316: gap of 100 bp
* 12317 146921: contig of 134605 bp in length.
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FEATURES
source

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BASE COUNT
ORIGIN

Query Match 22.8% Score 253 DB 2 Length 146921
Best Local Similarity 100.0% Pred. No. 2.2e-134
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 660 AGGCACTATGAGGAAAGTGGATGGAAGCTTCAAGATATGTCAGCGAAGAGAGGAT 719
DB 77486 AGGCACTATGAGGAAAGTGGATGGAAGCTTCAAGATATGTCAGCGAAGAGAGGAT 77427
QY 720 TTGCATCGCCCACTTCAAAATCTACAGTAATGCAAGGAGAGAGGCTTGTATAGCT 779
DB 77426 TTGCATCGCCCACTTCAAAATCTACAGTAATGCAAGGAGAGAGGCTTGTATAGCT 77367
QY 780 GCTGAAGAGCTCAAGTCACTTGTCCCAAGCCCGGTGTGGCTTACTTCTGTAGAGG 839
DB 77366 GCTGAAGAGCTCAAGTCACTTGTCCCAAGCCCGGTGTGGCTTACTTCTGTAGAGG 77307
QY 840 CATGACGGTGAAGGCTCTGTATGCGCATGAGCCCGCTGGGTCTTGTGGAGAAATTTCT 899
DB 77306 CATGACGGTGAAGGCTCTGTATGCGCATGAGCCCGCTGGGTCTTGTGGAGAAATTTCT 77247
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RESULT 14
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LOCUS AC130364
DEFINITION Homo sapiens chromosome 11, clone RP11-707M1, complete sequence.
ACCESSION AC130364
VERSION AC130364.5 GI:23683265
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 173032)
Birren, B., Nuebaum, C. and Lander, B.
Homo sapiens chromosome 11, clone RP11-707M1
Unpublished
2 (bases 1 to 173032)
Birren, B., Nuebaum, C., Lander, B., Ali, A., Allen, N., Anderson, S.,
Barra, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhgalter, B.,
Camara, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A.,
Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J., Dodge, S.,
Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B.,
Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A.,
Karatas, A., Kelle, C., Landers, T., Levine, R., Lindblad-Toh, K.,
Liu, G., Maclean, C., Macdonald, P., Major, J., Matthews, C.,
McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V.,
Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C. H.,
O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K.,
Phunkhang, P., Pterre, N., Raymond, C., Retta, R., Rise, C., Rogov, P.,
Roman, J., Roy, A., Schauer, S., Schnupack, R., Seaman, S., Severy, P.,
Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J.,
Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J.,

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TITLE
JOURNAL
REFERENCE
AUTHORS
3 (bases 1 to 173032)
Birren, B., Nuebaum, C., Lander, B., Ali, A., Allen, N., Anderson, S.,
Barra, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhgalter, B.,
Camara, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A.,
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Phunkhang, P., Pterre, N., Raymond, C., Retta, R., Rise, C., Rogov, P.,
Roman, J., Roy, A., Schauer, S., Schnupack, R., Seaman, S., Severy, P.,
Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J.,
Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J.,
Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (28-SEP-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
4 (bases 1 to 173032)
Birren, B., Nuebaum, C., Lander, B., Ali, A., Allen, N., Anderson, S.,
Barra, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhgalter, B.,
Camara, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A.,
Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J., Dodge, S.,
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Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J.,
Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (10-OCT-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Oct 10, 2002 this sequence version replaced gi:23343785.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/BW/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
----- Project Information
Center project name: 127973
Center clone name: 707_M_1
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 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
 Bacteria; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 173795)  
 Homo sapiens chromosome 11, clone RP13-871G20  
 Unpublished  
 2 (bases 1 to 173795)  
 Birren, B., Nusbaum, C., Lander, B., Ali, A., Allen, N., Anderson, S.,  
 Barina, N., Bastien, V., Bloom, T., Boguslavsky, L., Bouhgalter, B.,  
 Camarata, J., Chang, J., Chazaro, B., Choquet, Y., Collymore, A.,  
 Cook, A., Cooke, P., DeArrelano, K., Dewar, K., Diaz, J.S., Dodge, S.,  
 Fero, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J.,

TITLE  
JOURNAL  
REFERENCE  
AUTHORS

Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karakas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Maclean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrim, J., Menus, L., Milova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunhahang, P., Piere, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schuback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Teste, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Submitted (09-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
(bases 1 to 173795)

Bliren, B., Nussbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Bouhassal, B., Camarata, J., Chang, J., Chazaro, B., Chopel, Y., Collymore, A., Cook, A., Cooke, P., Dearrellano, K., Dewar, K., Diaz, J. S., Dodge, S., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karakas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Maclean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrim, J., Menus, L., Milova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunhahang, P., Piere, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schuback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Teste, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE  
JOURNAL  
COMMENT

Submitted (27-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Oct 10, 2002 this sequence version replaced gi:23477886.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WtBR  
Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
Project Information  
Center project name: L27938  
Center clone name: 871\_G\_20

NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

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\* 3811 3910: gap of 100 bp  
\* 3911 47222: contig of 43312 bp in length  
\* 47223 47322: gap of 100 bp  
\* 47323 47383: contig of 7461 bp in length  
\* 47384 54883: gap of 100 bp  
\* 54884 75151: contig of 20268 bp in length  
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BASE COUNT 51546 a 33677 c 33180 g 54838 t 554 others  
ORIGIN

Query Match 22.8%; Score 253; DB 2; Length 173795;  
Best Local Similarity 100.0%; Pred. No. 2.2e-134;  
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Search completed: December 14, 2003, 21:51:55  
Job time: 4199.38 secs



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RESULT 2  
US-09-695-481-5  
Sequence 5, Application US/09695481  
Patent No. 6534287  
GENERAL INFORMATION:  
APPLICANT: STORMANN, THOMAS M.  
APPLICANT: LEVINTHAL, CYNTHIA  
APPLICANT: STORJOHANN, LAURA  
APPLICANT: HAMMERLAND, LANCE G.  
APPLICANT: KRAPCHO, KAREN J.  
APPLICANT: NPS PHARMACEUTICALS, INC.  
TITLE OF INVENTION: A NOVEL HUMAN METABOTROPIC GLUTAMATE RECEPTOR  
FILE REFERENCE: 1094.2.6  
CURRENT APPLICATION NUMBER: US/09/695,481  
CURRENT FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: 60/161,481  
PRIOR FILING DATE: 1998-10-25  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 5  
LENGTH: 3129  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: Description of Artificial Sequence: Chimeric  
OTHER INFORMATION: molecule comprising portions of human mGluR4 and  
OTHER INFORMATION: the human calcium receptor.  
NAME/KEY: CDS  
LOCATION: ( )... (3129)  
US-09-695-481-5

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Best Local Similarity 99.1%; Pred. No. 2.9e-102;  
Matches 422; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
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RESULT 3  
US-09-016-434-1133  
Sequence 1133, Application US/09016434  
Patent No. 6500938  
GENERAL INFORMATION:  
APPLICANT: Janice Au-Young  
APPLICANT: Jeffrey J. Seilhammer  
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
NUMBER OF SEQUENCES: 1490  
CORRESPONDENCE ADDRESS:  
ADDRESSER: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 PORTER DRIVE  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
FILING DATE: HEREWITH  
APPLICATION NUMBER: US/09/016,434  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Zeller, Karen J.  
REGISTRATION NUMBER: 37,071  
REFERENCE/DOCKET NUMBER: PA-0002 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 845-4166  
TELEFAX: (650) 855-0555  
INFORMATION FOR SEQ ID NO: 1133:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4078 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GENBANK  
CLONE: g1408051  
US-09-016-434-1133

Query Match 20.0%; Score 222; DB 4; Length 4078;  
Best Local Similarity 99.1%; Pred. No. 2.9e-102;  
Matches 422; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
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RESULT 4  
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Sequence 1, Application US/08660148  
Patent No. 6211353  
GENERAL INFORMATION:  
APPLICANT: Burnett, J. P.  
APPLICANT: Mayne, Nancy G.  
APPLICANT: Sharp, Robert L.  
APPLICANT: Snyder, Yvonne M.  
TITLE OF INVENTION: EXCITATORY AMINO RECEPTOR PROTEIN AND  
TITLE OF INVENTION: RELATED NUCLEIC ACID COMPOUNDS  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Eli Lilly and Company  
STREET: Lilly Corporate Center  
CITY: Indianapolis  
STATE: Indiana  
COUNTRY: United States of America  
ZIP: 46285  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/660,148  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/282,853  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Gaylo, Paul J.  
REGISTRATION NUMBER: 36,808  
REFERENCE/DOCKET NUMBER: X-9419  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (317) 276-0756  
TELEFAX: (317) 276-3861  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4207 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 460..3999  
US-08-660-148-1

Query Match 20.0%; Score 222; DB 3; Length 4207;

Best Local Similarity 99.1%; Pred. No. 2,9e-102;  
Matches 422; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
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RESULT 5  
US-08-660-148-3  
Sequence 3, Application US/08660148  
Patent No. 6211353  
GENERAL INFORMATION:  
APPLICANT: Burnett, J. P.  
APPLICANT: Mayne, Nancy G.  
APPLICANT: Sharp, Robert L.  
APPLICANT: Snyder, Yvonne M.  
TITLE OF INVENTION: EXCITATORY AMINO RECEPTOR PROTEIN AND  
TITLE OF INVENTION: RELATED NUCLEIC ACID COMPOUNDS  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Eli Lilly and Company  
STREET: Lilly Corporate Center  
CITY: Indianapolis  
STATE: Indiana  
COUNTRY: United States of America  
ZIP: 46285  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/660,148  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/282,853  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Gaylo, Paul J.  
REGISTRATION NUMBER: 36,808  
REFERENCE/DOCKET NUMBER: X-9419  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (317) 276-0756

TELEFAX: (317) 276-3861  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4207 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: mRNA  
US-08-660-148-3

Query Match 20.0%; Score 222; DB 3; Length 4207;  
Best Local Similarity 76.3%; Pred. No. 2.9e-102;  
Matches 325; Conservative 97; Mismatches 4; Indels 0; Gaps 0;

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DB 1040 CAGAUUCUACGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1099  
QY 641 TATCAGCCGTCACACAGAAAGCCTATGAGAAAGTGGATGGAAGCTTCAAGATA 700  
DB 1100 UACACGCGGTCACACAGAAAGCCTATGAGAAAGTGGATGGAAGCCTTCAAGATA 1159  
QY 701 TGTCAAGGAGAGAGGATTTGCTGATGCTCCATCTTCAAAATCTAAGTATGACAGGG 760  
DB 1160 UGCACGAGAGAGAGGATTTGCTGATGCTCCATCTTCAAAATCTAAGTATGACAGGG 1219  
QY 761 AGCAGAGCTTTGATTAAGCTCTGAAGAGCTCAAGTCACTTCCCAAGCCCGGCTG 820  
DB 1220 AGCAGAGCTTTGATTAAGCTCTGAAGAGCTCAAGTCACTTCCCAAGCCCGGCTG 1279  
QY 821 TGCCCTACTTCTGTGAGGCGCATGACGGTGTGCTGATGAGCATGAGCGCTTG 880  
DB 1280 TGCCCTACTTCTGTGAGGCGCATGACGGTGTGCTGATGAGCATGAGCGCTTG 1339  
QY 881 GTCTAG 886  
DB 1340 GTCTAG 1345

## RESULT 6

US-08-660-148-4  
Sequence 4, Application US/08660148  
Patent No. 6211353  
GENERAL INFORMATION:  
APPLICANT: Burnette, J. P.  
APPLICANT: Mayne, Nancy G.  
APPLICANT: Sharp, Robert L.  
APPLICANT: Snyder, Yvonne M.  
TITLE OF INVENTION: EXCITATORY AMINO RECEPTOR PROTEIN AND  
NUMBER OF SEQUENCES: 6  
TITLE OF INVENTION: RELATED NUCLEIC ACID COMPOUNDS  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Eli Lilly and Company  
STREET: Lilly Corporate Center  
CITY: Indianapolis  
STATE: Indiana  
COUNTRY: United States of America  
ZIP: 46285  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/660,148

FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/282,853  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Gaylo, Paul J.  
REGISTRATION NUMBER: 36,808  
REFERENCE/DOCKET NUMBER: X-9419  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (317) 276-0756  
TELEFAX: (317) 276-3861  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4303 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 460..4095  
US-08-660-148-4

Query Match 20.0%; Score 222; DB 3; Length 4303;  
Best Local Similarity 99.1%; Pred. No. 2.9e-102;  
Matches 422; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 461 TAGCCATTGAGTCCAGAAATTTGCTTCAACATACCTCAGATTGCTTACTCAG 520  
DB 920 UACCCAUUCAGGCGCCAGAAATTTGCTTCAACATACCTCAGATTGCTTACTCAG 979  
QY 521 CAACCATCATGATCTGATGACAAAGCTCTTCAATATTTTCATGAGGGTTGTGCTT 580  
DB 980 CAACCGACGAGTCTGATGACAAAGCTCTTCAATATTTTCATGAGGGTTGTGCTT 1039  
QY 581 CAGATGCTCAGCAGCAGAGTCCATGATGATGATGATGATGATGATGATGATGATG 640  
DB 1040 CAGATGCTCAGCAGCAGAGTCCATGATGATGATGATGATGATGATGATGATGATG 1099  
QY 641 TATCAGCCGTCACACAGAAAGCCTATGAGAAAGTGGATGGAAGCTTCAAGATA 700  
DB 1100 TATCAGCCGTCACACAGAAAGCCTATGAGAAAGTGGATGGAAGCTTCAAGATA 1159  
QY 701 TGTCAAGGAGAGAGGATTTGCTGATGCTCCATCTTCAAAATCTAAGTATGACAGGG 760  
DB 1160 TGTCAAGGAGAGAGGATTTGCTGATGCTCCATCTTCAAAATCTAAGTATGACAGGG 1219  
QY 761 AGCAGAGCTTTGATTAAGCTCTGAAGAGCTCAAGTCACTTCCCAAGCCCGGCTG 820  
DB 1220 AGCAGAGCTTTGATTAAGCTCTGAAGAGCTCAAGTCACTTCCCAAGCCCGGCTG 1279  
QY 821 TGCCCTACTTCTGTGAGGCGCATGACGGTGTGCTGATGAGCATGAGCGCTTG 880  
DB 1280 TGCCCTACTTCTGTGAGGCGCATGACGGTGTGCTGATGAGCATGAGCGCTTG 1339  
QY 881 GTCTAG 886  
DB 1340 GTCTAG 1345

## RESULT 7

US-08-660-148-6  
Sequence 6, Application US/08660148  
Patent No. 6211353  
GENERAL INFORMATION:  
APPLICANT: Burnette, J. P.  
APPLICANT: Mayne, Nancy G.  
APPLICANT: Sharp, Robert L.  
APPLICANT: Snyder, Yvonne M.  
TITLE OF INVENTION: EXCITATORY AMINO RECEPTOR PROTEIN AND  
NUMBER OF SEQUENCES: 6  
TITLE OF INVENTION: RELATED NUCLEIC ACID COMPOUNDS



## CORRESPONDENCE ADDRESS:

ADDRESSEE: Eli Lilly and Company  
STREET: Lilly Corporate Center  
CITY: Indianapolis  
STATE: Indiana  
COUNTRY: United States of America  
ZIP: 46285

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/660,148  
FILING DATE:  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US/08/282,853  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Gaylo, Paul J.  
REGISTRATION NUMBER: 36,808  
REFERENCE/DOCKET NUMBER: X-9419  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (317) 276-0756  
TELEFAX: (317) 276-3861  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4303 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: mRNA  
US-08-660-148-6

Query Match 20.0%; Score 222; DB 3; Length 4303;  
Best Local Similarity 76.3%; Pred. No. 2,9e-102;

Matches 325; Conservative 97; Mismatches 4; Indels 0; Gaps 0;

QY 461 TAGCCATTGAGTCCAGAAATTTGCTCCAGTTTCAACATGCTGAGATTGCTTACTGAG 520  
DB 920 UAGCCAUUAGGUCAGAAUUGUCUCAGCUUUCACAAUACCUCAAGUUGUCUACUCAG 979  
QY 521 CAACCATGATGATCTGAGTGAAGCAAGACTGTCTCAATATTTTCATGAGGGTTGCTT 580  
DB 980 CAACGAGCAUUGAUUCGAGUGACAAACCTGUCUCAAUUAUUCAGAGGUGUUGCCUU 1039  
QY 581 CAGATCTGAGCAGGAGGAGGTCATGATGATGAGAGAGTAACTGAGCCTTCAAGCTATG 640  
DB 1040 CAGAGUCUACGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1099  
QY 641 TATCAGCCGTATACACAGAAAGGCACTATGAGAGAAAGTGGATGAGAGGCTTCAAGATA 700  
DB 1100 UUNACACCGUGACACAGAAAGGCAUUAUGAGAAAGUUGAGAGGAGGAGGAGGAGG 1159  
QY 701 TGTCAAGCGAAGAGGAGGATTTGATGATGCTTCACTTCAAAATCTTCAAGTATGCAAGG 760  
DB 1160 UGTCAAGCGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1219  
QY 761 AGCAGAGCTTTGATAGCTGCTGAGAGAGCTCAAGTCACTGAGGAGGAGGAGGAGGAGG 820  
DB 1220 AGCAGAGCTTTGATAGCTGCTGAGAGAGCTCAAGTCACTGAGGAGGAGGAGGAGG 1279  
QY 821 TGGCTTACTTCTGTGAGGAGGAGTACGCTGATGAGGAGGAGGAGGAGGAGGAGGAGG 880  
DB 1280 UGGCTTCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1339  
QY 881 GTCTAG 886  
DB 1340 GUCUAG 1345

RESULT 8

US-08-072-574-11

Sequence 11, Application US/08072574

Patent No. 5521297

GENERAL INFORMATION:

APPLICANT: Daggett, Lorrie

APPLICANT: Ellis, Steven B.

APPLICANT: Liaw, Chen

APPLICANT: Portisler, Aaron

TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,

TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME AND USES THEREOF

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pretty, Schroeder, Brueggemann &amp; Clark

STREET: 444 South Flower Street, Suite 2000

CITY: Los Angeles

STATE: CA

COUNTRY: USA

ZIP: 00719

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/072,574

FILING DATE: 19930604

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Reiter, Stephen E.

REGISTRATION NUMBER: 31,192

REFERENCE/DOCKET NUMBER: P41 9383

TELECOMMUNICATION INFORMATION:

TELEPHONE: 213-622-7700

TELEFAX: 213-489-4210

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 3282 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: both

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 370..3003

OTHER INFORMATION: /product= "HUMAN MGLUR5C"

US-08-072-574-11

Query Match 15.4%; Score 171; DB 1; Length 3282;  
Best Local Similarity 98.8%; Pred. No. 1.5e-76;

Matches 421; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 461 TAGCCATTGAGTCCAGAAATTTGCTCCAGTTTCAACATGCTGAGATTGCTTACTGAG 520  
DB 830 TAGCCATTGAGTCCAGAAATTTGCTCCAGTTTCAACATGCTGAGATTGCTTACTGAG 889  
QY 521 CAACCATGATGATCTGAGTGAAGCAAGACTGTCTCAATATTTTCATGAGGGTTGCTT 580  
DB 890 CAACGAGCAUUGAUUCGAGUGACAAACCTGUCUCAAUUAUUCAGAGGUGUUGCCUU 949  
QY 581 CAGATCTGAGCAGGAGGAGGTCATGATGATGAGAGAGTAACTGAGCCTTCAAGCTATG 640  
DB 950 CAGATCTGAGCAGGAGGAGGTCATGATGATGAGAGAGTAACTGAGCCTTCAAGCTATG 1009  
QY 641 TATCAGCCGTATACACAGAAAGGCACTATGAGAGAAAGTGGATGAGAGGCTTCAAGATA 700  
DB 1010 TATCAGCCGTATACACAGAAAGGCACTATGAGAGAAAGTGGATGAGAGGCTTCAAGATA 1069  
QY 701 TGTCAAGCGAAGAGGAGGATTTGATGATGCTTCACTTCAAAATCTTCAAGTATGCAAGG 760  
DB 1070 TGTCAAGCGAAGAGGAGGATTTGATGATGCTTCACTTCAAAATCTTCAAGTATGCAAGG 1129  
QY 761 AGCAGAGCTTTGATAGCTGCTGAGAGAGCTCAAGTCACTGAGGAGGAGGAGGAGGAGG 820

Db 1130 AGAGAGCTTGTATAGCTGCTAAGAGCTCAACTGCTGCCCCAAGCCCGGCTGG 1189  
QY 821 TGCCCTACTCTGTGAGGCGCATGCGGTGAGGTCTGATGAGCCATGAGCGGCTGG 880  
Db 1190 TGCCCTGCTTCTGTGTAGGCGCATGCGGTGAGGTCTGATGAGCCATGAGCGGCTGG 1249  
QY 881 GTCTAG 886  
Db 1250 GTCTAG 1255

RESULT 9  
US-08-486-270-11  
; Sequence 11, Application US/08486270  
; Patent No. 5807689  
; GENERAL INFORMATION:  
; APPLICANT: Daggett, Lorrie  
; APPLICANT: Ellis, Steven B.  
; APPLICANT: Liaw, Chen  
; APPLICANT: Pontsler, Aaron  
; APPLICANT: Johnson, Edwin C.  
; APPLICANT: Hess, Stephen D.  
; TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,  
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME AND USES THEREOF  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
; STREET: 444 South Flower Street, Suite 2000  
; CITY: Los Angeles  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/486,270  
; FILING DATE: 02-JUN-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/072,574  
; FILING DATE: 04-JUN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Reiter, Stephen E.  
; REGISTRATION NUMBER: 31,192  
; REFERENCE/DOCKET NUMBER: FP41 9772  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-546-4737  
; TELEFAX: 619-546-9392  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3282 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 370..3003  
; OTHER INFORMATION: /product= "HUMAN MGLUR5C"  
; OTHER INFORMATION: /note= "Variant of MGLUR5A with truncated 3' end."  
; US-08-486-270-11

Query Match 15.4%; Score 171; DB 1; Length 3282;  
Best Local Similarity 98.8%; Pred. No. 1.5e-76;  
Matches 421; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 461 TAGCATTAGAGTCCAGATTGCTGCTGAGCTTTTCAACATGCTGAGATTGCTTACTGAG 520  
Db 830 TAGCATTAGAGTCCAGATTGCTGCTGAGCTTTTCAACATGCTGAGATTGCTTACTGAG 889

QY 521 CAACATCATGATCTGATGACCAAGACTCTGTTCAATATTTTCATGAGGTTGCTT 580  
Db 890 CAACGAGATGATCTGATGACCAAGACTCTGTTCAATATTTTCATGAGGTTGCTT 949  
QY 581 CAGATCTCAGCAGGCAAGGCTCAGTGTGACATGATGAAAGGTCAACTGACCTTAG 640  
Db 950 CAGATCTCAGCAGGCAAGGCTCAGTGTGACATGATGAAAGGTCAACTGACCTTAG 1009  
QY 641 TATCAGCCGTACACAGAAAGCAACTATGAGAAAGTGGATGAAAGCTTCAAGATA 700  
Db 1010 TATCAGCCGTACACAGAAAGCAACTATGAGAAAGTGGATGAAAGCTTCAAGATA 1069  
QY 701 TGTACAGGAGGAGGAGGATTTGATGCCCACTCTTACAAAATCTACATGATGACGGG 760  
Db 1070 TGTACAGGAGGAGGAGGATTTGATGCCCACTCTTACAAAATCTACATGATGACGGG 1129  
QY 761 AGCAGACTTTGATTAAGCTGCTGAGAGAGCTCAAGTCACTTGCCTCAAGCCGGGTGG 820  
Db 1130 AGCAGACTTTGATTAAGCTGCTGAGAGAGCTCAAGTCACTTGCCTCAAGCCGGGTGG 1189  
QY 821 TGCCCTACTCTGTGAGGCGCATGCGGTGAGGTCTGATGAGCCATGAGCGGCTGG 880  
Db 1190 TGCCCTGCTTCTGTGTAGGCGCATGCGGTGAGGTCTGATGAGCCATGAGCGGCTGG 1249  
QY 881 GTCTAG 886  
Db 1250 GTCTAG 1255

RESULT 10  
US-08-367-264-11  
; Sequence 11, Application US/08367264  
; Patent No. 6001581  
; GENERAL INFORMATION:  
; APPLICANT: Daggett, Lorrie  
; APPLICANT: Ellis, Steven B.  
; APPLICANT: Liaw, Chen  
; APPLICANT: Pontsler, Aaron  
; APPLICANT: Johnson, Edwin C.  
; APPLICANT: Hess, Stephen D.  
; TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,  
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME AND USES THEREOF  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
; STREET: 444 South Flower Street, Suite 2000  
; CITY: Los Angeles  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/367,264  
; FILING DATE: 02-JUN-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/072,574  
; FILING DATE: 04-JUN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Reiter, Stephen E.  
; REGISTRATION NUMBER: 31,192  
; REFERENCE/DOCKET NUMBER: FP41 9772  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-546-4737  
; TELEFAX: 619-546-9392  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3282 base pairs

TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 370..3003  
OTHER INFORMATION: /product= "HUMAN MGLUR5C"  
OTHER INFORMATION: /note= "Variant of MGLUR5A with truncated 3' end."  
US-08-367-264-11

Query Match 15.4%; Score 171; DB 3; Length 3282;  
Best Local Similarity 98.8%; Pred. No. 1.5e-76;  
Matches 421; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 461 TAGCCATTGAGTCCGGAATTTCTCCAGCTTTTCAACATACCTGAGATTGCTTACTGAG 520  
DB 830 TAGCCATTGAGTCCGGAATTTCTCCAGCTTTTCAACATACCTGAGATTGCTTACTGAG 889  
QY 521 CAACCATCATGATCTGAGTGAAGAAGCTCTGTTCAATTTTCAATGAGGCTTGTGCTT 580  
DB 890 CAACCATCATGATCTGAGTGAAGAAGCTCTGTTCAATTTTCAATGAGGCTTGTGCTT 949  
QY 581 CAGATCTCAGCAGGCAAGGTCCTGATGAGTGAAGAAGTGAAGAAGTGAAGAAGTGAAGA 640  
DB 950 CAGATCTCAGCAGGCAAGGTCCTGATGAGTGAAGAAGTGAAGAAGTGAAGAAGTGAAGA 1009  
QY 641 TATCAGCCGTGACACAGAAAGGCACTGATGAGAAAGTGAAGAAGTGAAGAAGTGAAGA 700  
DB 1010 TATCAGCCGTGACACAGAAAGGCACTGATGAGAAAGTGAAGAAGTGAAGAAGTGAAGA 1069  
QY 701 TGTCAAGGAGGAAGGATTTGATGAGCCCACTTAACTTAACTTAACTTAACTTAACTTAA 760  
DB 1070 TGTCAAGGAGGAAGGATTTGATGAGCCCACTTAACTTAACTTAACTTAACTTAACTTAA 1129  
QY 761 AGCAGAGCTTTGATTAAGTCTGATGAGAGTCAAGTCACTTGAAGGCGCGGCTG 820  
DB 1130 AGCAGAGCTTTGATTAAGTCTGATGAGAGTCAAGTCACTTGAAGGCGCGGCTG 1189  
QY 821 TGGCCTACTTCTGTGAGGCGCATGACGCTGAGAGGCTCTGATGAGGCGCGGCTG 880  
DB 1190 TGGCCTACTTCTGTGAGGCGCATGACGCTGAGAGGCTCTGATGAGGCGCGGCTG 1249  
QY 881 GTCTAG 886  
DB 1250 GTCTAG 1255

RESULT 11  
US-09-153-757-11  
Sequence 11, Application US/09153757  
Patent No. 6413764

GENERAL INFORMATION:  
APPLICANT: Daggett, Lorrie  
Ellis, Steven B.

Liaw, Chen  
Pomblier, Aaron  
Johnson, Edwin C.  
Hees, Stephen D.

TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,  
NUCLEIC ACIDS ENCODING SAME AND USES THEREOF  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
STREET: 444 South Flower Street, Suite 2000  
CITY: Los Angeles  
STATE: CA  
COUNTRY: USA  
ZIP: 90071

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/153,757  
FILING DATE: 15-Sep-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,270  
FILING DATE: 02-JUN-1994  
APPLICATION NUMBER: US 08/072,574  
FILING DATE: 04-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen E.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: PP41 9772  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-546-4737  
TELEFAX: 619-546-9392  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3282 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 370..3003  
OTHER INFORMATION: /product= "HUMAN MGLUR5C"  
/note= "Variant of MGLUR5A with truncated 3' end."  
SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-09-153-757-11

Query Match 15.4%; Score 171; DB 4; Length 3282;  
Best Local Similarity 98.8%; Pred. No. 1.5e-76;  
Matches 421; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 461 TAGCCATTGAGTCCGGAATTTCTCCAGCTTTTCAACATACCTGAGATTGCTTACTGAG 520  
DB 830 TAGCCATTGAGTCCGGAATTTCTCCAGCTTTTCAACATACCTGAGATTGCTTACTGAG 889  
QY 521 CAACCATCATGATCTGAGTGAAGAAGCTCTGTTCAATTTTCAATGAGGCTTGTGCTT 580  
DB 890 CAACCATCATGATCTGAGTGAAGAAGCTCTGTTCAATTTTCAATGAGGCTTGTGCTT 949  
QY 581 CAGATCTCAGCAGGCAAGGTCCTGATGAGTGAAGAAGTGAAGAAGTGAAGAAGTGAAGA 640  
DB 950 CAGATCTCAGCAGGCAAGGTCCTGATGAGTGAAGAAGTGAAGAAGTGAAGAAGTGAAGA 1009  
QY 641 TATCAGCCGTGACACAGAAAGGCACTTAACTTAACTTAACTTAACTTAACTTAACTTAA 700  
DB 1010 TATCAGCCGTGACACAGAAAGGCACTTAACTTAACTTAACTTAACTTAACTTAACTTAA 1069  
QY 701 TGTCAAGGAGGAAGGATTTGATGAGCCCACTTAACTTAACTTAACTTAACTTAACTTAA 760  
DB 1070 TGTCAAGGAGGAAGGATTTGATGAGCCCACTTAACTTAACTTAACTTAACTTAACTTAA 1129  
QY 761 AGCAGAGCTTTGATTAAGTCTGATGAGAGTCAAGTCACTTGAAGGCGCGGCTG 820  
DB 1130 AGCAGAGCTTTGATTAAGTCTGATGAGAGTCAAGTCACTTGAAGGCGCGGCTG 1189  
QY 821 TGGCCTACTTCTGTGAGGCGCATGACGCTGAGAGGCTCTGATGAGGCGCGGCTG 880  
DB 1190 TGGCCTACTTCTGTGAGGCGCATGACGCTGAGAGGCTCTGATGAGGCGCGGCTG 1249  
QY 881 GTCTAG 886  
DB 1250 GTCTAG 1255

RESULT 12  
US-09-459-715-11  
Sequence 11, Application US/09459715  
Patent No. 6485919

GENERAL INFORMATION:  
APPLICANT: Daggett, Lorrie  
Ellis, Steven B.  
Liew, Chen  
Pontsler, Aaron  
Johnson, Edwin C.  
Hees, Stephen D.  
TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,  
NUCLEIC ACIDS ENCODING SAME AND USES THEREOF  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
STREET: 444 South Flower Street, Suite 2000  
CITY: Los Angeles  
STATE: CA  
COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/459,715  
FILING DATE: 13-Dec-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/367,264  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen E.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: P41 9772  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-546-4737  
TELEFAX: 619-546-9392  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3282 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 370..3003  
OTHER INFORMATION: /product= "HUMAN MGLUR5C"  
/note= "Variant of MGLUR5A with truncated 3' end."  
SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-09-459-715-11

Query Match 15.4%; Score 171; DB 4; Length 3282;  
Best Local Similarity 98.8%; Pred. No. 1.5e-76;  
Matches 421; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

461 TAGCCATTGAGTCCAGAAATTTGCTCCAGCTTTTCAACATACCTAGATTGCTTACTGAG 520  
830 TAGCCATTGAGTCCAGAAATTTGCTCCAGCTTTTCAACATACCTAGATTGCTTACTGAG 889  
521 CAACCATGATGATCTGATGACAGAACTCTGTTCAAAATATTTTCATGAGGGTTGTGCTT 580  
890 CAACCATGATGATCTGATGACAGAACTCTGTTCAAAATATTTTCATGAGGGTTGTGCTT 949  
581 CAATGCTGACGACGACAGAGTCCATGATGACATGAGAAAGTGGATGGAAGCCTTCAAGATA 640  
950 CAATGCTGACGACGACAGAGTCCATGATGACATGAGAAAGTGGATGGAAGCCTTCAAGATA 1009  
641 TATCAGCCGTCACACAGAGCAACTATGAGAAAGTGGATGGAAGCCTTCAAGATA 700  
1010 TATCAGCCGTCACACAGAGCAACTATGAGAAAGTGGATGGAAGCCTTCAAGATA 1069  
701 TGTCAAGCAAGAGGATTTGATGCGCCACTTTTCAAAATCTACATGATGCAAGGGG 760

DB 1070 TGTCAAGCAAGAGGATTTGATGCGCCACTTTTCAAAATCTACATGATGCAAGGG 1129  
QY 761 AGCAGAGCTTTGATTAAGTGTCTGAAGAGCTCAAGATGACTGAGCCCAAGCCGGGTGG 820  
DB 1130 AGCAGAGCTTTGATTAAGTGTCTGAAGAGCTCAAGATGACTGAGCCCAAGCCGGGTGG 1189  
QY 821 TGGCCTACTTCTGTGAGAGGATGACGATGAGAGGTCTGATGAGCCATGAGGCGCTGG 880  
DB 1190 TGGCCTACTTCTGTGAGAGGATGACGATGAGAGGTCTGATGAGCCATGAGGCGCTGG 1249  
QY 881 GTCTAG 886  
DB 1250 GTCTAG 1255

RESULT 13  
US-08-072-574-7  
Sequence 7, Application US/08072574  
Patent No. 5521297  
GENERAL INFORMATION:  
APPLICANT: Daggett, Lorrie  
Ellis, Steven B.  
Liew, Chen  
Pontsler, Aaron  
Johnson, Edwin C.  
Hees, Stephen D.  
TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,  
NUCLEIC ACIDS ENCODING SAME AND USES THEREOF  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
STREET: 444 South Flower Street, Suite 2000  
CITY: Los Angeles  
STATE: CA  
COUNTRY: USA  
ZIP: 00719  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/072,574  
FILING DATE: 19930604  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen E.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: P41 9383  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 213-622-7700  
TELEFAX: 213-489-4210  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4085 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 370..3912  
OTHER INFORMATION: /product= "HUMAN MGLUR5A"  
US-08-072-574-7

Query Match 15.4%; Score 171; DB 1; Length 4085;  
Best Local Similarity 98.8%; Pred. No. 1.6e-76;  
Matches 421; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

461 TAGCCATTGAGTCCAGAAATTTGCTCCAGCTTTTCAACATACCTAGATTGCTTACTGAG 520  
830 TAGCCATTGAGTCCAGAAATTTGCTCCAGCTTTTCAACATACCTAGATTGCTTACTGAG 889  
521 CAACCATGATGATCTGATGACAGAACTCTGTTCAAAATATTTTCATGAGGGTTGTGCTT 580

Db 890 CAACGACATGATCTGATGACAGACTCTGTTCAAAATTTTCATGAGGGTTGCTT 949  
QY 581 CAGATGCTGACGAGGAGGTCATGCTGAGCATAGTGAAGAGTCACTGACCTATG 640  
Db 950 CAGATGCTGACGAGGAGGTCATGCTGAGCATAGTGAAGAGTCACTGACCTATG 1009  
QY 641 TATCAGCCGTACACAGAGGCACTATGAGAAAGTGGATGGAAGCTTCAAGATA 700  
Db 1010 TATCAGCCGTGACACAGAGGCACTATGAGAAAGTGGATGGAAGCTTCAAGATA 1069  
QY 701 TGTGACGGAAGAGGATTTGATGAGCCCACTCTTCAAAATCTACAGTAATGACAGGG 760  
Db 1070 TGTGACGGAAGAGGATTTGATGAGCCCACTCTTCAAAATCTACAGTAATGACAGGG 1129  
QY 761 AGCAGAGCTTTGATAGCTGCTGAGAGGCTCAAGTCACTTGGCCCAAGCCCGGCTG 820  
Db 1130 AGCAGAGCTTTGATAGCTGCTGAGAGGCTCAAGTCACTTGGCCCAAGCCCGGCTG 1189  
QY 821 TGCCCTACTTCTGTGAGGCGATGACGGTGAAGAGTCTGTATGAGCCATGAGCGCTG 880  
Db 1190 TGCCCTACTTCTGTGAGGCGATGACGGTGAAGAGTCTGTATGAGCCATGAGCGCTG 1249  
QY 881 GTCTAG 886  
Db 1250 GTCTAG 1255

RESULT 14  
US-08-486-270-7  
Sequence 7, Application US/08486270  
Patent No. 5807689  
GENERAL INFORMATION:  
APPLICANT: Daggett, Lottie  
APPLICANT: Ellis, Steven B.  
APPLICANT: Liaw, Chen  
APPLICANT: Pontsler, Aaron  
APPLICANT: Johnson, Edwin C.  
APPLICANT: Hess, Stephen D.  
TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,  
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME AND USES THEREOF  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
STREET: 444 South Flower Street, Suite 2000  
CITY: Los Angeles  
STATE: CA  
COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,270  
FILING DATE: 02-JUN-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/072,574  
FILING DATE: 04-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen E.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: FP41 9772  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-546-4737  
TELEFAX: 619-546-9392  
INFORMATION FOR SEQ. ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4085 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both

MOLUCULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 370..3912  
OTHER INFORMATION: /product= "HUMAN MGLUR5A"  
US-08-486-270-7  
Query Match 15.4%; Score 171; DB 1; Length 4085;  
Best Local Similarity 98.8%; Pred. No. 1.6e-76;  
Matches 421; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 461 TAGCCATTGAGGTCAGAAATTTGCTCAGCTTTTCAAACTACTGATGCTTACTAG 520  
Db 830 TAGCCATTGAGGTCAGAAATTTGCTCAGCTTTTCAAACTACTGATGCTTACTAG 889  
QY 521 CAACCATGATGATCTGAGTGAACAAGACTCTGTGTAATTTTCATGAGGTTGCTT 580  
Db 890 CAACCATGATGATCTGAGTGAACAAGACTCTGTGTAATTTTCATGAGGTTGCTT 949  
QY 581 CAGATGCTGACGAGGAGGTCATGCTGAGCACTATGAGAAAGTGAAGCTTCAAGCTATG 640  
Db 950 CAGATGCTGACGAGGAGGTCATGCTGAGCACTATGAGAAAGTGAAGCTTCAAGCTATG 1009  
QY 641 TATCAGCCGTACACAGAGGCACTATGAGAAAGTGGATGGAAGCTTCAAGATA 700  
Db 1010 TATCAGCCGTGACACAGAGGCACTATGAGAAAGTGGATGGAAGCTTCAAGATA 1069  
QY 701 TGTGACGGAAGAGGATTTGATGAGCCCACTCTTCAAAATCTACAGTAATGACAGGG 760  
Db 1070 TGTGACGGAAGAGGATTTGATGAGCCCACTCTTCAAAATCTACAGTAATGACAGGG 1129  
QY 761 AGCAGAGCTTTGATAGCTGCTGAGAGGCTCAAGTCACTTGGCCCAAGCCCGGCTG 820  
Db 1130 AGCAGAGCTTTGATAGCTGCTGAGAGGCTCAAGTCACTTGGCCCAAGCCCGGCTG 1189  
QY 821 TGCCCTACTTCTGTGAGGCGATGACGGTGAAGAGTCTGTATGAGCCATGAGCGCTG 880  
Db 1190 TGCCCTACTTCTGTGAGGCGATGACGGTGAAGAGTCTGTATGAGCCATGAGCGCTG 1249  
QY 881 GTCTAG 886  
Db 1250 GTCTAG 1255

RESULT 15  
US-08-367-264-7  
Sequence 7, Application US/08367264  
Patent No. 6001581  
GENERAL INFORMATION:  
APPLICANT: Daggett, Lottie  
APPLICANT: Ellis, Steven B.  
APPLICANT: Liaw, Chen  
APPLICANT: Pontsler, Aaron  
APPLICANT: Johnson, Edwin C.  
APPLICANT: Hess, Stephen D.  
TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,  
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME AND USES THEREOF  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
STREET: 444 South Flower Street, Suite 2000  
CITY: Los Angeles  
STATE: CA  
COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/367,264  
FILING DATE: 02-JUN-1994

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/072,574  
FILING DATE: 04-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen E.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: FP41 9772  
TELEPHONE: 619-546-4737  
TELEFAX: 619-546-9392  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4085 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 370..3912  
OTHER INFORMATION: /product= "HUMAN MGURSA"  
US-08-367-264-7

Query Match 15.4%; Score 171; DB 3; Length 4085;  
Best Local Similarity 98.8%; Pred. No. 1.6e-76;  
Matches 421; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY	461	TAGCCATTGAGTTCAGAGATTGCTCCAGCTTTCAACATACCTCAGATTGCTTACTCAG	520
DB	830	TAGCCATTGAGTTCAGAGATTGCTCCAGCTTTCAACATACCTCAGATTGCTTACTCAG	889
QY	521	CAACCATCATGATCTGATGACAGACTGCTTCAATATTTGATGAGGGTTGCTT	580
DB	890	CAACCATCATGATCTGATGACAGACTGCTTCAATATTTGATGAGGGTTGCTT	949
QY	581	CAGATGCTCAGCAGGCAAGGTCATGCTGACATAGTGAAGAGGTACACTGACCTATG	640
DB	950	CAGATGCTCAGCAGGCAAGGTCATGCTGACATAGTGAAGAGGTACACTGACCTATG	1009
QY	641	TATCAGCCGTACACACAGAAAGCACTATGAGAAAGTGAGTGAAGCCTTCAGAGATA	700
DB	1010	TATCAGCCGTACACACAGAAAGCACTATGAGAAAGTGAGTGAAGCCTTCAGAGATA	1069
QY	701	TGTCAGGAGAGAAAGGATTGCAATGCCCCCACTCTTACAAATCTACAGTAATGCAAGGG	760
DB	1070	TGTCAGGAGAGAAAGGATTGCAATGCCCCCACTCTTACAAATCTACAGTAATGCAAGGG	1129
QY	761	AGCAGAGCTTGTAAAGCTGCTGAAGAAGCTCAAGTCACTTGCCCAAGGCCGGGTGG	820
DB	1130	AGCAGAGCTTGTAAAGCTGCTGAAGAAGCTCAAGTCACTTGCCCAAGGCCGGGTGG	1189
QY	821	TGGCCTACTTCTGTGAGGGCATGACGGTGAAGAGGTCTGCTGATGGCCATGAGGGCCTGG	880
DB	1190	TGGCCTACTTCTGTGAGGGCATGACGGTGAAGAGGTCTGCTGATGGCCATGAGGGCCTGG	1249
QY	881	GTCTAG 886	
DB	1250	GTCTAG 1255	

Search completed: December 14, 2003, 15:19:15  
Job time: 75.2844 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 14, 2003, 18:02:28 ; Search time 2532.22 Seconds  
(without alignments)  
10653.868 Million cell updates/sec

Title: US-10-027-923-3

Perfect score: 1110

Sequence: 1 atgagcctcctgtgctcct.....tgaggacagcctcatctaa 1110

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 22781392 seqs, 1215238056 residues

Word size : 0

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Listing first 45 summaries

Database :  
EST:  
1: em\_estba:\*  
2: em\_estbm:\*  
3: em\_estin:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
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12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_ges\_hum:\*  
18: em\_ges\_hnv:\*  
19: em\_ges\_pln:\*  
20: em\_ges\_vrt:\*  
21: em\_ges\_fun:\*  
22: em\_ges\_mam:\*  
23: em\_ges\_mus:\*  
24: em\_ges\_pro:\*  
25: em\_ges\_rtd:\*  
26: em\_ges\_phg:\*  
27: em\_ges\_vrt:\*  
28: gb\_ges1:\*  
29: gb\_ges2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	499	45.0	499	10	BE467477 h266d08.x
2	489	44.1	519	10	BE674422 7e01a04.x
3	412	37.1	442	9	AM015382 ur-H-B10-
4	384	34.6	414	10	BG150163 nad46b03.

Result No.	Score	Query Match	Length DB	ID	Description
5	347	31.3	449	14	CB153433 K-EST0210
6	209	18.8	515	13	BX280403
7	141	12.7	392	14	BX280403
8	131	11.8	1297	11	BC031602
9	113	10.2	664	12	B1826234
10	102	9.2	268	14	F05449
11	94	8.5	516	13	BX282658
12	73	6.6	456	9	AT201184
13	66	5.9	667	29	AC046849
14	59	5.3	682	10	BG695213
15	59	5.3	3879	11	AK032422
16	48	4.3	649	29	AC052404
17	43	3.9	715	10	B275390
18	43	3.9	742	12	B1093942
19	43	3.9	806	10	B125311
20	43	3.9	871	10	B8993553
21	43	3.9	888	13	B0154755
22	40	3.6	608	28	AQ376196
23	40	3.6	647	10	B8625841
24	40	3.6	661	14	BY721282
25	40	3.6	1013	13	BQ070358
26	34	3.1	409	28	AQ227301
27	27	3.0	507	10	BG187881
28	30	2.7	532	29	B2930457
29	29	2.6	463	28	AQ228293
30	28	2.5	960	10	BG335390
31	27	2.4	229	29	B2914334
32	27	2.4	997	10	BF025698
33	26	2.3	450	28	AQ471966
34	24	2.2	657	13	B0351729
35	24	2.2	669	13	B0393781
36	24	2.2	673	13	B0390603
37	23	2.1	746	10	AW941949
38	21	1.9	419	14	CA026495
39	21	1.9	480	13	BX279584
40	21	1.9	599	10	B8922880
41	21	1.9	629	10	BE409094
42	21	1.9	643	28	BH467481
43	21	1.9	700	28	AQ325894
44	21	1.9	1201	13	BX358386
45	20	1.8	231	9	AA339052

## ALIGNMENTS

RESULT 1  
LOCUS BE467477 499 bp mRNA linear EST 27-JUL-2000  
DEFINITION h266d08.x1 NCI\_CGAP\_Lu24 Homo sapiens CDNA clone IMAGE:3212943 3'  
similar to SW:MG95\_HUMAN PA1594 METABOTROPIC GLUTAMATE RECEPTOR 5  
PRECUSOR. /, mRNA sequence.

ACCESSION BE467477  
VERSION BE467477.1 GI:9513252

KEYWORDS EST.  
ORGANISM Homo sapiens (human)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 499)

NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
Tissue Procurement: Christopher Mokaluk, M.D., Ph.D., Michael R.  
Zimmer-Buck, M.D., Ph.D.

## JOURNAL COMMENT

CDNA Library Preparation: M. Bento Soares, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CCGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL, send email to:

InfoImage.lnl.gov  
Seq primer: -40UP from Gibco  
High quality sequence stop: 493.  
Location/Qualifiers

## FEATURES

source  
1. 499  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3212943"  
/issue\_type="carcinoid"  
/lab\_host="DH10B"  
/clone\_1lb="NCI CGAP Lu24"  
/note="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI CGAP Lu5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonoids 141920-1417991 and 1520904-1522439). Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 141 a 107 c 138 g 113 t  
ORIGIN

Query Match 45.0%; Score 499; DB 10; Length 499;  
Best Local Similarity 100.0%; Pred. No. 3,1e-234;  
Matches 499; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 497 ACATACCTGAGATTGCTTACTCAGCAACATCATGATCTGATGACAGACTCTGTTC A 556  
DB 1 ACATACCTGAGATTGCTTACTCAGCAACATCATGATCTGATGACAGACTCTGTTC A 60  
QY 557 AATATTTCAGAGGTTGCTTCTCAGATGCTCAGCGAGGAGGTCATGCTGACACTAG 616  
DB 61 AATATTTCAGAGGTTGCTTCTCAGATGCTCAGCGAGGAGGTCATGCTGACACTAG 120  
QY 617 TGAAGAGTCAACTGAGACCTATGATCAGCCGTCACACAGAAAGCACTATGAGAAA 676  
DB 121 TGAAGAGTCAACTGAGACCTATGATCAGCCGTCACACAGAAAGCACTATGAGAAA 180  
QY 677 GTGGAGTGAAGGCTTCAAGATATGTCAGCGAAGAAAGGATTTGATGCCCACTTT 736  
DB 181 GTGGAGTGAAGGCTTCAAGATATGTCAGCGAAGAAAGGATTTGATGCCCACTTT 240  
QY 737 ACAAAATCTTCAGTAATGCGAGGAGCAAGCTTTGATTAAGCTGCTGAAGAAGTCA 796  
DB 241 ACAAAATCTTCAGTAATGCGAGGAGCAAGCTTTGATTAAGCTGCTGAAGAAGTCA 300  
QY 797 GTCACTTGCCCAAGGCGCGGGTGGCTTACTTCTGTGAGGGGATGACGGTGAAGGTC 856  
DB 301 GTCACTTGCCCAAGGCGCGGGTGGCTTACTTCTGTGAGGGGATGACGGTGAAGGTC 360  
QY 857 TGGTGAATGCGCATGAGGCGCTGGGTCTAGTGGAGAAATTTCTGCTTCTGGGACGGGAC 916  
DB 361 TGGTGAATGCGCATGAGGCGCTGGGTCTAGTGGAGAAATTTCTGCTTCTGGGACGGGAC 420  
QY 917 CAGATGCGATCTTTATGAGATCTCAAGAAACAGATCTTATGAGAAAGCAAGAAAT 976  
DB 421 CAGATGCGATCTTTATGAGATCTCAAGAAACAGATCTTATGAGAAAGCAAGAAAT 480  
QY 977 GCCAAGTGGCTTCTCTCA 995  
DB 481 GCCAAGTGGCTTCTCTCA 499

RESULT 2  
BE674422 519 bp mRNA linear EST 08-SEP-2000  
LOCUS BE674422  
DEFINITION 7e0104.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3281166 3.  
ACCESSION BE674422  
VERSION BE674422.1 GI:10034963

KEYWORDS  
SOURCE  
ORGANISM

## REFERENCE

1 (bases 1 to 519)  
NCI CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: cgaaps-rc@mail.nih.gov  
Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL, send email to:  
InfoImage.lnl.gov  
Seq primer: -40UP from Gibco  
High quality sequence stop: 499.  
Location/Qualifiers

## FEATURES

source  
1. 519  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3281166"  
/issue\_type="carcinoid"  
/lab\_host="DH10B"  
/clone\_1lb="NCI CGAP Lu24"  
/note="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI CGAP Lu5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonoids 141920-1417991 and 1520904-1522439). Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 143 a 114 c 143 g 119 t  
ORIGIN

Query Match 44.1%; Score 489; DB 10; Length 519;  
Best Local Similarity 100.0%; Pred. No. 2,6e-225;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 508 ATTGCTTACTCAGCAACATCATGATCTGATGACAAAGCTCTGTTCAATTTTCATG 567  
DB 31 ATTGCTTACTCAGCAACATCATGATCTGATGACAAAGCTCTGTTCAATTTTCATG 90  
QY 568 AGGGTTGCTTCAAGTCTCAGCAGCGAAGGTCATGCTGAGCAATGTAAGAGCTAC 627  
DB 91 AGGGTTGCTTCAAGTCTCAGCAGCGAAGGTCATGCTGAGCAATGTAAGAGAGTAC 150  
QY 628 AACTGACCTATGATCAAGCCGTCACACAGAAAGCACTATGAGAAAGTGGAGTGA 687  
DB 151 AACTGACCTATGATCAAGCCGTCACACAGAAAGCACTATGAGAAAGTGGAGTGA 210  
QY 688 GCCTCAAGATATGTCAGCGAAGAGGATTTGATGCGCCCACTTTCAAAATCTAC 747  
DB 211 GCCTCAAGATATGTCAGCGAAGAGGATTTGATGCGCCCACTTTCAAAATCTAC 270  
QY 748 AGTAATGACAGGGAGAGAGCTTTGATTAAGCTGCTGAAGAGTCAAGATCACTTGC 807  
DB 271 AGTAATGACAGGGAGAGAGCTTTGATTAAGCTGCTGAAGAGTCAAGATCACTTGC 330  
QY 808 AAGGCGGCGGTGCTGCTTCTGATGAGGAGTACAGCTGAGAGTCTGCTGATGAGGC 867  
DB 331 AAGGCGGCGGTGCTGCTTCTGATGAGGAGTACAGCTGAGAGTCTGCTGATGAGGC 390  
QY 868 ATGAGCGCTGGGTCTAGTGGAGAAATTTGCTTCTGGGAGGAGCAAGATGCGATC 927



Db 391 ATAGAGCGCTGCTCTAGTGGAGAAATTTCTGCTTCTGGCAGGGAACCATGCCATC 450  
 Qy 928 TTTATTGAGATCTCAAGACAGCATCTTATGGGAGACAGAAAGAAATGCCAAGTCGC 987  
 Db 451 TTTATTGAGATCTCAAGACAGCATCTTATGGGAGACAGAAAGAAATGCCAAGTCGC 510  
 Qy 988 TTCTCTCAG 996  
 Db 511 TTCTCTCAG 519

RESULT 3  
 AMO15382 442 bp mRNA linear EST 10-SEP-1999  
 LOCUS UI-H-Bio-aat-d-06-0-UI-s1 NCI CGAP\_Sub1 Homo sapiens cDNA clone  
 DEFINITION IMAGE:2710331.3', mRNA sequence.  
 AMO15382.1 GI:5864139  
 VERSION EST.  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 REFERENCE 1 (bases 1 to 442)  
 AUTHORS NCI CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
 JOURNAL Unpublished  
 COMMENT Contact: Robert Straubeberg, Ph.D.  
 Email: cga@bbs-remail.nih.gov  
 0190-dt track not found, Not 1 site shown in beginning of sequence is likely internal to the message. cDNA library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution  
 Information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bdrp/image/image.html  
 Seg primer: M13 Forward  
 POLYA=No.

FEATURES  
 source  
 1..442  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2710331"  
 /lab\_host="DH10B (Life Technologies)"  
 /clone\_1lb="NCI CGAP Sub1"  
 /note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker, Site 1: Not I; Site 2: Eco RI; The NCI CGAP Sub1 library is a subtracted library derived from B1. B1 constitutes a mixture of 21 normalized or subtracted NCI CGAP libraries: NCI CGAP C04, NCI CGAP Pr22, NCI CGAP Pr28, NCI CGAP C010, NCI CGAP C016, NCI CGAP K1d5, NCI CGAP K1d12, NCI CGAP K1d3, NCI CGAP K1d11, NCI CGAP Lym2, NCI CGAP Br2, NCI CGAP C08, NCI CGAP C1d1, NCI CGAP Lym2, NCI CGAP Br23, NCI CGAP Lys, NCI CGAP Lys24, NCI CGAP Lys9, NCI CGAP G04, NCI CGAP G06, NCI CGAP Brn25. These 21 libraries were pooled and a single-stranded DNA preparation of the resulting mixture was used as a tracer in a subtractive hybridization with a driver whose composition is detailed below: NCI CGAP K1d3 pool 1 LAM 3334-3337, 3682-3683, 3798-3803 (IMAGE Cloneids 1322376-1323911, 1456008-1456775, 1500552-1502855) NCI CGAP K1d5 pool 1 LAM 3338-3342, 3752-3755, 3776-3778 (IMAGE Cloneids 1322912-1325831, 1471368-1472903, 1492104-1493253) NCI CGAP Lys pool 1 LAM 3575-3582, 3851-3854 (IMAGE Cloneids 1414920-1417991, 1520904-1522439) NCI CGAP G04 pool 1 LAM 3164-3167, 3716-3720, 3733-3735 (IMAGE Cloneids 1257096-1258631, 1469064-1470983, 1475592-1476743) NCI CGAP Pr22 pool 1 LAM 2457-2459, 2758-2759, 3062-3068 (IMAGE Cloneids 955608-986759, 1101192-1101959, 1217928-1220615) NCI CGAP C010 pool 1 LAM 2644-2653, 2871-2872 (IMAGE Cloneids 1057416-1061255, 1144584-1145551) The resulting subtracted library contained 530,000 recombinants.

Subtraction was performed as previously described [Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806.  
 TAG LIB=NCI CGAP Le12  
 TAG TISSUE=lelomyosarcoma  
 TAG\_SEQ=AAATCG"

BASE COUNT 118 a 97 c 127 g 100 t

ORIGIN

Query Match 37.1%; Score 412; DB 9; Length 442;  
 Best Local Similarity 100.0%; Pred. No. 2e-191;  
 Matches 412; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 486 CCAGCTTTCAACATACCTTCAGATTGCTTACTGACACACATCATGATGATGACAA 545  
 Db 7 CCAGCTTTCAACATACCTTCAGATTGCTTACTGACACACATCATGATGATGACAA 66  
 Qy 546 GACTGTGTCAAATATTTATGATGAGGGTGTGCTTCAGATGCTCAGCAGGCAAGTTCAT 605  
 Db 67 GACTGTGTCAAATATTTATGATGAGGGTGTGCTTCAGATGCTCAGCAGGCAAGTTCAT 126  
 Qy 606 GGTGACATATGTAAGAGGTACACTGACCTATGATACAGCGTACACAGAGGCAA 665  
 Db 127 GGTGACATATGTAAGAGGTACACTGACCTATGATACAGCGTACACAGAGGCAA 186  
 Qy 666 CTATGAGAAAGTGGAGTGAAGGCTTCAAGATATGTCAGCGAAGAGGATTTGCAT 725  
 Db 187 CTATGAGAAAGTGGAGTGAAGGCTTCAAGATATGTCAGCGAAGAGGATTTGCAT 246  
 Qy 726 CGCCCACTTTCAAAATATTAAGTAATGACAGGAGGAGGACCTTTGAATACCTGTGAA 785  
 Db 247 CGCCCACTTTCAAAATATTAAGTAATGACAGGAGGAGGACCTTTGAATACCTGTGAA 306  
 Qy 786 GAAGTCACTCACTGCTGAGCCCAAGGCCCGGGTGTGCTTCTGTGAGGGCATGAC 845  
 Db 307 GAAGTCACTCACTGCTGAGCCCAAGGCCCGGGTGTGCTTCTGTGAGGGCATGAC 366  
 Qy 846 GGTGAGAGTCTGCTGATGAGCCATGAGCGCTGTGCTTATGGAGAAATTT 897  
 Db 367 GGTGAGAGTCTGCTGATGAGCCATGAGCGCGCTGTGCTTATGGAGAAATTT 418

RESULT 4  
 BG150163 414 bp mRNA linear EST 05-FEB-2001  
 LOCUS nad46b03.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3368404.3'  
 DEFINITION similar to SW:MG85\_HUMAN P41594 METABOTROPIC GLUTAMATE RECEPTOR 5-  
 PRECURSOR. [1]', mRNA sequence.  
 BG150163 GI:12662193  
 VERSION EST.  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 REFERENCE 1 (bases 1 to 414)  
 AUTHORS NCI CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
 JOURNAL Unpublished  
 COMMENT Contact: Robert Straubeberg, Ph.D.  
 Email: cga@bbs-remail.nih.gov  
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmer-Buck, M.D., Ph.D.  
 cDNA library Prepared by: Greg Lennon, Ph.D.  
 cDNA library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov  
 Seg primer: -40bp from Gibco  
 High quality sequence stop: 354.

FEATURES  
source

Location/Qualifiers

1. 414  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3368404"  
/tissue\_type="carcinoid"  
/lab\_host="DH10B"  
/clone\_1lb="NCI\_CGAP\_Lu24"  
/note="Organ: lung; Vector: pT7TD-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI CGAP Lu2 was prepared, and ss circles were made in vitro. Following RAP purification, this DNA was used as tracer in a subtracted hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneids 1414920-1417991 and 1520904-1522439). Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT  
ORIGIN

Query Match 34.6%; Score 384; DB 10; Length 414;  
Best Local Similarity 100.0%; Pred. No. 1.2e-177;  
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

502 CCTCAGATTGCTTACCTGACCAACATGATGATGACAGACCTGTTCAATAT 561  
25 CCTCAGATTGCTTACCTGACCAACATGATGATGACAGACCTGTTCAATAT 84  
562 TTCTAGAGGGTGGCTTCAGATGCTCAGACGAGGATCCATGATGACATAGTAA 621  
85 TTCTAGAGGGTGGCTTCAGATGCTCAGACGAGGATCCATGATGACATAGTAA 144  
622 AGGTACACTGACCTATGATATCAGCCGTACACACAGAGGCACTATGAGAAAGTGG 681  
145 AGGTACACTGACCTATGATATCAGCCGTACACACAGAGGCACTATGAGAAAGTGG 204  
682 ATGGAACCTTCAAGATATGTCAGGAGGAGGATTTGCACTGGCCACTTACAA 741  
205 ATGGAACCTTCAAGATATGTCAGGAGGAGGATTTGCACTGGCCACTTACAA 264  
742 ATCTACAGTATGACGAGGAGCAGAGCTTGTATAGTGTGTAAGAGTCTACAACTAC 801  
265 ATCTACAGTATGACGAGGAGCAGAGCTTGTATAGTGTGTAAGAGTCTACAACTAC 324  
802 TTGCCCCAAGGCCCGGTGGTCTTCTGTGAGGCGCATGACGCTGAGAGTCTGCTG 861  
325 TTGCCCCAAGGCCCGGTGGTCTTCTGTGAGGCGCATGACGCTGAGAGTCTGCTG 384  
862 ATGGCCATGAGGCGCGCTGGGCTCA 885  
385 ATGGCCATGAGGCGCGCTGGGCTCA 408

## RESULT 5

CB153433

LOCUS CB153433 449 bp mRNA linear EST 29-JAN-2003  
DEFINITION K-EST0210877 B1T694954 Homo sapiens cDNA clone B1T694954-28-C09 5',  
mRNA sequence.

ACCESSION

CB153433

VERSION

CB153433.1

KEYWORDS

EST.

SOURCE

ORGANISM

Homo sapiens (human)

REFERENCE

ATTNORS

TITLE

JOURNAL

COMMENT

Contact: Kim YS

FEATURES  
source

Genome Research Center  
Korea Research Institute of Bioscience & Biotechnology  
52 Beom-dong Yuseong-gu, Daejeon 305-333, South Korea  
Tel: +82-42-860-4470  
Fax: +82-42-860-4409  
Email: yongsung@mail.kribb.re.kr  
Plate: 28 row: C column: 09  
High quality sequence stop: 449.

Location/Qualifiers

1. 449

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="B1T694954-28-C09"

/sex="M"

/lab\_host="Top10P"

/clone\_1lb="B1T694954"

/note="Organ: Brain; Vector: pcNS-D2; Site 1: EcoRI; Site 2: NotI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then dephosphorylated with tobacco acid pyrophosphatase (TAP). The dephosphorylated mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of 14 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10P by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

BASE COUNT  
ORIGIN

Query Match 31.3%; Score 347; DB 14; Length 449;  
Best Local Similarity 99.6%; Pred. No. 2e-159;  
Matches 447; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

120 CTTTCTGTTTCATCAGCCTTACTGTGACGAGTTTCATGAGAGAGTGTGGGCACT 179  
1 CTTTCTGTTTCATCAGCCTTACTGTGACGAGTTTCATGAGAGAGTGTGGGCACT 60  
180 CCGTGAACAGTATGAGATTCAGAGGTGAGAGGCGATGACCTGGAAGATCA 239  
61 CCGTGAACAGTATGAGATTCAGAGGTGAGAGGCGATGACCTGGAAGATCA 120  
240 TTGAGACCCACACTCTTGCCCAACATCACTGAGGCTGTGAGATTAAGGATTCCTGCTG 299  
121 TTGAGACCCACACTCTTGCCCAACATCACTGAGGCTGTGAGATTAAGGATTCCTGCTG 180  
300 GCATTGGCTGTGGCCCTTGAAGAGCAATGAGTTCAATAGATTCCTCATTTCTTC 359  
181 GCATTGGCTGTGGCCCTTGAAGAGCAATGAGTTCAATAGATTCCTCATTTCTTC 240  
360 GGAAGAGAGAGAGGCTTGGTATGCTCTGTGATGAGTGGCTCTCTCTCTCCGCTCCAA 419  
241 GGAAGAGAGAGAGGCTTGGTATGCTCTGTGATGAGTGGCTCTCTCTCTCCGCTCCAA 300  
420 GAAGCCATAGTATGAGGATCATTTGGGCTGTGATGAGTGGCTCTCTCTCTCCGCTCCAA 479  
301 GAAGCCATAGTATGAGGATCATTTGGGCTGTGATGAGTGGCTCTCTCTCTCCGCTCCAA 360  
480 TTGCTCCAGCTTTTCAACATACCTGAGATTGCTTACTGACCAACATCATCATGATCTGAG 539  
361 TTGCTCCAGCTTTTCAACATACCTGAGATTGCTTACTGACCAACATCATCATGATCTGAG 420  
540 TGACAGACTCTGTTCAATATTTTCATGA 568  
421 TGACAGACTCTGTTCAATATTTTCATGA 449

	RESULT 6
LOCUS	BX280403/c
DEFINITION	BX280403 NC1 CGAP Lu24 Homo sapiens cDNA clone IMAGE998A078034 ; IMAGE:3281166, mRNA sequence.
ACCESSION	BX280403
VERSION	BX280403.1 GI:28612394
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 515) Ebert,L., Hell,O., Hennig,S., Neubert,P., Paratch,E., Peters,M., Radelof,U., Schneider,D. and Korn,B. Human Unigeneset - RZPD3 Unpublished
TITLE	Contact: Ina Rolfs
JOURNAL	RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany RZPD; IMAGP998A078034. RZPDLIB; I.M.A.G.E. CDNA Clone Collection; Human Unigeneset - RZPD3 (RZPDLIB No.972) <a href="http://www.rzpd.de/CldoneCards/cgi-bin/showlib.pl.cgi/response?libNo=972">http://www.rzpd.de/CldoneCards/cgi- bin/showlib.pl.cgi/response?libNo=972</a> Contact: Ina Rolfs RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Heidenberg 6, D-14059 Berlin, Germany Tel.: +49 30 32639 101 Fax: +49 30 32639 111 <a href="http://www.rzpd.de">www.rzpd.de</a>
FEATURES	This clone is available royalty-free from RZPD; contact RZPD ( <a href="mailto:clone@rzpd.de">clone@rzpd.de</a> ) for further information. Seq primer: M13r, Primer sequence: TTTCACACAGGAAACAGCTATGAC. Location/Qualifiers 1..515 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGP998A078034 ; IMAGE:3281166" /tissue_type="carcinoid" /lab_host="DH10B" /clone_lib="NCI CGAP Lu24" /note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP Lu24 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 141920-1417991 and 1520904-1522439). Subtraction by Bencitc Soares and M. Fatima Bonaldo." 2 others
BASE COUNT	137 a 138 c 105 g 133 t
ORIGIN	
Query Match	18.8%; Score 209; DB 13; Length 515;
Best Local Similarity	100.0%; Pred. No. 1,8e-91;
Matches	209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy	TTCTGGGAGGGAACAGATGCATTATTAGATCCAAAGAACGATCCTATGGG 961
Dd	TTCTGGGAGGGAACCAATGTCATTATTAGATCTCAAAGAACCAGATCCTATGGG 407
Oy	AAGACAGAAAGAAATGCCAAGGTGGCTTCCTTCAGGGTTTTGGAGACAATTATTAACAGAAA 1021
Dd	AAGACAGAAAGAAATGCCAAGGTGGCTTCCTTCAGGGTTTTGGAGACAATTATTAACAGAAA 347
Oy	GTTGAGTCCGTCGTCGTGACACAAGCCCCCAGCCCTCTGAATCTTAGAGCTCAGTTCAAGGCCCA 1081
Dd	GTTGAGTCCGTCGTCGTGACACAAGCCCCCAGCCCTCTGAATCTTAGAGCTCAGTTCAAGGCCCA 287
Oy	TTACTGAGACTGAGGACAGGCTCATCTTAA 1110
Dd	TTACTGAGACTGAGGACAGGCTCATCTTAA 258

LOCUS	78107	392 bp	mRNA	linear	EST 07-MAR-1995
DEFINITION	yc8ba01.r1 Soares infant brain IN1B Homo sapiens cDNA clone IMAGE:23998 5' similar to SP-JC2132 JC2132 METABOTROPIC GLUTAMATE RECEPTOR 5 A - ; mRNA sequence.				
ACCESSION	78107				
VERSION	78107.1	GI:696616			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 (bases 1 to 392)				
AUTHORS	Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Matra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,P., Trevaekis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.				
TITLE	The Washu-Merck EST project				
JOURNAL	Unpublished				
COMMENT	Contact: Wilson RK Washington University School of Medicine 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@wustl.wustl.edu High quality sequence stops: 204 Source: IMAGE Consortium, LML This clone is available royalty-free through LML; contact the IMAGE Consortium (info@image.lml.gov) for further information. Seq primer: M13RPI High quality sequence stop: 204. Location/Qualifiers 1..392 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="GDB:396345" /db_xref="taxon:9606" /clone="IMAGE:23998" /sex="female" /dev_stage="73 days post natal" /lab_host="DH10B (ampicillin resistant)" /clone_lib="Soares infant brain IN1B" /note="Organ: whole brain; Vector: Lactid BA; Site_1: Not I; Site_2: Hind III; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' AAGCGAAGAAATCGCGCGCGCGAATTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Hind III adaptors (Pharmacia), digested with Not I and directionally cloned into the Not I and Hind III sites of the Lactid BA vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."				
BASE COUNT	85 a 96 c 95 g 108 t				
ORIGIN					
Query Match	12.7%; Score 141; DB 14; Length 392;				
Best Local Similarity	100.0%; Pred. No. 4.8e-58;				
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	461 TAGCCATTGAGGTCCAGAAATTTGCTCCAGCTTTTCAACATTAAGTTCAGTTCAG 520				
DB	74 TAGCCATTGAGGTCCAGAAATTTGCTCCAGCTTTTCAACATTAAGTTCAGTTCAG 133				
QY	521 CAACCATCATGATCTAGTGAACAAGACTGCTGTAATATTTTCATGAGGGTTGTCCT 580				
DB	134 CAACCATCATGATCTAGTGAACAAGACTGCTGTAATATTTTCATGAGGGTTGTCCT 193				
QY	581 CAGATGCTCAGCAGCAAGGT 601				
DB	194 CAGATGCTCAGCAGCAAGGT 214				

RESULT 8  
BC031602  
LOCUS BC031602 1297 bp mRNA linear HTC 04-MAR-2003  
DEFINITION Homo sapiens, clone IMAGE:5167902, mRNA.  
ACCESSION BC031602  
VERSION BC031602.1 GI:21594893  
KEYWORDS HTC.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 1297)  
AUTHORS Strausberg, R.  
TITLE Direct Submission  
JOURNAL Submitted (06-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
COMMENT Contact: GAGS help desk  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
Tissue Procurement: Life Technologies, Inc.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center  
Center code: BCM-HGSC  
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>  
Contact: [amg@bcm.tmc.edu](mailto:amg@bcm.tmc.edu)  
Gamarine, P.H., Garcia, A.M., Lu, X., Huiyk, S.W., Louised, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Wazny, D.M., Nanavali, A.N., Gibbs, R.A.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>  
Series: IRAC Plate: 51 Row: a Column: 11  
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4504142  
This clone has the following problem: retained intron.  
Location/Qualifiers  
1. 1297  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5167902"  
/tissue\_type="Brain, adult medulla"  
/clone\_lib="NIH\_MGC\_119"  
/lab\_host="DH10B"  
/note="Vector: PCMV-SPORT6"  
BASE COUNT 343 a 301 c 325 g 328 t  
ORIGIN  
Query Match 11.8%; Score 131; DB 11; Length 1297;  
Best Local Similarity 99.5%; Pred. No. 6.5e-53;  
Matches 181; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 178 GTCCTGAACAGATGATTCAGAGAGTGGAGCCATGCTGATACCTCGAAGAGATC 237  
Db 548 GTCCTGAACAGATGATTCAGAGAGTGGAGCCATGCTGATACCTCGAAGAGATC 607  
QY 238 AATTCAGACCCACACTCTTGCCCAACATCACTGGGCTGTGATTAAGGATTCCTGC 297  
Db 608 AATTCAGACCCACACTCTTGCCCAACATCACTGGGCTGTGATTAAGGATTCCTGC 667  
QY 298 TGGCATTGGCTGTGGCTTGAAGCAGACAGATTGATTCAATTAAGATTCCTCATTTCT 357  
Db 668 TGGCATTGGCTGTGGCTTGAAGCAGACAGATTGATTCAATTAAGATTCCTCATTTCT 727  
QY 358 TC 359  
Db 728 TC 729

RESULT 9  
B1826234  
LOCUS B1826234 664 bp mRNA linear EST 04-OCT-2001  
DEFINITION 603075928F1 NIH\_MGC\_119 Homo sapiens CDNA clone IMAGE:5167902 5', mRNA sequence.  
ACCESSION B1826234  
VERSION B1826234.1 GI:15937784  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 664)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
Tissue Procurement: Life Technologies, Inc.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>  
plate: LLAM1417 row: g column: 07  
High quality sequence scop: 662.  
Location/Qualifiers  
1. 664  
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/mol\_type="mRNA"  
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/clone="IMAGE:5167902"  
/tissue\_type="medulla"  
/lab\_host="DH10B"  
/clone\_lib="NIH\_MGC\_119"  
/note="Organ: brain; Vector: PCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH\_MGC Library."  
BASE COUNT 151 a 177 c 179 g 157 t  
ORIGIN  
Query Match 10.2%; Score 113; DB 12; Length 664;  
Best Local Similarity 100.0%; Pred. No. 3.6e-44;  
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 178 GTCCTGAACAGATGATTCAGAGAGTGGAGCCATGCTGATACCTCGAAGAGATC 237  
Db 547 GTCCTGAACAGATGATTCAGAGAGTGGAGCCATGCTGATACCTCGAAGAGATC 606  
QY 238 AATTCAGACCCACACTCTTGCCCAACATCACTGGGCTGTGATTAAGGATTC 290  
Db 607 AATTCAGACCCACACTCTTGCCCAACATCACTGGGCTGTGATTAAGGATTC 659  
RESULT 10  
F05449  
LOCUS F05449 268 bp mRNA linear EST 19-FEB-1995  
DEFINITION HSC0BC111 normalized infant brain CDNA Homo sapiens CDNA clone c-0bc11, mRNA sequence.  
ACCESSION F05449  
VERSION F05449.1 GI:669265  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 268)  
Auffray, C., Behar, G., Bois, F., Bouchier, C., da Silva, C., Devignes, M.D., Duprat, S., Houlgatte, R., Juneau, M.N., Lamy, B., Lorenzo, F., Mitchell, H., Mariage-Samson, R., Picu, G., Poullot, Y., Sebasticani-Kabitchis, C. and Tessier, A.  
IMAGE: molecular integration of the analysis of the human genome and its expression  
C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)  
95277534  
7757816  
Contact: Genethon  
Genexpress-Genethon  
Genethon Centre de recherche sur le Genome Humain  
1, rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE  
Tel: 33169472800  
Fax: 33160778698  
Email: genexpress@genethon.fr  
Single read.  
Genexpress\_library\_idt: C; Genexpress\_sequence\_idt: y1c-0bc11  
Seq primer: (-21)M13 universal.  
Location/Qualifiers  
1. 268  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="c-0bc11"  
/sex="Female"  
/tissue\_type="total brain"  
/dev\_stage="3 months old"  
/clone\_1b="normalized infant brain cDNA"  
/note="Organ: brain; Vector: lafmid B; Site\_1: HindIII; Site\_2: NotI; sex: Female; dev\_stage=3 months old; isolate=muscular atrophy patient; tissue\_type=total brain; total mRNA was oligo-(dT) primed and directionally cloned 5' -> 3' into the HindIII -> NotI sites of the lafmid BA vector. Clone library from B.Souares, Psychiatry Dept. Columbia University, USA. Normalization\_method: Bento Soares, P.N.A.S in press"  
BASE COUNT  
ORIGIN  
70 a 61 c 69 g 67 t 1 others

Query Match  
Best Local Similarity 100.0%; Pred. No. 6.5e-39;  
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 699 TATGTACGAGGAGGAGGATTCATCGCCCACTTTACAAATCTACAGTATGCAG 758  
DB 167 TATGTACGAGGAGGAGGATTCATCGCCCACTTTACAAATCTACAGTATGCAG 226

QY 759 GGAGCAGAGCTTTGATTAAGCTGCTGAAGAGCTCACAATCA 800  
DB 227 GGAGCAGAGCTTTGATTAAGCTGCTGAAGAGCTCACAATCA 268

RESULT 11  
BX282658  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

BX282658 516 bp mRNA linear EST 04-MAR-2003  
BX282658 NIH MGC 119 Homo sapiens cDNA clone IMAGE:5167902;  
IMAGE:5167902, mRNA sequence.  
BX282658 BX282658.1 GI:26613056  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 516)  
Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M., Radelet, U., Schneider, D. and Korn, B.  
Human Unigeneset - RZPD3  
Unpublished  
Contact: Ina Rolfe

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany  
RZPD, IMAGE99860711417.  
RZPDLIB: I.M.A.G.E. cDNA Clone Collection;  
Human Unigeneset - RZPD3 (RZPDLIB No. 972)  
http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi?response=11DN0972  
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
Heubnerweg 6, D-14059 Berlin, Germany  
Tel: +49 30 32639 101  
Fax: +49 30 32639 111  
www.rzpd.de  
This clone is available royalty-free from RZPD;  
contact RZPD (clone@rzpd.de) for further information. Seq primer:  
M13U. Primer sequence: GCTTGTAAACAGCCGCACT.  
Location/Qualifiers  
1. 516  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE99860711417; IMAGE:5167902"  
/tissue\_type="medulla"  
/lab\_host="DH10B"  
/clone\_1b="NIH MGC 119"  
/note="Organ: brain; Vector: pCMV-SPORT6; Site\_1: NotI; Site\_2: EcoRV (destroyed); RNA source: normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH MGC Library."  
BASE COUNT  
ORIGIN  
110 a 143 c 135 g 128 t

Query Match  
Best Local Similarity 100.0%; Pred. No. 7.3e-35;  
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTCTCTTCTGTGATCTCTGATCTTCTTCTTGAAGAAGATCCGAGAGTGA 60  
DB 371 ATGTCTCTTCTGTGATCTCTGATCTTCTTCTTGAAGAAGATCCGAGAGTGA 430

QY 61 CAGTCCAGTGAAGAGGAGGAGTGTGCTCAATGC 94  
DB 431 CAGTCCAGTGAAGAGGAGGAGTGTGCTCAATGC 464

RESULT 12  
AI201184  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AI201184 456 bp mRNA linear EST 14-OCT-1998  
qf70d05.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1755369  
3' similar to gb:Y00281 RIBOPHORIN I PRECURSOR (HUMAN);, mRNA  
sequence.  
AI201184  
AI201184.1 GI:3753790  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 456)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo  
Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www.bio.lnl.gov/db/ftp/image/image.html](http://www.bio.lnl.gov/db/ftp/image/image.html)

Seq primer: -40UP from Glibco  
High quality sequence stop: 432.

## FEATURES

## source

1. 456  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1755369"  
/sex="male"  
/lab\_host="DH10B"

/clone\_lib="Soares\_testis\_NHT"  
/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - Oligo(dT) primer [5', TGTTACCATCTGAGTGGAGCGGCCCATTTTCTTTTCTTTT 3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization to Cos5, and was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 122 a 100 c 90 g 144 t

## ORIGIN

Query Match 6.6%; Score 73; DB 9; Length 456;  
Best Local Similarity 100.0%; Pred. No. 1.5e-24;  
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 528 CATGATCTGAGGACAACTCTGTCAATATTTCATGAGGTTTGCTTCAGATGC 587  
DB 431 CATGATCTGAGGACAACTCTGTCAATATTTCATGAGGTTTGCTTCAGATGC 372  
QY 588 TCAGCAGGCAAG 600  
DB 371 TCAGCAGGCAAG 359

## RESULT 13

AG046849 667 bp DNA linear GSS 02-NOV-2001  
LOCUS AG046849

DEFINITION Pan troglodytes DNA, clone: PTB-026D03.F, genomic survey sequence.

ACCESSION AG046849.1 GI:16583741

VERSION GSS.

KEYWORDS Pan troglodytes (chimpanzee)

SOURCE

ORGANISM Pan troglodytes (chimpanzee)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.

REFERENCE

AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,  
Toto, Y., Watanabe, H. and Sakaki, Y.

TITLE BAC end sequences of library PTB

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 667)

AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,  
Toto, Y., Watanabe, H. and Sakaki, Y.

TITLE Direct Submission

JOURNAL Submitted (02-NOV-2001) Aaso Fujiyama, The Institute of Physical  
and Chemical Research (RIKEN), Genomic Sciences Center (GSC),  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
(E-mail: [chimbpe@gsc.riken.go.jp](mailto:chimbpe@gsc.riken.go.jp); URL: <http://hsp.gsc.riken.go.jp/>,  
Tel: 81-45-503-9111, Fax: 81-45-503-9170)

COMMENT Clones are derived from the chimpanzee BAC library PTB This BAC end  
was generated during the Rad process and may have higher chance of  
clone tracking errors.

PRIMERS

Sequencing: -21M13  
LIBRARY Vector : PKS145  
R.Site 1 : SacI

R.Site 2 : SacI.  
Location/Qualifiers  
1. 667

## FEATURES

## source

/organism="Pan troglodytes"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9598"  
/clone="PTB-026D03.F"

/cell\_type="lymphoblast"  
/clone\_lib="PTB Chimpanzee Male BAC Library"  
/clone 142 c 158 g 210 t 1 others

BASE COUNT 156 a 142 c 158 g 210 t

## ORIGIN

Query Match 5.9%; Score 66; DB 29; Length 667;  
Best Local Similarity 100.0%; Pred. No. 5e-21;  
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 178 GTCCGTGAACAGTATGATTCAGAGAGTGAAGCCATGTCATACCTGAAAGATC 237  
DB 132 GTCCGTGAACAGTATGATTCAGAGAGTGAAGCCATGTCATACCTGAAAGATC 191  
QY 238 AATTCA 243  
DB 192 AATTCA 197

## RESULT 14

AG695213 682 bp mRNA linear EST 04-MAY-2001

LOCUS AG695213

DEFINITION NISC i431g09.w1 Soares NMBP2 pituitary Mus musculus cDNA clone  
IMAGE:4317880 5', mRNA sequence.

ACCESSION AG695213 GI:13954900

VERSION EST.

KEYWORDS Mus musculus (house mouse)

SOURCE

ORGANISM Mus musculus (house mouse)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 682)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index

JOURNAL Unpublished

COMMENT Contact: Robert Straube, Ph.D.  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
CDNA Library Preparation: M. Bento Soares Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL  
DNA Sequencing by: National Institutes of Health Intramural  
Sequencing Center (NISC)  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>

MG1:1598648  
Plate: L14M9922 row: M column: 17  
Seq primer: T7 primer.  
Location/Qualifiers  
1. 682

## FEATURES

## source

/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
/clone="IMAGE:4317880"  
/issue\_type="pituitary gland"  
/dev\_stage="embryo, 14 dpc"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="Soares NMBP2 pituitary"  
/note="Organ: brain; Vector: pT73D-Pac; Site 1: NotI;  
Site 2: EcoRI; 1st strand cDNA was primed with a NotI -  
oligo(dT) primer  
5'-ACTGGAAGATTCGCGCGCGCGCTTTTCTTTTCTTTT-3';  
double-stranded cDNA was ligated to EcoRI adaptors  
5'-ATTGCGCAGG-3' AND 5'-CTGTGCGG-3' (Pharmacia),  
digested with NotI and cloned into the NotI and EcoRI  
sites of the pT73D-Pac vector. Library went through one

round of normalization, and was constructed in the laboratory of M. Bento Soares (University of Iowa).  
 BASE COUNT 190 a 121 c 162 g 209 t  
 ORIGIN

Query Match 5.3%; Score 59; DB 10; Length 682;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-17;  
 Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 691 TTCGAAGATATGTCAGCGAAGAGGATTTCATGCCCTTTACAAATCTACAG 749  
 Db 142 TTCGAAGATATGTCAGCGAAGAGGATTTCATGCCCTTTACAAATCTACAG 200

RESULT 15  
 AK032422 3879 bp mRNA linear HTC 05-DEC-2002  
 LOCUS  
 DEFINITION Mus musculus adult male olfactory brain cDNA, RIKEN full-length  
 enriched library, clone:6430542K11 product:METABOTROPIC GLUTAMATE  
 RECEPTOR MGLURS PRECURSOR homolog [Rattus norvegicus], full insert  
 sequence.

ACCESSION AK032422  
 VERSION AK032422.1 GI:26082838  
 KEYWORDS HTC; CAP trapper.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM

REFERENCE  
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 Carninci, P. and Hayashizaki, Y.  
 High-efficiency full-length cDNA cloning  
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
 MEDLINE 99279253  
 PUBMED 10349636

REFERENCE  
 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
 Itoh, M., Komoto, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.  
 Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new genes  
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
 MEDLINE 20493374  
 PUBMED 11042159

TITLE  
 JOURNAL  
 MEDLINE  
 PUBMED  
 REFERENCE  
 AUTHORS  
 3 Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P.,  
 Komoto, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M.,  
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,  
 Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,  
 Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M.,  
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,  
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.  
 RIKEN integrated sequence analysis (RISA) system-384-format  
 sequencing pipeline with 384 multicapillary sequencer  
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)  
 MEDLINE 20530913  
 PUBMED 11076861

TITLE  
 JOURNAL  
 MEDLINE  
 PUBMED  
 REFERENCE  
 AUTHORS  
 4 Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,  
 Aizawa, T., Hara, A., Fukunishi, Y., Komoto, H., Adachi, J., Fukuda, S.,  
 Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I.,  
 Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.,  
 Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,  
 Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H.,  
 Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G.,  
 Quackenbush, J., Schriml, L. M., Staudil, F., Suzuki, R., Tomita, M.,  
 Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,  
 Balarelli, R., Barsh, G., Blake, J., Botfield, D., Boujars, N.,  
 Carinci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C.,  
 Fletcher, C., Fujita, M., Gariboldi, M., Guernicchi, S., Hill, D.,  
 Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P.,  
 Marchionni, L., Mashima, U., Mazzarelli, J., Mombaur, P., Nordone, P.,  
 Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,  
 Sato, K., Schobach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H.,  
 Toyooka, K., Wang, K. H., Wetz, C., Whitaker, C., Wilmberg, L.,

Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, H., Kohseki, S.,  
 and Hayashizaki, Y.  
 Functional annotation of a full-length mouse cDNA collection  
 JOURNAL Nature 409 (6821), 685-690 (2001)  
 MEDLINE 21085660  
 PUBMED 11217851

REFERENCE  
 AUTHORS 5 The PANTOM Consortium and the RIKEN Genome Exploration Research  
 Group Phase I & II Team.  
 Analysis of the mouse transcriptome based on functional annotation  
 of 60,770 full-length cDNAs  
 JOURNAL Nature 420, 563-573 (2002)  
 MEDLINE 12108560  
 PUBMED 12108560

TITLE  
 JOURNAL  
 MEDLINE  
 PUBMED  
 REFERENCE  
 AUTHORS  
 6 (bases 1 to 3879)  
 Adachi, J., Aizawa, K., Akimura, T., Aizawa, T., Bono, H., Carninci, P.,  
 Fukuda, S., Furuno, M., Hasegawa, T., Hara, A., Hashizume, M.,  
 Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T.,  
 Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,  
 Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Komoto, H., Kondo, M.,  
 Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,  
 Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,  
 Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,  
 Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,  
 Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,  
 Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,  
 Muramatsu, M., and Hayashizaki, Y.

TITLE  
 JOURNAL  
 MEDLINE  
 PUBMED  
 REFERENCE  
 AUTHORS  
 Direct Submission  
 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of  
 Physical and Chemical Research (RIKEN), Laboratory for Genome  
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
 RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
 Kanagawa 230-0045, Japan (E-mail: genome-resgsc.riken.go.jp,  
 URL: http://genome.resgsc.riken.go.jp/, Tel: 81-45-503-9222,  
 Fax: 81-45-503-9216)

COMMENT  
 cDNA library was prepared and sequenced in Mouse Genome  
 Encyclopedia Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in Riken.  
 Division of Experimental Animal Research in Riken contributed to  
 prepare mouse tissues.  
 Please visit our web site for further details.  
 URL: http://genome.resgsc.riken.go.jp/  
 URL: http://phantom.resgsc.riken.go.jp/  
 Location/Qualifiers

FEATURES  
 source  
 1..3879  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C57BL/6J"  
 /db\_xref="PANTOM DB:6430542K11"  
 /db\_xref="taxon:10090"  
 /clone="6430542K11"  
 /sex="male"  
 /tissue\_type="olfactory brain"  
 /clone\_idb="RIKEN full-length enriched mouse cDNA library"  
 /dev\_stage="adult"

misc\_feature  
 1..3063  
 /note="METABOTROPIC GLUTAMATE RECEPTOR MGLURS PRECURSOR  
 homolog [Rattus norvegicus] (SPTR|BA01711, evidence:  
 FASTV, 98.5%ID, 87%length, match=3058)  
 putative"

BASE COUNT 1026 a 975 c 954 g 924 t  
 ORIGIN

Query Match 5.3%; Score 59; DB 11; Length 3879;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-17;  
 Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 691 TTCGAAGATATGTCAGCGAAGAGGATTTCATGCCCTTTACAAATCTACAG 749  
 Db 234 TTCGAAGATATGTCAGCGAAGAGGATTTCATGCCCTTTACAAATCTACAG 292

Search completed: December 14, 2003, 23:43:38  
 Job time : 2535.22 secs





GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 14, 2003, 06:51:47 ; Search time 4194.01 Seconds  
(without alignments)  
10827.282 Million cell updates/sec

Title: US-10-027-923-3

Perfect score: 1110

Sequence: 1 atgagcctctctgtgacccct.....tgagggacagcgtcactaa 1110

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

GenBml:.\*  
1: gb ba:.\*  
2: gb htg:.\*  
3: gb\_in:.\*  
4: gb\_ov:.\*  
5: gb\_ov:.\*  
6: gb\_ov:.\*  
7: gb\_ov:.\*  
8: gb\_ov:.\*  
9: gb\_ov:.\*  
10: gb\_ov:.\*  
11: gb\_ov:.\*  
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36: gb\_ov:.\*  
37: gb\_ov:.\*  
38: gb\_ov:.\*  
39: gb\_ov:.\*  
40: gb\_ov:.\*  
41: gb\_ov:.\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1110	100.0	1110	6	AX709349 Sequence
2	1110	100.0	1823	6	AX709347 Sequence
3	1106.8	99.7	2172	6	AX068372 Sequence
4	1050.8	94.7	2149	6	AX068374 Sequence
5	919.8	82.9	2349	6	AX068368 Sequence
6	907.8	81.8	2064	6	AX068376 Sequence
7	888.4	80.0	4078	6	AR270570 Sequence
8	888.4	80.0	4207	6	AR145364 Sequence
9	888.4	80.0	4207	6	AR145365 Sequence
10	888.4	80.0	4303	6	AR145367 Sequence
11	888.4	80.0	4518	6	AX548892 Sequence
12	888.4	80.0	4518	6	AX548892 Sequence
13	888.4	80.0	4518	6	AX548892 Sequence
14	888.4	80.0	4518	6	AX548892 Sequence
15	885.2	79.7	3282	6	AR038828 Sequence
16	885.2	79.7	3282	6	AR038828 Sequence
17	885.2	79.7	3282	6	AR038828 Sequence
18	885.2	79.7	3282	6	AR038828 Sequence
19	885.2	79.7	4085	6	AR038826 Sequence
20	885.2	79.7	4085	6	AR038826 Sequence
21	885.2	79.7	4085	6	AR038826 Sequence
22	885.2	79.7	4085	6	AR038826 Sequence
23	885.2	79.7	4181	6	AR038827 Sequence
24	885.2	79.7	4181	6	AR038827 Sequence
25	885.2	79.7	4181	6	AR038827 Sequence
26	885.2	79.7	4181	6	AR038827 Sequence
27	885.2	79.7	4181	6	AR038827 Sequence
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29	885.2	79.7	4181	6	AR038827 Sequence
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DEFINITION Sequence 3 from Patent WO02070708.  
ACCESSION AX709349  
VERSION AX709349.1 GI:29564891  
KEYWORDS  
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ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS Bates,B.G., Xie,Y., Gulukota,K. and Paulsen,J.B.  
TITLE Glutamate receptor modulatory proteins and nucleic acids encoding them

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 KEYWORDS  
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 ORGANISM  
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE  
 AUTHORS Bates,B.G., Xie,Y., Gulukota,K. and Paulsen,J.B.  
 TITLE Glutamate receptor modulatory proteins and nucleic acids encoding  
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ACCESSION AX068372  
VERSION AX068372.1 GI:12578537  
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 Schwarz, D.A. and Makl, R.A.  
Metabotropic glutamate receptors and methods of use therefor  
Patent: WO 0102566-A 7 11-JAN-2001;  
Neurocrine Biosciences, Inc. (US)  
Location/Qualifiers  
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SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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REFERENCE  
 1 Schwarz, D.A. and Maki, R.A.  
 Metabotropic glutamate receptors and methods of use therefor  
 Patent: WO 0102566-A 3 11-JAN-2001;  
 Neurocrine Biosciences, Inc. (US)

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 DEFINITION Sequence 11 from Patent WO0102566.  
 ACCESSION AX068376  
 VERSION AX068376.1 GI:12578539  
 KEYWORDS  
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
 1 Schwarz, D.A. and Maki, R.A.  
 Metabotropic glutamate receptors and methods of use therefor  
 Patent: WO 0102566-A 11 11-JAN-2001;  
 Neurocrine Biosciences, Inc. (US)

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AR270570 4078 bp DNA linear PAT 10-Apr-2003
LOCUS AR270570
DEFINITION Sequence 1133 from patent US 6500938.
ACCESSION AR270570
VERSION AR270570.1 GI:29701804
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4078)
AUTHORS Au-Young, J. and Sellhammer, J. J.
TITLE Composition for the detection of signaling pathway gene expression
JOURNAL Patent: US 6500938-A 1133 31-DEC-2002;
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BASE COUNT 994 a 1074 c 1076 g 934 t
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QY 901 CTTCTGGGCGAG 914
DB 1051 CTTCTGGGCGAG 1064

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RESULT 8  
LOCUS AR145364 4207 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 1 from patent US 6211353.  
ACCESSION AR145364  
VERSION AR145364.1 GI:15107231  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 4207)  
AUTHORS Burnett,J.Paul, Jr., Mayne,N.Gail., Sharp,R.Leon. and Snyder,Y.Marie.  
TITLE Isolated nucleic acid encoding a human mglurs  
JOURNAL Patent: US 6211353-A 1 03-APR-2001;  
FEATURES Location/Qualifiers  
source 1..4207  
/organism="unknown"  
BASE COUNT 1011 a 1120 c 1112 g 964 t  
ORIGIN  
Query Match 80.0%; Score 888.4; DB 6; Length 4207;  
Best Local Similarity 98.2%; Pred. No. 1.7e-250;  
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DB 460 ATGGTCCTTCTGTGATCCGTGACGCTTACTTTTGAAGAAGATGCGGGAGTGA 519  
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DB 760 CATTCGGCTGTGGCCCTTGAAGCAGAGCATTTAGATTCAATAAGATTCCCTCATTTCTTG 819  
QY 361 GAAGAGAAAGAGGGCTTGTATGCTGTGAGATGGCTCCCTCTTCCCTCCGCTCAAG 420  
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DEFINITION Sequence 3 from patent US 6211353.  
ACCESSION AR145365  
VERSION AR145365.1 GI:15107232  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 4207)  
AUTHORS Burnett,J.Paul, Jr., Mayne,N.Gail., Sharp,R.Leon. and Snyder,Y.Marie.  
TITLE Isolated nucleic acid encoding a human mglurs  
JOURNAL Patent: US 6211353-A 3 03-APR-2001;  
FEATURES Location/Qualifiers  
source 1..4207  
/organism="unknown"  
BASE COUNT 1010 a 1121 c 1112 g 964 t  
ORIGIN  
Query Match 80.0%; Score 888.4; DB 6; Length 4207;  
Best Local Similarity 98.2%; Pred. No. 1.7e-250;  
Matches 898; Conservative 0; Mismatches 16; Indels 0; Gaps 0;  
QY 1 ATGGTCCTTCTGTGATCCGTGACGCTTACTTTTGAAGAAGATGCGGGAGTGA 60  
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QY 481 TTGCTCAGCTTTTCAACATACCTCAGATTCCTTACTCAGACCATCATGATCTAGT 540  
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 LOCUS Sequence 4 from patent US 6211353.  
 DEFINITION ARI45366  
 ACCESSION ARI45366  
 VERSION ARI45366.1 GI:15107233  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 4303)  
 AUTHORS Burnet,J.Paul. Jr., Mayne,N.Gail., Sharp,R.Leon. and Snyder,Y.Marie.  
 TITLE Isolated nucleic acid encoding a human mglur5  
 JOURNAL Patent: US 6211353-A 4 03-APR-2001;  
 FEATURES Location/Qualifiers  
 source 1..4303  
 /organism="unknown"

BASE COUNT 1044 a 1138 c 1144 g 977 t  
 ORIGIN  
 Query Match 80.0%; Score 888.4; DB 6; Length 4303;  
 Best Local Similarity 98.2%; Pred. No. 1.7e-250;  
 Matches 898; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1 ATGCTCCTTCTGATCTGTCACTTACTTTGAAGAAGATGTCCTGGAGATGCA 60  
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 DEFINITION ARI45367  
 ACCESSION ARI45367  
 VERSION ARI45367.1 GI:15107234  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 4303)  
 AUTHORS Burnet,J.Paul. Jr., Mayne,N.Gail., Sharp,R.Leon. and Snyder,Y.Marie.  
 TITLE Isolated nucleic acid encoding a human mglur5  
 JOURNAL Patent: US 6211353-A 6 03-APR-2001;  
 FEATURES Location/Qualifiers  
 source 1..4303  
 /organism="unknown"

BASE COUNT 1043 a 1139 c 1144 g 977 t  
 ORIGIN

Query Match 80.0%; Score 888.4; DB 6; Length 4303;



Best Local Similarity 98.2%; Pred. No. 1.7e-250;  
Matches 898; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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DB 640 CCGAAGCAGTATGAGCATTGAGAGAGTGGAGCCATGCTGATACCTTGGAAAGATCAAT 699
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RESULT 12  
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LOCUS AX548892 4518 bp DNA linear PAT 26-NOV-2002  
DEFINITION Sequence 177 from Patent WO02061087.  
ACCESSION AX548892

VERSION AX548892.1 GI:25813755  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE  
AUTHORS Burner, G.C., Roush, C.L. and Brown, J.P.  
TITLE Antigenic peptides, such as for G protein-coupled receptors (GPCRs), antibodies thereto, and systems for identifying such antigenic peptides  
JOURNAL Patent: WO 02061087-A 177 08-AUG-2002;  
FEATURES  
source  
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location/Qualifiers  
BASE COUNT 1114 a 1170 c 1145 g 1089 t

Query Match 80.0%; Score 888.4; DB 6; Length 4518;  
Best Local Similarity 98.2%; Pred. No. 1.8e-250;  
Matches 898; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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RESULT 14  
HUMNGR55B  
LOCUS  
DEFINITION  
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Human mRNA for metabotropic glutamate receptor subtype 5b, complete cds.

ACCESSION  
D28539.1 GI:1408053  
KEYWORDS  
mglur5b; metabotropic glutamate receptor.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens

REFERENCE  
AUTHORS  
TITLE  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 4614)  
Minakami, R., Katsuki, F., Yamamoto, T., Nakamura, K. and Sugiyama, H.  
Molecular cloning and the functional expression of two isoforms of  
human metabotropic glutamate receptor subtype 5  
Biochem. Biophys. Res. Commun. 199 (3), 1136-1143 (1994)

JOURNAL  
MEDLINE  
PUBMED  
7908515  
2 (bases 1 to 4614)  
Katsuki, F.  
Direct Submission  
Submitted (14-FEB-1994) Fujika Katsuki, Faculty of Science, Kyushu  
University, Department of Biology; 6-10-1 Hakozaki, Higashi-ku,  
Fukuoka, Fukuoka 812, Japan (Tel:092-642-2630, Fax:092-642-2645)  
On Jul 10, 1996 this sequence version replaced GI:483426.  
Sequence updated (03-Jul-1996) by: Fujika Katsuki.

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VPLPGNGLILISCTFYAKTRNVNPNFPAKIAFTMTTTCIIMAFPIIYEGSNYK  
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/replace="cg"

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/replace="cg"

3'UTR  
BASE COUNT 1147 a 1188 c 1177 g 1102 t  
ORIGIN  
Query Match 80.0%; Score 888.4; DB 9; Length 4614;  
Best Local Similarity 98.2%; Pred. No. 1.8e-250;  
Matches 898; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1 ATGCTCTTCTGTGTAATCTCTGTCAGTCTTAATTTTGAAGAAGATGCTCGTGGAGTGA 60  
Db 151 ATGCTCTTCTGTGTAATCTCTGTCAGTCTTAATTTTGAAGAAGATGCTCGTGGAGTGA 210  
QY 61 CAGTCCAGTGAAGAGAGGGGTGGTCTCAGTCTGGTGGTGAATCTTAATTTAGAGCTTC 120  
Db 211 CAGTCCAGTGAAGAGAGGGGTGGTCTCAGTCTGGTGGTGAATCTTAATTTAGAGCTTC 270  
QY 121 TTTTCTGTTATCAGCAGGCTTACTGTGACGAAGTTTATGAGAGAAAGTGTGGGAGTTC 180  
Db 271 TTTTCTGTTATCAGCAGGCTTACTGTGACGAAGTTTATGAGAGAAAGTGTGGGAGTTC 330  
QY 181 CCGTGAACAGTATGAGCTTATGAGAGTGGAGGCTATGCTGATTCCTTGGAAAGATCAAT 240  
Db 331 CCGTGAACAGTATGAGCTTATGAGAGTGGAGGCTATGCTGATTCCTTGGAAAGATCAAT 390  
QY 241 TCAGACCCCACTCTTGCCCAACATCAGCTGGGCTGTGAGTAAAGGATTCCTGCTGG 300  
Db 391 TCAGACCCCACTCTTGCCCAACATCAGCTGGGCTGTGAGTAAAGGATTCCTGCTGG 450  
QY 301 CATTGCGCTGTGGCCCTTAGAGAGAGACATTTGATTAAGATTCCTCATTTCTTGG 360  
Db 451 CATTGCGCTGTGGCCCTTAGAGAGAGACATTTGATTAAGATTCCTCATTTCTTGG 510  
QY 361 GAAAGAGAAAGAGGCTTGTGATGCTGTGTGATGCTCTCTCTCTTCTTCCGCTCAAG 420  
Db 511 GAAAGAGAAAGAGGCTTGTGATGCTGTGTGATGCTCTCTCTCTTCTTCCGCTCAAG 570  
QY 421 AAGCCCATGATGAGGGGTCAATGGGCTGTTCAGTCTTTAGCCATTAAGCTCCAGAT 480  
Db 571 AAGCCCATGATGAGGGGTCAATGGGCTGTTCAGTCTTTAGCCATTAAGCTCCAGAT 630  
QY 481 TTGCTTCAGCTTTTCAACATTAATCTCATGATGCTTCACTGACCAACATCATGATCTGAGT 540  
Db 631 TTGCTTCAGCTTTTCAACATTAATCTCATGATGCTTCACTGACCAACATCATGATCTGAGT 690  
QY 541 GACAGACTCTGTTCAATATTTTCAATGAGGCTTCTCTTCAATGCTCAGCAGGCAAG 600  
Db 691 GACAGACTCTGTTCAATATTTTCAATGAGGCTTCTCTTCAATGCTCAGCAGGCAAG 750  
QY 601 TCCATGCTGACATGTAAGAGTCACTGACCTTAATGTAATGACCCGTACACAGAA 660  
Db 751 TCCATGCTGACATGTAAGAGTCACTGACCTTAATGTAATGACCCGTACACAGAA 810  
QY 661 GGCACATATGAGAAAGTGGATGGAAGCTTCAAGATATGTCACGAGAAAGAGGATTT 720  
Db 811 GGCACATATGAGAAAGTGGATGGAAGCTTCAAGATATGTCACGAGAAAGAGGATTT 870  
QY 721 TGCATGCCCACTCTTAACAAATCTACAGTAATGACGGGAGACAGCTTTGATTAAGCTG 780  
Db 871 TGCATGCCCACTCTTAACAAATCTACAGTAATGACGGGAGACAGCTTTGATTAAGCTG 930  
QY 781 CTGAAGAAGCTCAAGATCACTTGCACAGGCTGGGTGTGGCTTAATTTGTGAGGGC 840  
Db 931 CTGAAGAAGCTCAAGATCACTTGCACAGGCTGGGTGTGGCTTAATTTGTGAGGGC 990  
QY 841 ATGACGATGAGAGTCTGTGATGAGCAGGCTGGGTCTAGTGGAGAAATTTCTG 900  
Db 991 ATGACGATGAGAGTCTGTGATGAGCAGGCTGGGTCTAGTGGAGAAATTTCTG 1050  
QY 901 CTTCTGGGAGGGA 914  
Db 1051 CTTCTGGGAGGGA 1064

RESULT 15  
AR038828  
LOCUS AR038828 3282 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 11 from patent US 5807689.  
ACCESSION AR038828  
VERSION AR038828.1 GI:5958191  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 3282)  
Daggett, L., Ellis, S.B., Liaw, C., Pontsler, A., Johnson, E.C. and  
Hess, S.D.  
TITLE Methods for identifying compounds that modulate metabotropic  
glutamate receptor activity  
JOURNAL Patent: US 5807689-A 11 15-SEP-1998;  
FEATURES  
Location/Qualifiers  
Source 1..3282  
BASE COUNT 840 a 769 c 848 g 825 t  
ORIGIN  
Query Match 79.7%; Score 885.2; DB 6; Length 3282;  
Best Local Similarity 98.0%; Pred. No. 1.5e-249;  
Matches 896; Conservative 0; Mismatches 18; Indels 0; Gaps 0;  
QY 1 ATGGCTCTGCTGTGATCCGTGCTGCTTCTTGAAGAAGATGCCGGGAGTGA 60  
DB 370 ATGGCTCTGCTGTGATCCGTGCTGCTTCTTGAAGAAGATGCCGGGAGTGA 429  
QY 61 CAGTCCAGTGAAGAGAGGAGTGTGCTCAATGCTGGGTGACATATTATGAGCTCTC 120  
DB 430 CAGTCCAGTGAAGAGAGGAGTGTGCTCAATGCTGGGTGACATATTATGAGCTCTC 489  
QY 121 TTTTCTGTTCATCAACGCTTCTGTGACGAAGTTCATGAGGAAGTGTGGGCAATC 180  
DB 490 TTTTCTGTTCATCAACGCTTCTGTGACGAAGTTCATGAGGAAGTGTGGGCAATC 549  
QY 181 CGTGAACAGTATGGCATTCAAGAGTGAAGCCATGCTGATACCTCTGGAAGAATCAAT 240  
DB 550 CGTGAACAGTATGGCATTCAAGAGTGAAGCCATGCTGATACCTCTGGAAGAATCAAT 609  
QY 241 TCAGACCCCACTCTTGCCCAATCACTGGGCTGTGAGATTAAGGAATTCCTGCTGG 300  
DB 610 TCAGACCCCACTCTTGCCCAATCACTGGGCTGTGAGATTAAGGAATTCCTGCTGG 669  
QY 301 CATTGGCTGTGGCCCTAGAGCAGAGCATTGAGTTCAATAAGATTCCCTCATTTCTTG 360  
DB 670 CATTGGCTGTGGCCCTAGAGCAGAGCATTGAGTTCAATAAGATTCCCTCATTTCTTG 729  
QY 361 GAAGAGAAAGAGGCTGTGATGCTGTGATGGCTCTCTTCTTCCGCTCCAAG 420  
DB 730 GAAGAGAAAGAGGCTGTGATGCTGTGATGGCTCTCTTCTTCCGCTCCAAG 789  
QY 421 AAGCCCATAGTAGGGGCTATTGGGCTGTGCTTCCAGTCTTTAGCCATTCAAGTCCAGAA 480  
DB 790 AAGCCCATAGTAGGGGCTATTGGGCTGTGCTTCCAGTCTTTAGCCATTCAAGTCCAGAA 849  
QY 481 TTGCTCAGCTTTTCAACATCACTCAGATTGCTTACTCAGCAACCATCATGATCTGAGT 540  
DB 850 TTGCTCAGCTTTTCAACATCACTCAGATTGCTTACTCAGCAACCATCATGATCTGAGT 909  
QY 541 GACAAGACTGTCTTCAATTTTTCATAGGGTGTGCTTCAAGTGTCTCAGCAGGCAAG 600  
DB 910 GACAAGACTGTCTTCAATTTTTCATAGGGTGTGCTTCAAGTGTCTCAGCAGGCAAG 969  
QY 601 TCCATGCTGACATAGTGAAGAGGTACATGACCTATATATCAGCCGTACACAGAA 660  
DB 970 GCCATGCTGACATAGTGAAGAGGTACATGACCTATATATCAGCCGTACACAGAA 1029  
QY 661 GGCACCTATGAGAAAGTGGATGGAAGCCTTCAAGATATGTCAGGGAAGAGGATT 720  
DB 1030 GGCACCTATGAGAAAGTGGATGGAAGCCTTCAAGATATGTCAGGGAAGAGGATT 1089

QY 721 TGCATGCCCACTTTACAAAATCTACAGTAATGACGGGAGAGAGCTTTGATTAAGCTG 780  
DB 1090 TGCATGCCCACTTTACAAAATCTACAGTAATGACGGGAGAGAGCTTTGATTAAGCTG 1149  
QY 781 CTGAGAAGCTCAAGAGTCACTTGCCCAAGGCCGGGCTGTGCTTCTGTGAGGGC 840  
DB 1150 CTGAGAAGCTCAAGAGTCACTTGCCCAAGGCCGGGCTGTGCTTCTGTGAGGGC 1209  
QY 841 ATGACGGTGAAGAGTCTGTGATGAGCCATGAGGCGCTGGTCTAGTGGAGAAATTTCTG 900  
DB 1210 ATGACGGTGAAGAGTCTGTGATGAGCCATGAGGCGCTGGTCTAGCAGGAATTTCTG 1269  
QY 901 CTTCTGGGACAGGA 914  
DB 1270 CTTCTGGGACAGTA 1283

Search completed: December 14, 2003, 13:24:31  
Job time : 4202.01 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 14, 2003, 06:48:22 ; Search time 319.792 Seconds  
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9369.765 Million cell updates/sec

Title: US-10-027-923-3

Perfect score: 1110  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%  
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Listing first 45 summaries

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26: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match length	DB	ID	Description
1	1110	100.0	1823	24	ABV73899	Human glutamate re
2	1108	99.8	1788	24	AA562274	CDNA sequence #61
3	1106.8	99.7	2172	22	AA299993	Human GRKX-1E DNA.
4	1050.8	94.7	2149	22	AA299994	Human GRKX-1F DNA.
5	919.8	82.9	2349	22	AA299990	Human GRKX-1B DNA.
6	907.8	81.8	2064	22	AA299995	Human GRKX-1G DNA.
7	888.4	80.0	2826	22	AA299995	CDNA encoding meta
8	888.4	80.0	3129	22	AA299995	CDNA encoding chim

9	888.4	80.0	4078	25	ACA56535	Human signalling p
10	888.4	80.0	4207	22	AA049990	Human metabotropic
11	888.4	80.0	4207	22	AA050029	Human metabotropic
12	888.4	80.0	4207	22	AA050030	Human metabotropic
13	888.4	80.0	4207	22	AA050033	Human metabotropic
14	888.4	80.0	4303	22	AA049991	Human metabotropic
15	888.4	80.0	4303	22	AA050031	Human metabotropic
16	888.4	80.0	4303	22	AA050032	Human metabotropic
17	888.4	80.0	4303	22	AA050033	Human metabotropic
18	888.4	80.0	4303	22	AA050034	Human metabotropic
19	888.4	80.0	4303	22	AA050035	Human metabotropic
20	888.4	80.0	4303	22	AA050036	Human metabotropic
21	888.4	80.0	4303	22	AA050037	Human metabotropic
22	888.4	80.0	4303	22	AA050038	Human metabotropic
23	888.4	80.0	4303	22	AA050039	Human metabotropic
24	888.4	80.0	4303	22	AA050040	Human metabotropic
25	888.4	80.0	4303	22	AA050041	Human metabotropic
26	888.4	80.0	4303	22	AA050042	Human metabotropic
27	888.4	80.0	4303	22	AA050043	Human metabotropic
28	888.4	80.0	4303	22	AA050044	Human metabotropic
29	888.4	80.0	4303	22	AA050045	Human metabotropic
30	888.4	80.0	4303	22	AA050046	Human metabotropic
31	888.4	80.0	4303	22	AA050047	Human metabotropic
32	888.4	80.0	4303	22	AA050048	Human metabotropic
33	888.4	80.0	4303	22	AA050049	Human metabotropic
34	888.4	80.0	4303	22	AA050050	Human metabotropic
35	888.4	80.0	4303	22	AA050051	Human metabotropic
36	888.4	80.0	4303	22	AA050052	Human metabotropic
37	888.4	80.0	4303	22	AA050053	Human metabotropic
38	888.4	80.0	4303	22	AA050054	Human metabotropic
39	888.4	80.0	4303	22	AA050055	Human metabotropic
40	888.4	80.0	4303	22	AA050056	Human metabotropic
41	888.4	80.0	4303	22	AA050057	Human metabotropic
42	888.4	80.0	4303	22	AA050058	Human metabotropic
43	888.4	80.0	4303	22	AA050059	Human metabotropic
44	888.4	80.0	4303	22	AA050060	Human metabotropic
45	888.4	80.0	4303	22	AA050061	Human metabotropic

#### ALIGNMENTS

RESULT 1	ABV73899	standard; CDNA, 1823 BP.
XX	ABV73899	
XX	08-JUN-2003	(first entry)
XX	Human glutamate receptor modulatory protein mGluR5m CDNA.	
XX	Metabotropic glutamate receptor subtype 5 modulatory protein;	
XX	mGluR5m; human; G-protein coupled receptor; receptor; schizophrenia;	
XX	schizophrenia; bipolar affective disorder; bipolar affective disorder;	
XX	unipolar affective disorder; adolescent conduct disorder;	
XX	neuroleptic; neuroprotective; neuroleptic; chromosome 11;	
XX	gene therapy; gene; ss.	
XX	Homo sapiens.	
XX	Key	Location/Qualifiers
XX	CDS	4..1113
XX	FT	/*tag= a
XX	FT	/product= "mGluR5m"
XX	FT	/note= "the CDS is specifically claimed in Claim 1"
XX	FT	sig_peptide
XX	FT	4..63
XX	FT	/*tag= b
XX	FT	mat_peptide
XX	FT	64..1110
XX	FT	/*tag= c
XX	PN	MO200270708-A2.

PD	12-SEP-2002.
XX	
PF	21-DEC-2001; 2001WO-US49817.
XX	
PR	22-DEC-2000; 2000US-257589P.
XX	
PA	(AMHP ) WYETH.
XX	
PI	Bates BG, Xie Y, Gulukota K, Paulsen JE;
XX	
DR	WP1; 2002-750462/81.
DR	P-PSDB; ABP54921.
XX	
PT	New mgluR5M nucleic acid molecules and proteins, useful for treating
PT	neurological or psychiatric disorders such as schizophrenia,
PT	schizoaffective disorder, bipolar or unipolar affective disorder, or
PT	adolescent conduct disorder -
PS	Claim 11; Fig 1A; 99pp; English.
XX	
CC	The present sequence is that of cDNA clone Y1176 (deposited as
CC	ATCC PTA-2775) encoding a novel human metabotropic glutamate
CC	receptor subtype modulatory protein (mgluR5M). The cDNA was
CC	isolated from a human brain cDNA library. Expression of mgluR5M
CC	is predominant in cells and tissues of the central nervous system.
CC	The gene maps to a region of chromosome 11 associated with
CC	schizophrenia and related psychiatric disorders. The invention
CC	provides mgluR5M polypeptides and nucleic acids, and methods for
CC	their detection, as well as methods for using them to identify
CC	compounds that modulate metabotropic receptor (mgluR) activity.
CC	Such modulators include a mgluR5M nucleic acid, a mgluR5M antibody,
CC	a ribozyme, an antisense oligonucleotide, a small molecule
CC	modulator, a peptide and a peptidomimetic. They can be used in a
CC	claimed method for treating a subject having a neurological
CC	disorder, especially a psychiatric disorder selected from
CC	schizophrenia, schizoaffective disorder, bipolar affective disorder,
CC	unipolar affective disorder or adolescent conduct disorder (all
CC	claimed). mgluR5M polypeptides, nucleic acids and antibodies are
CC	also useful for screening assays, and in predictive medicine, e.g.
CC	diagnostic assays (e.g. chromosome mapping and tissue typing),
CC	prognostic assays, monitoring clinical trials, and pharmacogenomics.
XX	
SQ	Sequence 1823 BP; 488 A; 397 C; 444 G; 493 T; 1 other;
	Query Match 100.0%; Score 1110; DB 24; Length 1823;
	Best Local Similarity 100.0%; Pred. No. 0;
	Matches 1110; Conservative 0; Mismatches 0; Indels 0; Gaps 0
OY	1 ATGGGCTCTTCGTTGATCTGTCGATCTCTTAATTGGAAGAAGATGTCGGTAGATGA 60
DB	4 ATGGGCTCTTCGTTGATCTGTCGATCTCTTAATTGGAAGAAGATGTCGGTAGATGA 63
OY	61 CAGTCCAGTGAAGAGAGGGTGTGCTCACTGCTGGTGATCATATTATGAGCTCTC 120
DB	64 CAGTCCAGTGAAGAGAGGGTGTGCTCACTGCTGGTGATCATATTATGAGCTCTC 123
OY	121 TTTTCTGTTTCATCACAGCTTACTGTGACGAAGTTTCATGAGAGAAAGTGTGGGCACTC 180
DB	124 TTTTCTGTTTCATCACAGCTTACTGTGACGAAGTTTCATGAGAGAAAGTGTGGGCACTC 183
OY	181 CGTGAACAGTATGAGATTCAGAGATGAGGCGCATCTGTCATATCCTGGAAAGATCAAT 240
DB	184 CGTGAACAGTATGAGATTCAGAGATGAGGCGCATCTGTCATATCCTGGAAAGATCAAT 243
OY	241 TCAGACCCCACTCTTGGCCCAACATCACTCGGGCTGTGAGATTAAGGATTCCTGTGG 300
DB	244 TCAGACCCCACTCTTGGCCCAACATCACTCGGGCTGTGAGATTAAGGATTCCTGTGG 303
OY	301 CATTGGCTGTGGCCCTTAGAGCAGAGACTTGATTCATTAAGATATTCCTCATTTCTTGG 360
DB	304 CATTGGCTGTGGCCCTTAGAGCAGAGACTTGATTCATTAAGATATTCCTCATTTCTTGG 363
OY	361 GAAGAGAAAGAGGCTGTGATGCTCTGTGTGATGAGTGCCTCTCTTCTTCCTCCGCTCAAG 420

Db	364	GAAAGGAAGAGGGGTTGGTATGCTCTGTGATGGCTCTCTCTTCTCGCTCAAG	423
Qy	421	AAGCCCATAGTAggggTCATTGGGCTGGTTCAGTCTTTAAGCATTCAGGTCCAGAT	480
Db	424	AAGCCCAATAGTAggggTCATTGGGCTGGTGTTCAGTCTTTAAGCATTCAGGTCCAGAT	483
Qy	481	TTGCTCCAGCTTTTCAACATACCTCAGATGCTTACTCAGAACCATCATGAGATCTGAGT	540
Db	484	TTGCTCCAGCTTTTCAACATACCTCAGATGCTTACTCAGAACCATCATGAGATCTGAGT	543
Qy	541	GACAAGACTCTGTTCAATATTTTCAATGAGGGTGTGCTTCAGATGCTCAGCAGGCAAG	600
Db	544	GACAAGACTCTGTTCAATATTTTCAATGAGGGTGTGCTTCAGATGCTCAGCAGGCAAG	603
Qy	601	TCATGTGTGACATAGTGAAGAGGTACAACCTGACCTTATGATCAGCCGTACACAGAA	660
Db	604	TCATGTGTGACATAGTGAAGAGGTACAACCTGATGTATCAGCCGTACACACAAA	663
Qy	661	GGCAACTATGGAAGAAAGTGGATGGAAGCCCTTCAAGATATGTGACGGAGAAGAGGATT	720
Db	664	GGCAACTATGGAAGAAAGTGGATGGAAGCCCTTCAAGATATGTGACGGAGAAGAGGATT	723
Qy	721	TGCATGCGCCACTCTTACAAATATCTACAGTATGACAGGGAGCAGAGCTTTGATTAAGCTG	780
Db	724	TGCATGCGCCACTCTTACAAATATCTACAGTATGACAGGGAGCAGAGCTTTGATTAAGCTG	783
Qy	781	CTGAAGAAGCTCACAAAGTCATTGSCCAAGGCCCGGGGTGTGTGGCTTACTTCTGTAGGGC	840
Db	784	CTGAAGAAGCTCACAAAGTCATTGSCCAAGGCCCGGGGTGTGTGGCTTACTTCTGTAGGGC	843
Qy	841	ATGACGGTGAAGGTCGTCTGTATATGGCCATGAGGGCCCTGGGTCTAATGAGGAGAAATTTCTG	900
Db	844	ATGACGGTGAAGGTCGTCTGTATATGGCCATGAGGGCCCTGGGTCTAATGAGGAGAAATTTCTG	903
Qy	901	CTTCTGGGCAAGGAAACAGATGCCATCTTTATTAAGATCTCAAGAAACAGGATCCTATGG	960
Db	904	CTTCTGGGCAAGGAAACAGATGCCATCTTTATTAAGATCTCAAGAAACAGGATCCTATGG	963
Qy	961	GAAACAGAAAGAAATGCAAGGTCCTTCTTCAAGGTTTGAAGACATATTACACAGA	1020
Db	964	GAAACAGAAAGAAATGCAAGGTCCTTCTTCAAGGTTTGAAGACATATTACACAGA	1023
Qy	1021	AGTAGAGTCCTGCTGCTGTCACATATGCCAGCCTCTGAATCTAAGAGCTCAGTTCAAGGCCC	1080
Db	1024	AGTAGAGTCCTGCTGCTGTCACATATGCCAGCCTCTGAATCTAAGAGCTCAGTTCAAGGCCC	1083
Qy	1081	ATCACTGAGACTGAGGAGCAGGCTCATCTAA	1110
Db	1084	ATCACTGAGACTGAGGAGCAGGCTCATCTAA	1113
RESULT 2			
AAS62274			
XX	AA62274	standard; cDNA; 1788 BP.	
XX	AA62274;		
XX	14-FEB-2002	(first entry)	
DE	CDNA	sequence #61 encoding novel human secreted protein.	
XX	Human	secreted protein; hyperproliferative disorder; autoimmune disorder;	
KW	immune	deficiency disorder; blood disorder; inflammatory disorder;	
KM	infectious	disorder; gene therapy; antimicrobial; hepatotropic;	
KX	immunopressive;	antirheumatic; ss.	
OS	Homo sapiens.		
XX	WO200177291-A2.		
XX	18-OCT-2001.		
PD			
XX			

PF 29-MAR-2001; 2001WO-US10485.  
 XX  
 PR 06-APR-2000; 2000US-195604P.  
 XX  
 PA (GENY ) GENETICS INST INC.  
 XX  
 PI Wong GG, Clark HF, Fechtel K, Agostino MJ, Howes SH, Resnick RJ,  
 PI Gulukota K, Graham JR;  
 XX  
 DR WPI; 2002-010900/01.  
 XX  
 PT New polynucleotides encoding secreted proteins useful for treating e.g.  
 PT asthma, HIV and Crohn's disease -  
 PS  
 PS Claim 1; Page 106-107; 391pp; English.  
 CC The present invention relates to the isolation of novel cDNA sequences  
 CC which encode human secreted proteins. The cDNA sequences have been  
 CC derived from a variety of human tissues. The invention also provides  
 CC a method for producing proteins from these polynucleotide sequences.  
 CC The proteins are useful for identifying compounds that modulate their  
 CC activity and production, and the cell is also useful for identifying  
 CC compounds that modulate expression of the polynucleotide sequences  
 CC useful for treating diseases such as hyperproliferative disorders  
 CC (e.g. cancer), immune deficiency disorders (e.g. severe combined  
 CC immunodeficiency (SCID)), autoimmune disorders (e.g. multiple  
 CC sclerosis), blood disorders (e.g. thrombocytopenia), inflammatory  
 CC disorders (e.g. arthritis) and infectious disorders (e.g. hepatitis).  
 CC The polynucleotide sequences of the invention are also useful in gene  
 CC therapy. AAS62214-AAS62838 represent the cDNA sequences of the  
 CC invention that encode for novel human secreted proteins.  
 XX  
 SQ Sequence 1788 BP; 454 A; 398 C; 444 G; 492 T; 0 other;  
 Query Match 99.8%; Score 1108; DB 24; Length 1788;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 481 GCTCCAGCTTTTCAACATACCTCAGATTGCTTACTACAGCAACCATCATGATCTGAGTA 540  
 QY 543 CAAGACTCTGTTCAATATATTTATGAGGGTATGCTTCAAGATGCTCAGACAGCAAGATC 602  
 DB 541 CAAGACTCTGTTCAATATATTTATGAGGGTATGCTTCAAGATGCTCAGACAGCAAGATC 600  
 QY 603 CATGTGACATAGTGAAGAGGTACAACTGACCTATGATAGCCGTACACAGAAAG 662  
 DB 601 CATGTGACATAGTGAAGAGGTACAACTGACCTATGATAGCCGTACACAGAAAG 660  
 QY 663 CAATATGAGAAAGTGGATGAAAGCTTCAAGATATGTCAGCGAAGAAAGGATTTG 722  
 DB 661 CAATATGAGAAAGTGGATGAAAGCTTCAAGATATGTCAGCGAAGAAAGGATTTG 720  
 QY 723 CATGCCCACTTTTCAAAATCTACATGATATGAGGAGAGAGCTTTGATAGCTGCT 782  
 DB 721 CATGCCCACTTTTCAAAATCTACATGATATGAGGAGAGAGCTTTGATAGCTGCT 780  
 QY 783 GAAGAAGCTCACAAGTCACTTCCCAAGGCCGGGTGAGCTTCTGTGAGGGCAT 842  
 DB 781 GAAGAAGCTCACAAGTCACTTCCCAAGGCCGGGTGAGCTTCTGTGAGGGCAT 840  
 QY 843 GACGGTGAAGGTCTGCTGATGAGGAGGCGCTGGCTTATGAGGAAATTTCTGCT 902  
 DB 841 GACGGTGAAGGTCTGCTGATGAGGAGGCGCTGGCTTATGAGGAAATTTCTGCT 900  
 QY 903 TCTGGGCGAGGAAACCATGATCCATCTTATATGATATCTAAAGAACAGATCTTATGGA 962  
 DB 901 TCTGGGCGAGGAAACCATGATCCATCTTATATGATATCTAAAGAACAGATCTTATGGA 960  
 QY 963 ACACAGAAAGAAATGCAAGTGTGCTTCTTCAAGGTTTGGAGACATTTACACAGAAG 1022  
 DB 961 ACACAGAAAGAAATGCAAGTGTGCTTCTTCAAGGTTTGGAGACATTTACACAGAAG 1020  
 QY 1023 TGAATCCGTGCTGTCACATGCCCCAGCTCTGAATCTAGAGCTTCAAGGCCAT 1082  
 DB 1021 TGAATCCGTGCTGTCACATGCCCCAGCTCTGAATCTAGAGCTTCAAGGCCAT 1080  
 QY 1083 CACTGACCTGAGGAGACAGGCTCATCTAA 1110  
 DB 1081 CACTGACCTGAGGAGACAGGCTCATCTAA 1108

RESULT 3  
 AAF29993  
 ID AAF29993 standard; DNA; 2172 BP.  
 XX  
 AC AAF29993;  
 XX  
 DT 06-APR-2001 (first entry)  
 XX  
 DE Human GRMx-1e DNA.  
 XX  
 KW Human; metabotropic glutamate receptor; schizophrenia; GRMx;  
 KW Alzheimer's; Parkinson's; stroke; depression; anxiety; pain; ds.  
 OS Homo sapiens.  
 PN WO200102566-A1.  
 PD 11-JAN-2001.  
 PF 27-JUN-2000; 2000WO-US17798.  
 PR 02-JUL-1999; 99US-0346326.  
 PA (NEUR-) NEUROCRINE BIOSCIENCES INC.  
 PI Schwarz DA, Maki RA;  
 DR WPI; 2001-123112/13.  
 XX Novel metabotropic glutamate receptor for prevention, treatment of





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QY 1 ATGCTCTTCTGTGATCTGTCACTTACTTTGAAGAAGATGCGTGGAGTGA 60
DB 365 ATGCTCTTCTGTGATCTGTCACTTACTTTGAAGAAGATGCGTGGAGTGA 424
QY 61 CAGTCCAGTGAAGAGAGGTGTGCTCACATGCTGGGTACATCATTAATGAGCTTC 120
DB 425 CAGTCCAGTGAAGAGAGGTGTGCTCACATGCTGGGTACATCATTAATGAGCTTC 484
QY 121 TTTTCTGTTCATCAACGAGCTACTGTGAGAGAAATTCAAGAGAGAAAGTGTGGGCAATC 180
DB 485 TTTTCTGTTCATCAACGAGCTACTGTGAGAGAAATTCAAGAGAGAAAGTGTGGGCAATC 544
QY 181 CGTGAACAGTATGAGCACTTGAAGAGTGAAGCCATGCTGATCCCTGGAAGAGATCAAT 240
DB 545 CGTGAACAGTATGAGCACTTGAAGAGTGAAGCCATGCTGATCCCTGGAAGAGATCAAT 604
QY 241 TCAGACCCCACTCTTGGCCCAATCACTGGGCTGTGAGATTAAGAGATTCCTGCTG 300
DB 605 TCAGACCCCACTCTTGGCCCAATCACTGGGCTGTGAGATTAAGAGATTCCTGCTG 664
QY 301 CATTGGCTGTGGCCCTTAAGAGAGAGATTAAGATTAAGATTAAGATTAAGATTAAGAT 360
DB 665 CATTGGCTGTGGCCCTTAAGAGAGAGATTAAGATTAAGATTAAGATTAAGATTAAGAT 724
QY 361 GAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 725 GAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 784
QY 421 AAGCCCATAGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
DB 785 AAGCCCATAGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 844
QY 481 TTGCTCAGCTTTTCAACATACCTCAGATTCCTTAATCAAGAACATCATGATCTGAGT 540
DB 845 TTGCTCAGCTTTTCAACATACCTCAGATTCCTTAATCAAGAACATCATGATCTGAGT 904
QY 541 GACAAGAGCTGTGCAATTTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
DB 905 GACAAGAGCTGTGCAATTTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 964
QY 601 TCCATGTGAGCATAGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
DB 965 TCCATGTGAGCATAGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1024
QY 661 GGCACATAGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
DB 1025 GGCACATAGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1084
QY 721 TGCATGCCCCACTCTTCAAAAATCTACAGTAATGACAGAGAGAGAGAGAGAGAGAG 780
DB 1085 TGCATGCCCCACTCTTCAAAAATCTACAGTAATGACAGAGAGAGAGAGAGAGAGAG 1144
QY 781 CTGAAGAAGCTCAAGTCACTTGCCCAAGCCGGGTGTGGCTTAATCTGTGAAGGCG 840
DB 1145 CTGAAGAAGCTCAAGTCACTTGCCCAAGCCGGGTGTGGCTTAATCTGTGAAGGCG 1204
QY 841 ATGACGGTGAAGAGTCTGCTGATGAGCCATGAGCGCGCTGGGTCTAGTGGAGAAATTC 900
DB 1205 ATGACGGTGAAGAGTCTGCTGATGAGCCATGAGCGCGCTGGGTCTAGTGGAGAAATTC 1264
QY 901 CTCTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
DB 1265 CTCTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1324
QY 961 GAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
DB 1325 GAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1361
QY 1021 AGTGAAGTCCGTGCTGACATGAGCCAGCTCTGATCTGAATCTGAAGCTCAAGGAGCC 1080
DB 1362 AGTGAAGTCCGTGCTGACATGAGCCAGCTCTGATCTGAATCTGAAGCTCAAGGAGCC 1421

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QY 1081 ATCACTGACTGAGGAGACAGCTCATCTAA 1110
DB 1422 ATCACTGACTGAGGAGACAGCTCATCTAA 1451
RESULT 5
AAF29990
ID AAF29990 strand; DNA; 2349 BP.
XX
AC AAF29990;
XX
DT 06-APR-2001 (first entry)
XX
DE Human GRMx-1b DNA.
XX
KW Human; metabotropic glutamate receptor; schizophrenia; GRMx;
KW Alzheimer's; Parkinson's; stroke; depression; anxiety; pain; de.
XX
OS Homo sapiens.
XX
PN M0200102566-A1.
XX
PD 11-JAN-2001.
XX
PF 27-JUN-2000; 2000MO-US17798.
XX
PR 02-JUL-1999; 99US-0346326.
XX
PA (NEUR-) NEUROCRINE BIOSCIENCES INC.
XX
PI Schwarz DA, Maki RA;
XX
DR WPI; 2001-123112/13.
XX
PT Novel metabotropic glutamate receptor for prevention, treatment of
PT conditions associated with undesirable glutamate levels, e.g.
PT Alzheimer's, Parkinson's disease, stroke, depression, anxiety, pain and
PT schizophrenia -
XX
PS Claim 2; Fig 3; 59pp; English.
XX
CC The present invention relates to human metabotropic glutamate
CC receptor. An agent that decreases expression or activity of the
CC metabotropic glutamate receptor is useful for treating schizophrenia.
CC Metabotropic glutamate receptor polynucleotides, polypeptides
CC are useful for treating diseases associated with undesirable
CC levels of glutamate, such as Alzheimer's disease, Parkinson's
CC disease, stroke, depression, anxiety, pain and schizophrenia.
XX
SQ Sequence 2349 BP; 588 A; 538 C; 586 G; 637 T; 0 other;
Query Match 82.9%; Score 919.8; DB 22; Length 2349;
Best Local Similarity 86.1%; Pred. No. 1.8e-280;
Matches 1108; Conservative 0; Mismatches 2; Indels 177; Gaps 1;
QY 1 ATGCTCTTCTGTGATCTGTCACTTACTTTGAAGAAGATGCGTGGAGTGA 60
DB 365 ATGCTCTTCTGTGATCTGTCACTTACTTTGAAGAAGATGCGTGGAGTGA 424
QY 61 CAGTCCAGTGAAGAGAGGTGTGCTCACATGCTGGGTACATCATTAATGAGCTTC 120
DB 425 CAGTCCAGTGAAGAGAGGTGTGCTCACATGCTGGGTACATCATTAATGAGCTTC 484
QY 121 TTTTCTGTTCATCAACGAGCTACTGTGAGAGAAATTCAAGAGAGAAAGTGTGGGCAATC 180
DB 485 TTTTCTGTTCATCAACGAGCTACTGTGAGAGAAATTCAAGAGAGAAAGTGTGGGCAATC 544
QY 181 CGTGAACAGTATGAGCACTTGAAGAGTGAAGCCATGCTGATCCCTGGAAGAGATCAAT 240
DB 545 CGTGAACAGTATGAGCACTTGAAGAGTGAAGCCATGCTGATCCCTGGAAGAGATCAAT 604
QY 241 TCAGACCCCACTCTTGGCCCAATCACTGGGCTGTGAGATTAAGAGATTCCTGCTG 300
DB 605 TCAGACCCCACTCTTGGCCCAATCACTGGGCTGTGAGATTAAGAGATTCCTGCTG 664

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Db      605 TCAGACCCCACTCTTGGCCCAATCATCACTGGGCTGTGAGATTAAGGATTCCTGCTGG 664
Qy      301 CATTGGCTGTGGCCCTTAGAGCAGAGATTGAGTTCAATAGATTCCTCATTTCTTCG 360
Db      665 CATTGGCTGTGGCCCTTAGAGCAGAGATTGAGTTCAATAGATTCCTCATTTCTTCG 724
Qy      361 GAAGAGAAAGAGGCTGTGATGCTGTGATGAGCTGCTCTTCTCTCCGCTCCAG 420
Db      725 GAAGAGAAAGAGGCTGTGATGCTGTGATGAGCTGCTCTTCTCTCCGCTCCAG 784
Qy      421 AAGCCCATAGTAGGGGCTATTGGGCTGTGATGAGCTGCTCTTCTCTCCGCTCCAG 480
Db      785 AAGCCCATAGTAGGGGCTATTGGGCTGTGATGAGCTGCTCTTCTCTCCGCTCCAG 844
Qy      481 TTGCTCAGCTTTTCAACATACCTCAGATTGCTTACTGACCAACCATATGATGATGAGT 540
Db      845 TTGCTCAGCTTTTCAACATACCTCAGATTGCTTACTGACCAACCATATGATGATGAGT 904
Qy      541 GACAAAGCTGTGTTCAAAATATTTTCAATGAGGTTGTGCTTCAATGCTCAGAGCAAG 600
Db      905 GACAAAGCTGTGTTCAAAATATTTTCAATGAGGTTGTGCTTCAATGCTCAGAGCAAG 964
Qy      601 TCCATGTGTGACATAGTAAAGAGTACACTGACCTATATGATCAGCCGTACACAGAA- 659
Db      965 TCCATGTGTGACATAGTAAAGAGTACACTGACCTATATGATCAGCCGTACACAGAA 1024
Qy      660 ----- 659
Db      1025 GGTTCAGATATTTCTCAATGCTTCCAAATTTGCTGGGATTATGGCATAGCCACC 1144
Qy      660 ----- 659
Db      1085 CCTCAAGTATCTGCTGCTTGGCTTCCAAATTTGCTGGGATTATGGCATAGCCACC 1144
Qy      660 ----- AGGC 663
Db      1145 ACAGACCCGCGCAGTCCGCACTTTAGAACACTCTTGAGGCTGTTCTGATTTTATAGGC 1204
Qy      664 AACTATGAGAAAGTGGGATGAGAAAGCTTCAAAAGTATGTCAGAGAGAAAGGATTTGC 723
Db      1205 AACTATGAGAAAGTGGGATGAGAAAGCTTCAAAAGTATGTCAGAGAGAAAGGATTTGC 1264
Qy      724 ATGCCCCACTCTTCAAAATCTAAGTATAGCAGAGGAGCAGAGCTTTGATTAAGCTCTG 783
Db      1265 ATGCCCCACTCTTCAAAATCTAAGTATAGCAGAGGAGCAGAGCTTTGATTAAGCTCTG 1324
Qy      784 AAGAAGCTCACAAGTCACTTGCCCAAGGCGCGGTGTGCTTACTTCTGTAGAGGCGATG 843
Db      1325 AAGAAGCTCACAAGTCACTTGCCCAAGGCGCGGTGTGCTTACTTCTGTAGAGGCGATG 1384
Qy      844 ACGGTGAGAGTCTGTGATGAGCAGATGAGGCGCTGTGCTTACTTCTGTAGAGGCGATG 903
Db      1385 ACGGTGAGAGTCTGTGATGAGCAGATGAGGCGCTGTGCTTACTTCTGTAGAGGCGATG 1444
Qy      904 CTGGGCGAGGAAACCAAGATGCACTTTATTTAGATCTCAAGAAACAGATCTTATGAGAA 963
Db      1445 CTGGGCGAGGAAACCAAGATGCACTTTATTTAGATCTCAAGAAACAGATCTTATGAGAA 1504
Qy      964 GACAGAAAGAAATGCAAGGTGCTTCTTCAAGGTTTGGAGACATATTAACAGAAAGT 1023
Db      1505 GACAGAAAGAAATGCAAGGTGCTTCTTCAAGGTTTGGAGACATATTAACAGAAAGT 1564
Qy      1024 GAGTCCCTGTGCTGCAATGCCCCAGCTTGAATCTAAGAGTCAAGTTCAGGGCCATC 1083
Db      1565 GAGTCCCTGTGCTGCAATGCCCCAGCTTGAATCTAAGAGTCAAGTTCAGGGCCATC 1624
Qy      1084 ACTGAGCTGAGGAGCAGGCTCATCTAA 1110
Db      1625 ACTGAGCTGAGGAGCAGGCTCATCTAA 1651

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ID      AAF29995 standard; DNA; 2064 BP.
XX
AC      AAF29995;
XX
DT      06-APR-2001 (first entry)
XX
DE      Human GRMx-Ig DNA.
XX
KW      Human; metabotropic glutamate receptor; schizophrenia; GRMx;
XX      Alzheimer's; Parkinson's; stroke; depression; anxiety; pain; ds.
XX
OS      Homo sapiens.
XX      MO200102566-A1.
XX
PD      11-JAN-2001.
XX
PF      27-JUN-2000; 200MO-US17798.
XX
PR      02-JUL-1999; 99US-0346326.
XX
PA      (NEUR-) NEUROCRINE BIOSCIENCES INC.
XX
PI      Schwarz DA, Maki RA;
XX
PT      WPI; 2001-123112/13.
XX
DR      Novel metabotropic glutamate receptor for prevention, treatment of
XX      conditions associated with undesirable glutamate levels, e.g.
XX      Alzheimer's, Parkinson's disease, stroke, depression, anxiety, pain and
XX      schizophrenia -
XX
PS      Claim 2; Fig 11; 59pp; English.
XX
CC      The present invention relates to human metabotropic glutamate
XX      receptor. An agent that decreases expression or activity of the
XX      metabotropic glutamate receptor is useful for treating schizophrenia.
XX      Metabotropic glutamate receptor polynucleotides, polypeptides
XX      are useful for treating diseases associated with undesirable
XX      levels of glutamate, such as Alzheimer's disease, Parkinson's
XX      disease, stroke, depression, anxiety, pain and schizophrenia.
XX
SQ      Sequence 2064 BP; 518 A; 466 C; 519 G; 561 T; 0 other;
Query Match      81.8%; Score 907.8; DB 22; Length 2064;
Best Local Similarity 99.8%; Pred. No. 1.1e-276;
Matches 909; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy      1 ATGATCCTTCTGTGATCTGTCAGTCTTACTTTGAAAGAGATGCTCGAGAGTGA 60
Db      365 ATGATCCTTCTGTGATCTGTCAGTCTTACTTTGAAAGAGATGCTCGAGAGTGA 424
Qy      61 CAGTCCAGTGAAGAGAGGCTGTGCTCACATGCTGGGTGACATCATTTATGAGCTCTC 120
Db      425 CAGTCCAGTGAAGAGAGGCTGTGCTCACATGCTGGGTGACATCATTTATGAGCTCTC 484
Qy      121 TTTTCTGTTCAATACACAGCTTACTGTGACGAGGTTCAAGAGAGAGTGTGGGCGATG 180
Db      485 TTTTCTGTTCAATACACAGCTTACTGTGACGAGGTTCAAGAGAGAGTGTGGGCGATG 544
Qy      181 CGTGAACAGTATGAGCATTGAGAGTGAAGGCGCATGCTGATACCTCTGAAAGATCAAT 240
Db      545 CGTGAACAGTATGAGCATTGAGAGTGAAGGCGCATGCTGATACCTCTGAAAGATCAAT 604
Qy      241 TCAGACCCCACTCTTGGCCCAATCATCACTGGGCTGTGAGATTAAGGATTCCTGCTGG 300
Db      605 TCAGACCCCACTCTTGGCCCAATCATCACTGGGCTGTGAGATTAAGGATTCCTGCTGG 664
Qy      301 CATTGGCTGTGGCCCTTAGAGCAGAGATTGAGTTCAATAGATTCCTCATTTCTTCG 360
Db      665 CATTGGCTGTGGCCCTTAGAGCAGAGATTGAGTTCAATAGATTCCTCATTTCTTCG 724
Qy      361 GAAGAGAAAGAGGCTGTGATGCTGTGATGAGCTGCTCTCTCTTCTCCGCTCCAG 420

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Db	725	GAAAGGAGAGAGGGCTTGGTGTGCTCTGTGGATGGCTCTCTCTCTTCCGCTCCAG	784
Qy	421	AAGCCCATAGTAGGGGTCATTGGGCTTGATTCAGTTCTTTAGCCATTCAAGTCCAGAT	480
Db	785	AAGCCCATAGTAGGGGTCATTGGGCTTGATTCAGTTCTTTAGCCATTCAAGTCCAGAT	844
Qy	481	TTGCTCCAGCTTTTCCACATACCTCAGATTGGCTTCTCAGCAACCATTAGATCTGAGT	540
Db	845	TTGCTCCAGCTTTTCCACATACCTCAGATTGGCTTCTCAGCAACCATTAGATCTGAGT	904
Qy	541	GACAAAGACTCTGTTCAATATTTTCATGAGGCTTGTCCTTCAGATGCTCAGAGCCAGG	600
Db	905	GACAAAGACTCTGTTCAATATTTTCATGAGGCTTGTCCTTCAGATGCTCAGAGCCAGG	964
Qy	601	TCCATGGTGGACATAGTGAAGAGGACAACTGGACCTATGTATCAAGCCGTACACAAAG	660
Db	965	TCCATGGTGGACATAGTGAAGAGGACAACTGGACCTATGTATCAAGCCGTACACAAAG	1024
Qy	661	GGCAACTATGAGAGAAAGTGGAGTGGAGAGCCCTTCAAGATATGTGCGAGAGAGAGGATT	720
Db	1025	GGCAACTATGAGAGAAAGTGGAGTGGAGAGCCCTTCAAGATATGTGCGAGAGAGAGGATT	1084
Qy	721	TGCATGCGCCCACTCTTACAAATCTACAGTATGCAAGGGAGACAGACTTTGATTAAGCTG	780
Db	1085	TGCATGCGCCCACTCTTACAAATCTACAGTATGCAAGGGAGACAGACTTTGATTAAGCTG	1144
Qy	781	CTGAAGAAAGCTCACAAGTCACTTGGCCCAAGGCCGGGTGTGTGGCTTACTTGTGTAGGGC	840
Db	1145	CTGAAGAAAGCTCACAAGTCACTTGGCCCAAGGCCGGGTGTGTGGCTTACTTGTGTAGGGC	1204
Qy	841	ATGACGGTGAAGAGTCTGCTGTATGGCCATGAGGGCCCTGGGCTCTTAGTGGAGAAATTTCTG	900
Db	1205	ATGACGGTGAAGAGTCTGCTGTATGGCCATGAGGGCCCTGGGCTCTTAGTGGAGAAATTTCTG	1264
Qy	901	CTTCTGGGCGAG 911	
Db	1265	CTTCTGGGCGAG 1275	

XX	RESULT 7
XX	AAC85785
ID	AAC85785 standard; cDNA; 2826 BP.
XX	
AC	AAC85785;
XX	
XX	
DT	18-JUL-2001 (first entry)
XX	
DE	cDNA encoding metabotropic glutamate receptor.
XX	
XX	Human; metabotropic glutamate receptor; mglur; splice variant;
KM	mgluR5; G-protein-coupled receptor; glutamate; neurological disorder
XX	anticonsvulsant; neuroprotectant; analgesic; cognitive enhancer;
KM	muscle relaxant; ss.
XX	
OS	Homo sapiens.
XX	
XX	WO200130829-A1.
PN	
XX	
PD	03-MAY-2001.
XX	
PF	25-OCT-2000; 2000WO-US29356.
XX	
PR	25-OCT-1999; 99US-0161481.
XX	
PR	24-OCT-2000; 2000US-0695481.
XX	
PA	(NPSF-) NPS PHARM INC.
XX	
PI	Krapcho K, Storchmann T, Levinthal C, Hammerland L, Storchmann L;
XX	
DR	WPI; 2001-308615/32.
XX	
DR	P-PSDB; AAB47217.
XX	

PT New nucleic acid encoding an isoform of human metabotropic glutamate  
PT receptor, for identifying potential therapeutic agents for neurological  
PT disease  
XX  
Claim 2: Page 51-56; 86pp; English.  
PS  
P8

CC This sequence encodes a human metabotropic glutamate receptor (mglur) .  
CC mglur is a splice variant of human metabotropic glutamate receptor 5  
CC (mglur5). mglur's are G-protein-coupled receptors capable of activating  
CC a variety of intracellular second messenger systems following the  
CC binding of glutamate. Recombinant mglur DNA and compounds that bind to,  
CC or modulate activity of mglur are useful for diagnosing or treating  
CC neurological disorders, e.g. as anticonvulsants, neuroprotectants,  
CC analgesics, cognitive enhancers and muscle relaxants.

**SQ** Sequence 2826 BP; 729 A; 679 C; 712 G; 706 T; 0 other;

Query Match	80.0%;	Score 888.4;	DB 22;	Length 2826;
Best Local Similarity	98.2%;	Pred NC 1	Re=270.	

Matches 898; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

1 ATGCTCCTTCTGTGATCCTGTCACTTACTTTTGAAGAGATGTCCTGGAGTGCA 60

Db 1 ATGTCCTTCTGTTGATCCTGTCAGTCTTACTTTTGAAGAAGATGTCCGTGGAGTGCA 60

61 CAGTCCAGTGAGAGGGTGGCTCACATGCTGGGTGACATCATTTGGAGCTCTC 122

Db 61 CAGTCCAGTGAGAGGAGGGTGGCTCACATGCCGGTGACATCATTTGGAGCTCTC 12

121 TTTTCTGTTATCACCAGCCTACTGTGGACGAAGTTCATGAGAGGAAGTGTGGGCAGTC 18

Db 121 TTTTCTGTCATCACCAGCCTACTGTGGACAAAGTTCATGAGAGGAAGTGTGGCGCTC 18

181 CGTGACAGTATGGCATT CAGAGAGTGGAGGCCATGCTGCATACCTGGAAAGGATCAAT 24

Db 181 CGTGACAGTATGGCATT CAGAGAGTGGAGGCCATGCTGCATACCCCTGGAAAGGATCAAT 24

241 TCAGACCCCACTCTTGCCCAATCACA CACTGGGCTGTGAGATAAGGATTCCTGCTGG 300

Db 241 TCAGACCCACACTCTTGCCCAACATCACA CTGGGCTGTGAGATAAGGACTCCTGCTGG 300

301 CATTGGGCTGTGGCCCTAGAGCAGAGCATTGAGTTCATAGAAGATTCCCTCATTCTTCG 360

Db 301 CATTGGCTGTGGCCCTAGAGCAGAGCATTTGAGTTCATAAGAGATTTCCCTCATTTCTTCA 36

361 GAAGAGGAGGGCTTGGTATGCTCTGTGATGGCTCCTCCTCTTCCTTCCGGCTCCAAG 422

Db 361 GAAGAGGAAGGCTTGGTACGCTGTGTGATGGCTCCTCCTCTTCTCCGCTCCAAG 42

421 AAGCCATAGGGGTCATTGGCCTGGTCCAGTCTTTAGCCATTCAAGTCCAGAT 48

Db 421. AAGCCATAGTAGGGTCATTGGGCTGCGTCCAGTCTGTAGCCATTCAAGTCCAGAT 48

481 TTGCTCCAGCTTTTCAACATACCTCAGATTGCTTACTCAGCAACCATCATGGATCTGAGT 54

Db 481 TTGCTCCAGCTTTTCAACATACCTCAGATTGCTTACTCAGCAACCAAGCATGATCTGAGT 54

541 GACAGACTCTGTTCAATATTTTCATGAGGGTTGTGCCCTTCAGATGCTCAGCAGGCAAGG 600

Db 541 GACAGACTCTGTTCAATATTTCA<sup>2</sup>TGAGGCTTGTGCCCTTCAGATGCTCAGCAGGCAAGG 60

601 TCCATGGTGACATAGTGAAGAGGTACAACTGGACCTATGTATCAGCCGTACACACAGAA 66

Db 601 GCCATGGTGACATAGTGAAGAGGTACAACCTGACCTATGTATCAGCCGTGCACACAGAA 66

661 GGCACTATGAGAAAGTGGATGGAAGCCTTCAAGATATGTCAGCGAAGGAGGATT 72

Db 661 GGCAACTATGGAGAAGTGGATGGAAGCCTTCAAGATATGTCAGCGAAGGAAGGATT 72

721 TGCATCGCCACTCTTACAAAATCTACAGTAATGCAGGGAGCAGAGCTTTGATAAGCTG 78

Db 721 TGCATCGCCCACTCTTACAAATCTACAGTAATGCAGGGAGCAGAGCTTTGATAAGCTG 78

QY 781 CTGAAGAGCTCAAGAGTCACTTCCCAAGAGCCCGGATGAGCTTACTTCTGAGAGGC 840  
DB 781 CTGAAGAGCTCAAGAGTCACTTCCCAAGAGCCCGGATGAGCTTACTTCTGAGAGGC 840  
QY 841 ATGACGGTGAAGAGTCTGCTGATGAGCATGAGGCTGAGTCTAGTGGAGAAATTTCTG 900  
DB 841 ATGACGGTGAAGAGTCTGCTGATGAGCATGAGGCTGAGTCTAGTGGAGAAATTTCTG 900  
QY 901 CTTCTGGGAGGGA 914  
DB 901 CTTCTGGGAGGGA 914

RESULT 8  
AAC85787  
ID AAC85787 standard; cDNA; 3129 BP.  
XX AAC85787;  
XX 18-JUL-2001 (first entry)  
XX  
XX cDNA encoding chimeric receptor containing hmGluR5d portion.  
XX Human; metabotropic glutamate receptor; mglur; splice variant;  
XX mglur5; G-protein-coupled receptor; glutamate; neurological disorder;  
XX anticonvulsant; neuroprotectant; analgesic; cognitive enhancer;  
XX muscle relaxant; calcium receptor; CaR; mglur5d; ss.  
XX Chimeric - Homo sapiens.  
XX MO200130829-A1.  
XX 03-MAY-2001.  
XX 25-OCT-2000; 2000MO-US29356.  
XX PF 25-OCT-1999; 99US-0161481.  
XX PR 24-OCT-2000; 2000US-0695481.  
XX (NPSF-) NPS PHARM INC.  
XX Krapcho K, Stormann T, Levinthal C, Hammerland L, Storchmann L;  
XX WPI; 2001-308615/32.  
XX DR P-PSDB; AABA7219.  
XX  
XX New nucleic acid encoding an isoform of human metabotropic glutamate  
XX receptor, for identifying potential therapeutic agents for neurological  
XX disease  
XX  
XX Claim 18; Page 70-75; 86pp; English.  
XX  
XX This sequence encodes a chimeric receptor comprising the intracellular  
XX cytoplasmic tail of the human calcium receptor (CaR) and the extra-  
XX cellular and seven transmembrane domains of the human metabotropic  
XX glutamate receptor (mglur) splice variant of human metabotropic  
XX glutamate receptor 5 (mglur5), mglur5d. mglur5 are G-protein-coupled  
XX receptors capable of activating a variety of intracellular second  
XX messenger systems following the binding of glutamate. Recombinant  
XX mglur5d DNA and compounds that bind to, or modulate activity of it  
XX are useful for diagnosing or treating neurological disorders, e.g.  
XX as anticonvulsants, neuroprotectants, analgesics, cognitive enhancers  
XX and muscle relaxants.  
XX  
XX Sequence 3129 BP; 806 A; 782 C; 804 G; 737 T; 0 other;

QY Query Match 80.0%; Score 888.4; DB 22; Length 3129;  
Best Local Similarity 98.2%; Pred. No. 1, 9e-270;  
Matches 898; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1 ATGGTCTTGTGATCTGTCAGTCTTACTTTGAAAGAGATGTCCTGGAGATGCA 60  
DB 1 ATGGTCTTGTGATCTGTCAGTCTTACTTTGAAAGAGATGTCCTGGAGATGCA 60

QY 61 CAGTCCAGTGAAGAGAGGGATGAGGCTCAATGCTGGGTGACATCATTTATTTGAGCTCTC 120  
DB 61 CAGTCCAGTGAAGAGAGGGATGAGGCTCAATGCTGGGTGACATCATTTATTTGAGCTCTC 120  
QY 121 TTTTCTGTTTCATCAGAGCTTACTTGTGACGAAGTTTCATGAGAGAGTGGGGAGTC 180  
DB 121 TTTTCTGTTTCATCAGAGCTTACTTGTGACGAAGTTTCATGAGAGAGTGGGGAGTC 180  
QY 181 CGTGAACAGTATGAGCATTCAGAGAGTGAAGGCCATGCTGATCCCTGGAAAGATCAAT 240  
DB 181 CGTGAACAGTATGAGCATTCAGAGAGTGAAGGCCATGCTGATCCCTGGAAAGATCAAT 240  
QY 241 TCAGACCCCACTCTTGGCCCAATCACTGAGGCTGTGAGATTAAGAGATTCCTGCTG 300  
DB 241 TCAGACCCCACTCTTGGCCCAATCACTGAGGCTGTGAGATTAAGAGATTCCTGCTG 300  
QY 301 CATTGGCTGTGAGCCCTAGAGCAGAGCATTTAGATTAAGAGATTCCTGATTTCTTGC 360  
DB 301 CATTGGCTGTGAGCCCTAGAGCAGAGCATTTAGATTAAGAGATTCCTGATTTCTTGC 360  
QY 361 GAAGAGAGAGAGGCTTTGATGCTCTGTGAGATGCTCTCTTCTTCCGCTCCAG 420  
DB 361 GAAGAGAGAGAGGCTTTGATGCTCTGTGAGATGCTCTCTTCTTCCGCTCCAG 420  
QY 421 AAGCCCATAGTAGGGGTCAATGGGCTGCTCAGTTCTTTAGCCATTGAGTCCAGAAAT 480  
DB 421 AAGCCCATAGTAGGGGTCAATGGGCTGCTCAGTTCTTTAGCCATTGAGTCCAGAAAT 480  
QY 481 TTGCTCAGCTTTTCAACATCTCAATGCTTACTCAAGCAACATCATGATCTGAGT 540  
DB 481 TTGCTCAGCTTTTCAACATCTCAATGCTTACTCAAGCAACATCATGATCTGAGT 540  
QY 541 GACAAAGCTCTGTTCAAAATTTTCATGAGAGGTTGCTTCAATGCTCAAGAGGCAAG 600  
DB 541 GACAAAGCTCTGTTCAAAATTTTCATGAGAGGTTGCTTCAATGCTCAAGAGGCAAG 600  
QY 601 TCCATGATGACATGATGAGAGGATCAACTGAGCCTATGATCAACCCGTACACAGAA 660  
DB 601 TCCATGATGACATGATGAGAGGATCAACTGAGCCTATGATCAACCCGTACACAGAA 660  
QY 661 GGCACATATGAGAAAGTGGATGAGAGGCTTCAAAAGATATGTCAGCGAAGAGGAT 720  
DB 661 GGCACATATGAGAAAGTGGATGAGAGGCTTCAAAAGATATGTCAGCGAAGAGGAT 720  
QY 721 TGCATGCCCCACTCTTACAAATCTACAGTAATGACGGGAGAGAGCTTTGATTAAGCTG 780  
DB 721 TGCATGCCCCACTCTTACAAATCTACAGTAATGACGGGAGAGAGCTTTGATTAAGCTG 780  
QY 781 CTGAAGAGCTCAAGAGTCACTTGGCCCAAGAGCCCGGATGAGCTTACTTCTGAGAGG 840  
DB 781 CTGAAGAGCTCAAGAGTCACTTGGCCCAAGAGCCCGGATGAGCTTACTTCTGAGAGG 840  
QY 841 ATGACGGTGAAGAGTCTGCTGATGAGCATGAGGCTGAGTCTAGTGGAGAAATTTCTG 900  
DB 841 ATGACGGTGAAGAGTCTGCTGATGAGCATGAGGCTGAGTCTAGTGGAGAAATTTCTG 900  
QY 901 CTTCTGGGAGGGA 914  
DB 901 CTTCTGGGAGGGA 914

RESULT 9  
ACAS6535  
ID ACAS6535 standard; cDNA; 4078 BP.  
XX ACAS6535;  
XX 06-JUN-2003 (first entry)  
XX  
XX Human signalling pathway polynucleotide probe SEQ ID NO 1133.  
XX Human; probe; ss; array element; Parkinson's disease;

KM	signalling pathway population; cancer; adenocarcinoma; leukaemia;
RN	immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.
XX	
OS	Homo sapiens.
XX	
PN	US6500938-B1.
PD	31-DEC-2002.
PF	30-JAN-1998; 98US-0016434.
PR	30-JAN-1998; 98US-0016434.
XX	(INCY-) INCYTE GENOMICS INC.
PA	Au-Young J, Sellhammer JJ;
XX	WPI; 2003-352189/33.
PT	Combination of polynucleotide probes, useful as array elements in a
FT	microarray for monitoring the expression of a number of target
PT	polynucleotides -
XX	
XX	Claim 1; SEQ ID NO 1133; 65pp; English.
CC	The invention relates to a combination which, comprises a number of
CC	polynucleotide probes comprising a sequence selected from one of the 1490
CC	sequences mentioned in the specification. The combination is useful as an
CC	array element in a microarray for monitoring the expression of a number
CC	of target polynucleotides. The microarray is particularly useful in the
CC	diagnosis and treatment of cancer and immunopathology and neuropathology.
CC	The microarray is useful in diagnostics and treatment regimens, drug
CC	discovery and development, toxicological and carcinogenically studies,
CC	forensics and pharmacogenomics. The microarray is also useful for
CC	monitoring progression of diseases and for developing sophisticated
CC	profiles for the effects of currently available therapeutic drugs. The
CC	combination is also useful for purifying a subpopulation of mRNAs, cDNAs
CC	and genomic fragments and in research and diagnostic applications. The
CC	array can detect changes in expression in a large number of genes coding
CC	for different signalling pathway populations which can be used to diagnose
CC	various diseases including cancer e.g. adenocarcinoma and leukaemia,
CC	immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease
CC	and Parkinson's disease. The present sequence represents a polynucleotide
CC	probe of the invention.
CC	Note: The sequence data for this patent did not form part of the printed
CC	specification but was obtained in electronic format directly from USPTO
CC	at seqdata.uspto.gov/sequence.html?docID=06500938B1.
XX	
SQ	Sequence 4078 BP; 994 A; 1074 C; 1076 G; 934 T; 0 other;
	Query Match 80.0%; Score 888.4; DB 25; Length 4078;
	Best Local Similarity 98.2%; Pred. No. 2,3e-270;
	Matches 898; Conservative 0; Mismatches 16; Indels 0; Gaps 0
QY	1 ATGCTCCTTCGTGGATCTCTGCACTTTACTTTTGAAGAAGATGTCGTGGAGTGCA 60
DB	151 ATGCTCCTTCGTGGATCTCTGCACTTTACTTTTGAAGAAGATGTCGTGGAGTGCA 210
QY	CAGTCACAGTAGAGAGGGGTGGTGCCTCACATGCTGGGGGACATCATATTATGAGCTGC 120
DB	211 CAGTCACAGTAGAGAGGGGTGGTGCCTCACATGCCGGGTGACATCATTTTGAAGCTTTC 270
QY	121 TTTTCTGTTCATCACAGCCTTA CTGTGGACGAAGTTTCATGAGAGGAAGTGTGGGCACTC 180
DB	271 TTTTCTGTTCATCACAGCCTTA CTGTGGACGAAGTTTCATGAGAGGAAGTGTGGGCGCTC 330
QY	181 CGTGAACGATATGGATTTCAGAGAGTGAAGGCCATGCTGCATACCCTGGAAAGATCAAT 240
DB	331 CGTGAACGATATGGATTTCAGAGAGTGAAGGCCATGCTGCATACCCTGGAAAGATCAAT 390
QY	241 TCAGACCCCACACCTTTGGCCCCAATCAACATCGGGGCTGGAGATAAAGGATTCCTCGCTGG 300
DB	391 TCAGACCCCACACCTTTGGCCCCAATCAACATCGGGGCTGGAGATAAAGGATTCCTCGCTGG 450

QY	301	CATTGGCTGGGCGCCCTAGAGCAGAGCATTGAGTTCAATAGAGATTCCTCATTTCTTCG	360
Db	451	CATTGGCTGGGCGCCCTAGAGCAGAGCATTGAGTTCAATAGAGATTCCTCATTTCTTCA	510
QY	361	GAAGAGGAAGAGGCGTTGGTATGCTCTGTGTGANTGGCTCTCTCTTCCCTTCGCTCAAG	420
Db	511	GAAGAGGAAGAGGCGTTGGTATGCTCTGTGTGANTGGCTCTCTCTTCCCTTCGCTCAAG	570
QY	421	AAGGCCATPAGAGGGGTCATTGGGCGCGTTCGACGTTCTTTAGGCATTGAGGTCCAGAT	480
QY	571	AAGGCCATPAGAGGGGTCATTGGGCGCGTTCGACGTTCTTTAGGCATTGAGGTCCAGAT	630
Db	631	TTGCTCCAGCTTTTCAACATATCCTCAATGCTTACTCAGAACACAGATGGATCTGAGT	690
QY	541	GACAAAGACTGTGTTCAAAATATTTTCATGAGGTTGTGCTTCAATGCTCAGCAGGCAAG	600
Db	691	GACAAAGACTGTGTTCAAAATATTTTCATGAGGTTGTGCTTCAATGCTCAGCAGGCAAG	750
QY	601	TTCATGTGTGACATATGGAAGAGGTAACTGACGACCTATGATCAGCGCTACACAGAA	660
Db	751	GCCATGTGTGACATATGGAAGAGGTAACTGACGACCTATGATCAGCGCTACACAGAA	810
QY	661	GGCAACTATGAGAGAAATGGGATGGAAGCCTTCAAAATATATGTCAGCGAAGAAAGGATT	720
Db	811	GGCAACTATGAGAGAAATGGGATGGAAGCCTTCAAAATATATGTCAGCGAAGAAAGGATT	870
QY	721	TGCATGCGCCCACTTTACAAATATCTACATATGACGAGGAGACAGAGCTTTGATTAAGCTG	780
Db	871	TGCATGCGCCCACTTTACAAATATCTACATATGACGAGGAGACAGAGCTTTGATTAAGCTG	930
QY	781	CTGAAAGAGCTCAACAATCACTGGCCCAAGGCGCGGGTGGTGGCTACTCTCTGTGAGAGGC	840
Db	931	CTGAAAGAGCTCAACAATCACTGGCCCAAGGCGCGGGTGGTGGCTACTCTCTGTGAGAGGC	990
QY	841	ATGACGGTGAAGAGTCTGCTGATGATGGCCATGAGGCGCCTGGGTCATGATGAGAAATTTCTG	900
Db	991	ATGACGGTGAAGAGTCTGCTGATGATGGCCATGAGGCGCCTGGGTCATGAGGAGAAATTTCTG	1050
QY	901	CTTCTGGGGCAGGGA 914	
Db	1051	CTTCTGGGGCAGTGA 1064	
RESULT 10			
AAD04990			
ID	AAD04990 standard; cDNA; 4207 BP.		
AC	AAD04990;		
XX	17-JUL-2001 (first entry)		
XX	Human metabotropic glutamate receptor, mgluR5A cDNA mutant.		
XX	Human; metabotropic glutamate receptor; mgluR5A; excitatory amino acid;		
KW	EAA; central nervous system; CNS; presynaptic release; neurotransmitter;		
KW	postsynaptic sensitivity; glutamate excitation; mutant; 88.		
XX	Homo sapiens.		
OS	Synthetic.		
XX	Key		
PH	mutation		
FT	mutation		
FT	mutation		
XX	US6211353-B1.		
XX	03-APR-2001.		
XX			

PF 07-JUN-1996; 96US-0660148.  
 XX 29-JUL-1994; 94US-0282853.  
 XX (BLIL ) LILLY & CO ELI.  
 XX Burnett JP, Mayne NG, Sharp RL, Snyder YM;  
 PI WPI; 2001-289639/30.  
 XX  
 XX New isolated nucleic acids for producing human metabotropic glutamate  
 PT receptor, which are useful for modulating the presynaptic release of  
 PT glutamate or the postsynaptic sensitivity of the neuronal cell to  
 PT glutamate excitation -  
 XX  
 PS Disclosure; Column -; 53bp; English.  
 XX  
 CC The present sequence is a cDNA mutant encoding human metabotropic  
 CC glutamate receptor, mGluR5A. L-glutamate, the most abundant  
 CC neurotransmitter in the central nervous system (CNS), mediates excitatory  
 CC pathway in mammals. L-glutamate is referred to as excitatory amino acid  
 CC (EAA) and the receptors that respond to glutamate are EAA receptors. The  
 CC receptors are useful for modulating the presynaptic release of glutamate  
 CC and the postsynaptic sensitivity of the neuronal cell to glutamate  
 CC excitation.  
 CC Note: The present sequence is not shown in the specification, but is  
 CC derived from the sequence referred as SEQ ID NO:1, shown in column  
 CC 59-68 (AAd05029) of the specification.  
 CC  
 XX Sequence 4207 BP; 1010 A; 1121 C; 1112 G; 964 T; 0 other;  
 XX  
 Query Match 80.0%; Score 888.4; DB 22; Length 4207;  
 Best Local Similarity 98.2%; Pred. No. 2.3e-270;  
 Matches 898; Conservative 0; Mismatches 16; Indels 0; Gaps 0;  
 QY 1 ATGGCTCTTCTGTTGATCTGTCACTCTTACTTTTGAAGAAGATCCGTGGAGATGCA 60  
 DB 460 ATGGCTCTTCTGTTGATCTGTCACTCTTACTTTTGAAGAAGATCCGTGGAGATGCA 519  
 QY 61 CAGTCCAGTGAAG 120  
 DB 520 CAGTCCAGTGAAG 579  
 QY 121 TTTTCTGTTATCAACGACCTACTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180  
 DB 580 TTTTCTGTTATCAACGACCTACTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 639  
 QY 181 CGTGAACAGTATGATGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 240  
 DB 640 CGTGAACAGTATGATGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 699  
 QY 241 TCAGAACCCCACTCTTGGCCCAATCACTCTGCTGTGATGAAGAGATTCCTGCTGG 300  
 DB 700 TCAGAACCCCACTCTTGGCCCAATCACTCTGCTGTGATGAAGAGATTCCTGCTGG 759  
 QY 301 CATTCGGCTGTGGCCCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATTC 360  
 DB 760 CATTCGGCTGTGGCCCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATTC 819  
 QY 361 GAAG 420  
 DB 820 GAAG 879  
 QY 421 AAGCCATAGTAAAGAT 480  
 DB 880 AAGCCATAGTAAAGAT 939  
 QY 481 TTGCTCAGCTTTTCAACATACCTCAATGCTTAACTCAGAAACATCAAGAGATAGT 540  
 DB 940 TTGCTCAGCTTTTCAACATACCTCAATGCTTAACTCAGAAACATCAAGAGATAGT 999  
 QY 541 GACAAAGCTGTGTTCAATATTTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600

DB 1000 GACAAAGCTGTGTTCAATATTTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1059  
 QY 601 TCATAGTGGACATAGTGAAGAGATCAACTGAGACCTATGATCAGCCGACACAGAA 660  
 DB 1060 GCCATGATGACATAGTGAAGAGATCAACTGAGACCTATGATCAGCCGACACAGAA 1119  
 QY 661 GGCACATATGAT 720  
 DB 1120 GGCACATATGAT 1179  
 QY 721 TCATAGTGGACATAGTGAAGAGATCAACTGAGACCTATGATCAGCCGACACAGAA 780  
 DB 1180 TCATAGTGGACATAGTGAAGAGATCAACTGAGACCTATGATCAGCCGACACAGAA 1239  
 QY 781 CTGAGAGAGCTCAAGATCACTGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840  
 DB 1240 CTGAGAGAGCTCAAGATCACTGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1299  
 QY 841 ATGACGATGATTC 900  
 DB 1300 ATGACGATGATTC 1359  
 QY 901 CTCTGATTC 914  
 DB 1360 CTCTGATTC 1373  
 RESULT 11  
 AAD05029  
 ID AAD05029 standard; cDNA; 4207 BP.  
 XX  
 AC AAD05029;  
 XX  
 DT 17-JUL-2001 (first entry)  
 XX  
 DE Human metabotropic glutamate receptor, mGluR5A cDNA.  
 XX  
 KW Human; metabotropic glutamate receptor; mGluR5A; excitatory amino acid;  
 KW EAA; central nervous system; CNS; presynaptic release; neurotransmitter;  
 KW postsynaptic sensitivity; glutamate excitation; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 460..402  
 FT /product= "Human metabotropic glutamate receptor,  
 FT mGluR5A"  
 XX  
 PN US6211353-B1.  
 XX  
 PD 03-APR-2001.  
 XX  
 PP 07-JUN-1996; 96US-0660148.  
 XX  
 XX 29-JUL-1994; 94US-0282853.  
 XX  
 PA (BLIL ) LILLY & CO ELI.  
 XX  
 PI Burnett JP, Mayne NG, Sharp RL, Snyder YM;  
 DR WPI; 2001-289639/30.  
 XX  
 DR P-PSDB; AAB01156.  
 XX  
 XX New isolated nucleic acids for producing human metabotropic glutamate  
 PT receptor, which are useful for modulating the presynaptic release of  
 PT glutamate or the postsynaptic sensitivity of the neuronal cell to  
 PT glutamate excitation -  
 XX  
 XX Claim 2; Column 59-68; 53bp; English.  
 XX  
 CC The present sequence is a cDNA encoding human metabotropic glutamate  
 CC receptor, mGluR5A. L-glutamate, the most abundant neurotransmitter in

CC the central nervous system (CNS), mediates excitatory pathway in  
CC mammals. l-glutamate is referred to as excitatory amino acid (EAA) and  
CC the receptors that respond to glutamate are EAA receptors. The receptors  
CC are useful for modulating the presynaptic release of glutamate and the  
CC postsynaptic sensitivity of the neuronal cell to glutamate excitation.  
CC Note: The present sequence is stated as being the same as that shown as  
CC SEQ ID NO:1 (AA05033) in column 7-18 of the specification. However the  
CC sequences differ at several positions.

5Q Sequence 4207 BP; 1011 A; 1120 C; 1112 G; 964 T; 0 other;

Query Match	80.0%	Score 888.4	DB 22	Length 4207
Best Local Similarity	98.2%	Pred. NO. 2.3e-270		
Matches 898	Conservative	0	Mismatches 16	Indels 0
			Gaps	0

Qy	ATGGCCCTTCGTGGATCTCTGACGCTTTACCTTTGAAAGAAAGATGTCCTGGAGATGCA	60
Db	ATGGCTCTTCGTGGATCTCTGACGCTTTACCTTTGAAAGAAAGATGTCCTGGAGATGCA	519
Qy	CAGTCCAGTAGAGAGAGGGGTGGCTCAATGCTGGGTGACATCATTTATTTGGACCTCTC	120
Db	CAGTCCAGTAGAGAGAGGGGTGGCTCAATGCCGGGTGACATCATTTATTTGGACCTCTC	579
Qy	TTTTCTGTTCATCACCAAGCTTACTGTGACGAAGTTCAATAGAGGAAGTGTGGGCAAGTC	180
Db	TTTTCTGTTCATCACCAAGCTTACTGTGACGAAGTTCAATAGAGGAAGTGTGGGCGGTGC	639
Qy	CGTAAACGTATGGCATTCAGAGAGTGAAGGCATGCTGCATACCTGTGAAAGATTCAT	240
Db	CGTAAACGTATGGCATTCAGAGAGTGAAGGCATGCTGCATACCTGTGAAAGATTCAT	699
Qy	TCAGACCCCACTCTTGGCCCAACATCACACTGGGCTGTGAGATTAAGGATTCCTGCTGG	300
Db	TCAGACCCCACTCTTGGCCCAACATCACACTGGGCTGTGAGATTAAGGATTCCTGCTGG	759
Qy	CATTGGGCTGTGGCCCTTAGAGACAGCATTTGAGTTCAATAGAGATTTCCCTCATTTCTTGG	360
Db	CATTGGGCTGTGGCCCTTAGAGACAGCATTTGAGTTCAATAGAGATTTCCCTCATTTCTTCA	819
Qy	GAAGAGGAAGGGGCTGGTATGCTGCTGTGATGAGATGGCTCTCTCTTCCCTCCGCTCCAG	420
Db	GAAGAGGAAGGGGCTGGTATGCTGCTGTGATGAGATGGCTCTCTCTTCCCTCCGCTCCAG	879
Qy	AAGCCCATAGTAGGGGTCATTGGGCTGTGCTCAAGTTCTTTAGCCATTCAAGTCCAGAT	480
Db	AAGCCCATAGTAGGGGTCATTGGGCTGTGCTCAAGTTCTTTAGCCATTCAAGTCCAGAT	939
Qy	TTGCTCCAAGCTTTTCAACATACCTTCAGATTGCTTACTCAGCAACAGCATGGATCTGAGT	540
Db	TTGCTCCAAGCTTTTCAACATACCTTCAGATTGCTTACTCAGCAACAGCATGGATCTGAGT	999
Qy	GACAAAGACTCGTTCAAAATATTTTCAATGAGGGGTGGCTTCAGATGCTCAGAGGCAAG	600
Db	GACAAAGACTCGTTCAAAATATTTTCAATGAGGGGTGGCTTCAGATGCTCAGAGGCAAG	1055
Qy	TCCATGGTGCATATAGTGAAAGAGGTCACTGACCTATGTATGACCCGTACACACAGA	660
Db	TCCATGGTGCATATAGTGAAAGAGGTCACTGACCTATGTATGACCCGTGACACACAGA	1119
Qy	GGCAACTATGTGAGAAAGTGGAGTGAAGCCTTCAAAAGTATGTCAAGCAAGAGAGGATTT	720
Db	GGCAACTATGTGAGAAAGTGGAGTGAAGCCTTCAAAAGTATGTCAAGCAAGAGAGGATTT	1179
Qy	TGCATCGCCCACTCTTACAAATATCAACGTATGTAGGAGGGAGACAGAGCTTTGATAGCTG	780
Db	TGCATCGCCCACTCTTACAAATATCAACGTATGTAGGAGGGAGACAGAGCTTTGATAGCTG	1233
Qy	CTGAAGAAGCTCACAAAGTCACTTGGCCCAAGGCCCGGGTGTGTGCCCTTCTGTGAGGGC	840
Db	CTGAAGAAGCTCACAAAGTCACTTGGCCCAAGGCCCGGGTGTGTGCCCTTCTGTGAGGGC	1299
Qy	ATGACGGTGAAGGCTCTGCTGATGGCCATTAAGCGGCTTGGGCTTATGTGGAGAAATTTCTG	900
Db	ATGACGGTGAAGGCTCTGCTGATGGCCATTAAGCGGCTTGGGCTTATGTGGAGAAATTTCTG	

Db 1300 ATGACGGTGAGAGTCTGCTGATGGCCATGAGGCGCTGGTCTAGCGGAGATTCTG 1359

901 CTTCTGGGCAAGGA 914

Db 1360 CTTCTGGGCAGTGA 1373

RESULT 12

ID AAD05030 standard; mRNA; 4207 BP.

AC AAD05030 ;

DT 17-JUL-2001 (first entry)

DE Human metabotropic glutamate receptor, mGluR5 mRNA

KW Human; metabotropic glutamate receptor; mGluR5A; excitatory amino acid;

**КВ** **роствынартис**

OS Homo sapiens

FH	Key	Location/Qualifiers
1	1	1
2	2	2
3	3	3
4	4	4
5	5	5
6	6	6
7	7	7
8	8	8
9	9	9
10	10	10
11	11	11
12	12	12
13	13	13
14	14	14
15	15	15
16	16	16
17	17	17
18	18	18
19	19	19
20	20	20
21	21	21
22	22	22
23	23	23
24	24	24
25	25	25
26	26	26
27	27	27
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91	91	91
92	92	92
93	93	93
94	94	94
95	95	95
96	96	96
97	97	97
98	98	98
99	99	99
100	100	100

RT

PT

PN US6211353-B1.

PD 03-APR-2001.

PF 07-JUN-1996; 96US-066

PR 29-JUL-1994; 94US-0282853.

PA (ELIL ) LILLY &amp; CO E

PI Burnett JP, Mayn

DR WPI; 2001-289639/30.

XX

PT receptors, which are

PT glutamate excitator

PS Claim 2; Column 43-44

CC The present sequence

CC the central nervous

CC the receptors that

CC postsynaptic sensitivity

**SQ Sequence 4207 BP; 10**

Query Match

Matches 675; Conservation

QY 1 ATGGTCCTTCT

Db 460 AUGGUCCUUCU

61 CAGTCCAGTGA

Db 520 CAGUCCAGUGA





Best Local Similarity 98.2%; Pred. No. 2.3e-270;  
Matches 898; Conservative 0; Mismatches 16; Indels 0; Gaps 0

QY	1	ATGGCCCTTGGTGAATCTCGTCACTCTTAACTTTTGAAGAAGATGTCGGTGGATGCA	60
Db	460	ATGGTCTCTTCTGTATCTCTGCACTCTTACTTTTGAAGAAGATGTCGGTGGATGCA	519
QY	61	CAGTCCAGTGAAGAGGGGTGGTCAATGCTGGGTGACATCAATTAATGGACTCTC	120
Db	520	CAGTCCAGTGAAGAGGGGTGGTCAATGCTGGGTGACATCAATTAATGGACTCTC	579
QY	121	TTTTCTGTTCATCACACGCTTACTGTGACGAATTCATGAGGAAGTGTGGGCACTC	180
Db	580	TTTTCTGTTCATCACACGCTTACTGTGACGAATTCATGAGGAAGTGTGGGCGCTC	639
QY	181	CGTGAACGTATGGGCAATCAGAGATGGAAGGCATGCTGCATACCTGTGAAGAATCAAT	240
Db	640	CGTGAACGTATGGGCAATCAGAGATGGAAGGCATGCTGCATACCTGTGAAGAATCAAT	699
QY	241	TCAGACCCCAACTCTTCCCAACATCAACTGCGGCTGTGAGATTAAGGAAATTCGCTGG	300
Db	700	TCAGACCCCAACTCTTCCCAACATCAACTGCGGCTGTGAGATTAAGGAAATTCGCTGG	759
QY	301	CATTGGCTGTGGCCCTTAAAGCAGCAATGAGTTCATPAAGATTCCTCATTTCTTTCG	360
Db	760	CATTGGCTGTGGCCCTTAAAGCAGCAATGAGTTCATPAAGATTCCTCATTTCTTTCG	819
QY	361	GAAAGGGAAGAGGCGTTGGTATGCTCTGTGATAGTGGCTCTCCTCTTCTTCGCTCCAG	420
Db	820	GAAAGGGAAGAGGCGTTGGTATGCTCTGTGATAGTGGCTCTCCTCTTCTTCGCTCCAG	879
QY	421	AAGCCCATAGTAGGGGTCATTGGGCGCTGGTTCAGATCTTTAGCCATTCAAGGTCAGAAAT	480
Db	880	AAGCCCATAGTAGGGGTCATTGGGCGCTGGTTCAGATCTTTAGCCATTCAAGGTCAGAAAT	939
QY	481	TTGCTCCAAGCTTTTCACATACCTCAATGCTTACTCAGCAACCATATGATCTAGT	540
Db	940	TTGCTCCAAGCTTTTCACATACCTCAATGCTTACTCAGCAACCATATGATCTAGT	999
QY	541	GACAAGACTCGTTCAAAATATTTCAATGAGGTTGGCCCTTCAAGATGCTCAGAGCCAGG	600
Db	1000	GACAAGACTCGTTCAAAATATTTCAATGAGGTTGGCCCTTCAAGATGCTCAGAGCCAGG	1055
QY	601	TCCATGTGTGACATAGTGAAGAGGTACAATGSACTTAATGATCAGCGGTACACAGAA	660
Db	1060	GCCATGTGTGACATAGTGAAGAGGTACAATGSACTTAATGATCAGCGGTACACAGAA	1119
QY	661	GGCAACTATGAGAAAGTGGGATGAGACCTTCAAAAGATATGTCAGCGAAGAAAGGATTT	720
Db	1120	GGCAACTATGAGAAAGTGGGATGAGACCTTCAAAAGATATGTCAGCGAAGAAAGGATTT	1179
QY	721	TGCAATCGCCCACTCTTACAAAATCTACAGTATGCAAGGGAGCAGAGCTTTGATTAAGCTG	780
Db	1180	TGCAATCGCCCACTCTTACAAAATCTACAGTATGCAAGGGAGCAGAGCTTTGATTAAGCTG	1238
QY	781	CTGAAGAAGCTCACAAAGTCACTTGGCCCAAGGCGCGGGGTGGGCTACTTCTGTGAAGGCG	840
Db	1240	CTGAAGAAGCTCACAAAGTCACTTGGCCCAAGGCGCGGGGTGGGCTACTTCTGTGAAGGCG	1299
QY	841	ATGACGGTGAAGGTCGTGCTGATGCGCCATGAGCGGCTTGGGCTTAATGAGGAATTTCTTG	900
Db	1300	ATGACGGTGAAGGTCGTGCTGATGCGCCATGAGCGGCTTGGGCTTAATGAGGAATTTCTTG	1355
QY	901	CTTCTGGGCAAGGA 914	
Db	1360	CTTCTGGGCAAGGA 1373	

RESULT14	
AAD04991	
ID	AAD04991 standard; cDNA; 4303 BP.
XX	
AC	AAD04991;

[illegible]

```
QY 301 CATTGGCTGGGCGCTAGAGCAGACATTGAGTTCAATAGAGATTCCTCATTTCTCG 360
DB 760 CATTGGCTGGGCGCTAGAGCAGACATTGAGTTCAATAGAGATTCCTCATTTCTCA 819
QY 361 GAAGAGAGAGAGGCGCTGATATGCTCTGTGAGATGAGCTCTCTCTTCCGCTCAAG 420
DB 820 GAAGAGAGAGAGGCGCTGATATGCTCTGTGAGATGAGCTCTCTCTTCCGCTCAAG 879
QY 421 AAGCCCTATAGAGGCGCTGATATGCTCTGTGAGATGAGCTCTCTTCCGCTCAAG 480
DB 880 AAGCCCTATAGAGGCGCTGATATGCTCTGTGAGATGAGCTCTCTTCCGCTCAAG 939
QY 481 TTGCTCAGCTTTTCAACATACCTCAGATTGCTTACTCAGAACACAGATGATCTGAGT 540
DB 940 TTGCTCAGCTTTTCAACATACCTCAGATTGCTTACTCAGAACACAGATGATCTGAGT 999
QY 541 GACAGAGCTCTGTTCAATATTTTCATGAGAGGTTGTGCTTCAATGCTCAGACAGCAAG 600
DB 1000 GACAGAGCTCTGTTCAATATTTTCATGAGAGGTTGTGCTTCAATGCTCAGACAGCAAG 1059
QY 601 TCCATGCTGACATAGTGAAGAGGTACACTGACCTATGATATGAGCCGTACACACAGAA 660
DB 1060 TCCATGCTGACATAGTGAAGAGGTACACTGACCTATGATATGAGCCGTACACACAGAA 1119
QY 661 GGCACATGAGAGAGAGGTGAGATGAGAGCCCTTCAAGATATGTCAGAGAGAGAGGATT 720
DB 1120 GGCACATGAGAGAGAGGTGAGATGAGAGCCCTTCAAGATATGTCAGAGAGAGAGGATT 1179
QY 721 TGCAATGCGCCACTCTTACAAATCTACATGATGACAGAGAGAGAGAGCTTGAATAGCTG 780
DB 1180 TGCAATGCGCCACTCTTACAAATCTACATGATGACAGAGAGAGAGAGCTTGAATAGCTG 1239
QY 781 CTGAAGAGAGCTCAAGTCACTTGGCCCAAGGCCGGGTGTGCTCTCTGTGAGAGGC 840
DB 1240 CTGAAGAGAGCTCAAGTCACTTGGCCCAAGGCCGGGTGTGCTCTCTGTGAGAGGC 1299
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DB 1300 ATGACGGTGAAGAGTGTGATGATGAGCAGAGAGCCCTGAGGCTTATGAGAGAAATTTCTG 1359
QY 901 CTTCTGGGAGAGGA 914
DB 1360 CTTCTGGGAGAGTGA 1373
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RESULT 15  
AAD05031  
ID AAD05031 standard; cDNA; 4303 BP.

XX  
AC AAD05031;

XX  
DT 17-JUL-2001 (first entry)

XX  
DE Human metabotropic glutamate receptor, mGluR5B cDNA.

XX  
KM Human; metabotropic glutamate receptor; mGluR5B; excitatory amino acid;  
KW EAA; central nervous system; CNS; presynaptic release; neurotransmitter;  
KW postsynaptic sensitivity; glutamate excitation; ss.

XX  
OS Homo sapiens.

XX  
FH Key Location/Qualifiers

FT CDS 460..4098

FT /tag= a  
FT /product= "Human metabotropic glutamate receptor,  
mGluR5B"

XX  
PN US6211353-B1.

XX  
PD 03-APR-2001.

XX  
PF 07-JUN-1996; 96US-0660148.

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XX  
PR 29-JUL-1994; 94US-0282853.  
XX  
PA (BLI ) LILLY & CO BLI.  
XX  
PI Burnette JP, Mayne NG, Sharp RL, Snyder YM;  
XX  
DR WPI; 2001-289639/30.  
XX  
DR P-PSDB; AAB01157.  
XX  
PT New isolated nucleic acids for producing human metabotropic glutamate  
PT receptors, which are useful for modulating the presynaptic release of  
PT glutamate or the postsynaptic sensitivity of the neuronal cell to  
PT glutamate excitation -  
XX  
PS Claim 15; Column 77-86; 53pp; English.  
XX  
CC The present sequence is a cDNA encoding human metabotropic glutamate  
CC receptor, mGluR5B. L-glutamate, the most abundant neurotransmitter in  
CC the central nervous system (CNS), mediates excitatory pathway in  
CC mammals. L-glutamate is referred to as excitatory amino acid (EAA) and  
CC the receptors that respond to glutamate are EAA receptors. The receptors  
CC are useful for modulating the presynaptic release of glutamate and the  
CC postsynaptic sensitivity of the neuronal cell to glutamate excitation.  
XX  
SQ Sequence 4303 BP; 1044 A; 1138 C; 1144 G; 977 T; 0 other;
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Query Match 80.0%; Score 888.4; DB 22; Length 4303;  
Best Local Similarity 98.2%; Pred. No. 2.3e-270;  
Matches 898; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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DB 460 ATGGTCTTCTGTGATCTGTCAGTCTTACTTTGAAAGAGATGCGTGAGAGTGA 519
QY 61 CAGTCAATGAGAGAGGAGTGTGCTCAATGCTGGGTGACATCATTTGAGACTCTC 120
DB 520 CAGTCAATGAGAGAGGAGTGTGCTCAATGCTGGGTGACATCATTTGAGACTCTC 579
QY 121 TTTTCTGTCATACCAAGCTTACTGTGAGAGAGTTCATGAGAGAGAGTGTGGGGAGTC 180
DB 580 TTTTCTGTCATACCAAGCTTACTGTGAGAGAGTTCATGAGAGAGAGTGTGGGGAGTC 639
QY 181 CGTGAACAGTATGAGATTCAGAGAGTGAAGAGCCATGCTGATACCTCTGAAAGATCAAT 240
DB 640 CGTGAACAGTATGAGATTCAGAGAGTGAAGAGCCATGCTGATACCTCTGAAAGATCAAT 639
QY 241 TCAGACCCCACTCTTGGCCCAACATCACATGAGGCTGTGAGATTAAGGATTCCTGCTGG 300
DB 700 TCAGACCCCACTCTTGGCCCAACATCACATGAGGCTGTGAGATTAAGGATTCCTGCTGG 759
QY 301 CATTGGCTGGGCGCTAGAGCAGACATTGAGTTCAATAGAGATTCCTCATTTCTTCG 360
DB 760 CATTGGCTGGGCGCTAGAGCAGACATTGAGTTCAATAGAGATTCCTCATTTCTTCG 819
QY 361 GAAGAGAGAGAGGCGCTGATATGCTCTGTGAGATGAGCTCTCTTCCGCTCAAG 420
DB 820 GAAGAGAGAGAGGCGCTGATATGCTCTGTGAGATGAGCTCTCTTCCGCTCAAG 879
QY 421 AAGCCCTATAGAGGCGCTGATATGCTCTGTGAGATGAGCTCTCTTCCGCTCAAG 480
DB 880 AAGCCCTATAGAGGCGCTGATATGCTCTGTGAGATGAGCTCTCTTCCGCTCAAG 939
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DB 1000 GACAGAGCTCTGTTCAATATTTTCATGAGAGGTTGTGCTTCAATGCTCAGACAGCAAG 1059
QY 601 TCCATGCTGACATAGTGAAGAGGTACACTGACCTATGATATGAGCCGTACACACAGAA 660
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Db      1360 CTTCTGGGCAGTGA 1373
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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 14, 2003, 04:35:06 : Search time 72.2844 Seconds  
(without alignments)  
6777.889 Million cell updates/sec

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Sequence: 1 atgagctctctgtgtgctcctc.....tgaggagacagcctcactctaa 1110

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	888.4	80.0	2826	4 US-09-695-481-1	Sequence 1, Appl1
2	888.4	80.0	3129	4 US-09-695-481-5	Sequence 5, Appl1
3	888.4	80.0	4078	4 US-09-016-434-1133	Sequence 1133, Ap
4	888.4	80.0	4207	3 US-08-660-148-1	Sequence 1, Appl1
5	888.4	80.0	4207	3 US-08-660-148-3	Sequence 3, Appl1
6	888.4	80.0	4303	3 US-08-660-148-4	Sequence 4, Appl1
7	888.4	80.0	4303	3 US-08-660-148-6	Sequence 6, Appl1
8	885.2	79.7	3282	1 US-08-072-574-11	Sequence 11, Appl1
9	885.2	79.7	3282	1 US-08-486-270-11	Sequence 11, Appl1
10	885.2	79.7	3282	3 US-08-367-264-11	Sequence 11, Appl1
11	885.2	79.7	3282	4 US-09-153-757-11	Sequence 11, Appl1
12	885.2	79.7	3282	4 US-09-459-715-11	Sequence 11, Appl1
13	885.2	79.7	4085	1 US-08-072-574-7	Sequence 7, Appl1
14	885.2	79.7	4085	1 US-08-486-270-7	Sequence 7, Appl1
15	885.2	79.7	4085	1 US-08-367-264-7	Sequence 7, Appl1
16	885.2	79.7	4085	4 US-09-153-757-7	Sequence 7, Appl1
17	885.2	79.7	4085	4 US-09-459-715-7	Sequence 7, Appl1
18	885.2	79.7	4181	1 US-08-072-574-9	Sequence 9, Appl1
19	885.2	79.7	4181	1 US-08-486-270-9	Sequence 9, Appl1
20	885.2	79.7	4181	3 US-08-367-264-9	Sequence 9, Appl1
21	885.2	79.7	4181	4 US-09-153-757-9	Sequence 9, Appl1
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23	458.2	41.3	3321	1 US-08-486-270-1	Sequence 1, Appl1
24	458.2	41.3	3321	3 US-08-367-264-1	Sequence 1, Appl1
25	458.2	41.3	3321	4 US-09-153-757-1	Sequence 1, Appl1
26	458.2	41.3	3321	4 US-09-459-715-1	Sequence 1, Appl1
27	458.2	41.3	3582	4 US-08-538-526-2	Sequence 2, Appl1

28	458.2	41.3	4074	4 US-09-016-434-1475	Sequence 1475, Ap
29	449.2	40.5	3219	2 US-08-687-289A-3	Sequence 3, Appl1
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32	449.2	40.5	3384	4 US-09-435-897-1	Sequence 1, Appl1
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45	143.6	12.9	3431	4 US-09-641-318-1	Sequence 1, Appl1

#### ALIGNMENTS

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RESULT 1
US-09-695-481-1
; Sequence 1, Application US/09695481
; Patent No. 6534287
; GENERAL INFORMATION:
; APPLICANT: STORMANN, THOMAS M.
; APPLICANT: LEVINTHAL, CYNTHIA
; APPLICANT: STORJOHAN, LAURA
; APPLICANT: HAMMERLAND, LANCE G.
; APPLICANT: KAPCHO, KAREN J.
; APPLICANT: NNS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: A NOVEL HUMAN METABOTROPIC GLUTAMATE RECEPTOR
; FILE REFERENCE: 1094.2.6
; CURRENT APPLICATION NUMBER: US/09/695,481
; CURRENT FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 60/161,481
; PRIOR FILING DATE: 1999-10-25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2826
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2826)
US-09-695-481-1

Query Match      80.0%; Score 888.4; DB 4; Length 2826;
Best Local Similarity 98.2%; Pred. No. 3,5e+269;
Matches 898; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1 ATGCTCTCTGTGTAATCTCTGATGCTTACTTTTGAAGAATATGCTGGAGTGA 60
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DB 1 ATGCTCTCTGTGTAATCTCTGATGCTTACTTTTGAAGAATATGCTGGAGTGA 60

QY 61 CAGTCCAGTGAAGAGAGGGGTGTGCTCAATGCTGGTGAATCATTTATGAGCTCTC 120
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DB 61 CAGTCCAGTGAAGAGAGGGGTGTGCTCAATGCTGGTGAATCATTTATGAGCTCTC 120

QY 121 TTTTCTGTCATCAGCAGCTTACTGTGAGCAAGATTATGAGAGAGAGTGTGGAGTGC 180
   |||
DB 121 TTTTCTGTCATCAGCAGCTTACTGTGAGCAAGATTATGAGAGAGAGTGTGGAGTGC 180

QY 181 CCGGAACAGTATGAGCATTTAGAGAGTGAAGGCGATGCTGATACCTTGAGAAAGATCAAT 240
   |||
DB 181 CCGGAACAGTATGAGCATTTAGAGAGTGAAGGCGATGCTGATACCTTGAGAAAGATCAAT 240

QY 241 TCAGACCCCAACTCTTGCCCAATCATCATGCTGGGCTGTGAGTAAGGAGTTCTGCTGG 300
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DB 241 TCAGACCCCAACTCTTGCCCAATCATCATGCTGGGCTGTGAGTAAGGAGTTCTGCTGG 300
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Db      241 TCAGACCCCACTCTTGCCCAATCATCACTGGGCTGTGATGAAGAAGGACTCTGCTGG 300
Qy      301 CATTCGGCTGTGGCCCTTAGAGAGAGATTGATTCATTAAGAGTTCCCTCATTTCTTGG 360
Db      301 CATTCGGCTGTGGCCCTTAGAGAGAGATTGATTCATTAAGAGTTCCCTCATTTCTTCA 360
Qy      361 GAAGAGAGAGAGGCTGTGATGCTGTGTGATGGCTCTCTCTCTCTCTCTCTCTCTCAAG 420
Db      361 GAAGAGAGAGAGGCTGTGATGCTGTGTGATGGCTCTCTCTCTCTCTCTCTCTCTCAAG 420
Qy      421 AAGCCATAGTAGGGGTCATTTGGGCTGTGCTCAAGTTCTTTAGCCATTCAAGTCCAGAT 480
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Qy      541 GACAAAGCTCTGTTCAATATTTTCATGAGGGTTGCTTCAAGTCTCAAGCAAGCAAG 600
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Qy      661 GGCAACTATGAGAAAGTGGATGGAGAGCTTCAAAATATATGTCAGGAGAGAGAGAT 720
Db      661 GGCAACTATGAGAAAGTGGATGGAGAGCTTCAAAATATATGTCAGGAGAGAGAGAT 720
Qy      721 TGATCGCCCACTCTTCAAAATCTACAGTATGACAGGAGAGAGAGAGAGATGATGAT 780
Db      721 TGATCGCCCACTCTTCAAAATCTACAGTATGACAGGAGAGAGAGAGAGATGATGAT 780
Qy      781 CTGAAGAGCTCACAACTCACTGCCCCAGGCGGGGTGTGCTGATCTGTGAGGGC 840
Db      781 CTGAAGAGCTCACAACTCACTGCCCCAGGCGGGGTGTGCTGATCTGTGAGGGC 840
Qy      841 ATGACGGTGAAGGTCTGCTGATGAGCCATGAGGGCGCTGAGTCTAGTGGAGAAATTTCTG 900
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Qy      901 CTCTGGGAGAGGA 914
Db      901 CTCTGGGAGAGTA 914

RESULT 2
US-09-695-481-5
; Sequence 5, Application US/09695481
; Patent No. 6534287
; GENERAL INFORMATION:
; APPLICANT: STORMANN, THOMAS M.
; APPLICANT: LEVINTHAL, CYNTHIA
; APPLICANT: STORJOHAN, LAURA
; APPLICANT: HAMBERLAND, LANCE G.
; APPLICANT: KRABCHO, KAREN J.
; APPLICANT: NRS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: A NOVEL HUMAN METABOTROPIC GLUTAMATE RECEPTOR
; FILE REFERENCE: 1094.2.6
; CURRENT APPLICATION NUMBER: US/09/695,481
; PRIOR APPLICATION NUMBER: 60/161,481
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 3129
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Chimeric
; OTHER INFORMATION: molecule comprising portions of human mGluR5d and

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; OTHER INFORMATION: the human calcium receptor.
; NAME/KEY: CDS
; LOCATION: (1..3129)
US-09-695-481-5

Query Match      80.0%; Score 888.4; DB 4; Length 3129;
Best Local Similarity 98.2%; Pred. No. 3,7e-269;
Matches 898; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Qy      1 ATGGTCTTGTGTTGATCTGTCAAGTCTTACTTTGAAAGAAATGTCCTGGAGAGTCA 60
Db      1 ATGGTCTTGTGTTGATCTGTCAAGTCTTACTTTGAAAGAAATGTCCTGGAGAGTCA 60
Qy      61 CAGTCCAGTGAAGAGGGGTGTGAGTCAATGCTGGTGTGATCATATTTAGAGCTCTC 120
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Qy      121 TTTTCTGTTTCATCACAGCCTTACTGTGAGCAAGTTTATGAGAGAAAGTGTGGGCGATC 180
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Qy      181 CTTGAACAGTATGAGCATTCAGAGAGTGAAGCCATGCTGATACCTTGGAAAGATTCAT 240
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Qy      481 TTGCTCCAGCTTTTCAATACCTCAATGCTTACTCAAGAACCAATCAATGATCTGAGT 540
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Db      781 CTGAAGAGCTCACAACTCACTGCCCCAGGCGGGGTGTGCTGATCTGTGAGGGC 840
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Qy      901 CTCTGGGAGAGGA 914
Db      901 CTCTGGGAGAGTA 914

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RESULT 3  
US-09-016-434-1133  
Sequence 1133, Application US/09016434  
Patent No. 6500938  
GENERAL INFORMATION:  
APPLICANT: Janice Au-Young  
APPLICANT: Jeffrey J. Sellhammer  
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
NUMBER OF SEQUENCES: 1490  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 PORTER DRIVE  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/016,434  
FILING DATE: HEREMITH  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Zeller, Karen J.  
REGISTRATION NUMBER: 37,071  
REFERENCE/DOCKET NUMBER: PA-0002 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 855-0555  
TELEFAX: (650) 845-4166  
INFORMATION FOR SEQ ID NO: 1133:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4078 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GENBANK  
CLONE: g1408051  
US-09-016-434-1133

Query Match 80.0%; Score 888.4; DB 4; Length 4078;  
Best Local Similarity 98.2%; Pred. No. 4.3e-269;  
Matches 898; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1 ATGGCTCTTCTGTTGATCTGTGCTGCTTCTTTGAAAGAGATGCCGGGAGAGTGA 60  
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QY 361 GAAGAGAGAGAGGCTTGTGTATGCTGTGTGATGAGTCTCTCTTCTTGGGCTCAAG 420  
DB 511 GAAGAGAGAGAGGCTTGTGTATGCTGTGTGATGAGTCTCTCTTCTTGGGCTCAAG 570  
QY 421 AAGCCATGATGAGGATCATTTGGGCTGTGCTCAAGTCTTACCATTTAGGATTCAGAAAT 480  
DB 571 AAGCCATGATGAGGATCATTTGGGCTGTGCTCAAGTCTTACCATTTAGGATTCAGAAAT 630  
QY 481 TTGCTCAGCTTTCAACATCTCAGATTTGCTTACAGAACCATCATGATGATGAGT 540  
DB 631 TTGCTCAGCTTTCAACATCTCAGATTTGCTTACAGAACCATCATGATGATGAGT 690  
QY 541 GACAGACTCTGTTCAATATTTCATGAGGTTGCTTCAAGATCTCAGAGCAAGG 600  
DB 691 GACAGACTCTGTTCAATATTTCATGAGGTTGCTTCAAGATCTCAGAGCAAGG 750  
QY 601 TCCATGATGATCATGATGAAGAGTCACTGAGACCTATGATACCCGATCAACAGAA 660  
DB 751 GCCATGATGATCATGATGAAGAGTCACTGAGACCTATGATACCCGATCAACAGAA 810  
QY 661 GGCACATATGAGAGAGTGGATGAGAGCTTCAAGATATGTCAGAGAGAGAGGATT 720  
DB 811 GGCACATATGAGAGAGTGGATGAGAGCTTCAAGATATGTCAGAGAGAGAGGATT 870  
QY 721 TGCATGCCCACTCTTCAAAATCTACATATGACAGGAGAGAGCTTGTATGAGCTG 780  
DB 871 TGCATGCCCACTCTTCAAAATCTACATATGACAGGAGAGAGCTTGTATGAGCTG 930  
QY 781 CTGAAGAGCTCAAGATCACTTGTCCCAAGGCCCGGATGTGCTTCTGTGAGGCT 840  
DB 931 CTGAAGAGCTCAAGATCACTTGTCCCAAGGCCCGGATGTGCTTCTGTGAGGCT 990  
QY 841 ATGACGATGAGAGTGTGCTGATGAGCATGAGGCGCTGGGTCTAGTGGAGAAATTTCTG 900  
DB 991 ATGACGATGAGAGTGTGCTGATGAGCATGAGGCGCTGGGTCTAGTGGAGAAATTTCTG 1050  
QY 901 CTTCTGGGAGAGGA 914  
DB 1051 CTTCTGGGAGAGTGA 1064

RESULT 4  
US-08-660-148-1  
Sequence 1, Application US/08660148  
Patent No. 6211353  
GENERAL INFORMATION:  
APPLICANT: Burnette, J. P.  
APPLICANT: Mayne, Nancy G.  
APPLICANT: Sharp, Robert L.  
APPLICANT: Snyder, Yvonne M.  
TITLE OF INVENTION: EXCITATORY AMINO RECEPTOR PROTEIN AND  
TITLE OF INVENTION: RELATED NUCLEIC ACID COMPOUNDS  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Eli Lilly and Company  
STREET: Lilly Corporate Center  
CITY: Indianapolis  
STATE: Indiana  
COUNTRY: United States of America  
ZIP: 46285  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/660,148  
FILING DATE:  
CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/282,853  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Gaylo, Paul J.  
REGISTRATION NUMBER: 36,808  
REFERENCE/DOCKET NUMBER: X-9419  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (317) 276-0756  
TELEFAX: (317) 276-3861  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4207 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 460..3999  
US-08-660-148-1

Query Match 80.0%; Score 888.4; DB 3; Length 4207;  
Best Local Similarity 98.2%; Pred. No. 4,4e-269;  
Matches 898; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

1 ATGGTCTTCTGTGATCCCTGCTGCTTCTTCTTGAAGAAGATGTCCTGGAGTGA 60  
460 ATGGTCTTCTGTGATCCCTGCTGCTTCTTCTTGAAGAAGATGTCCTGGAGTGA 519  
61 CAGTCCAGTGAAGAGAGGAGTGTGCTCACTACGCTGGGTGATCATTTATGAGCTTC 120  
520 CAGTCCAGTGAAGAGAGGAGTGTGCTCACTACGCTGGGTGATCATTTATGAGCTTC 579  
121 TTTTCTGTTCATCAACGACCTACTGTGAGCAAGATTATGAGAGAGTGTGGGAGTC 180  
580 TTTTCTGTTCATCAACGACCTACTGTGAGCAAGATTATGAGAGAGTGTGGGAGTC 639  
181 CGTGAACAGTATGATTCATGAGAGTGTGAGAGGCTGCTGATACCTCTGGAAGATCAAT 240  
640 CGTGAACAGTATGATTCATGAGAGTGTGAGAGGCTGCTGATACCTCTGGAAGATCAAT 699  
241 TCAGACCCCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300  
700 TCAGACCCCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 759  
301 CATTGGCTGTGGCCCTAGAGACAGAGCATTTGATTAAAGATTCCCTCATTTCTTCG 360  
760 CATTGGCTGTGGCCCTAGAGACAGAGCATTTGATTAAAGATTCCCTCATTTCTTCG 819  
361 GAAGAGAGAGAGGCTGTGATGCTGTGATGCTGTGATGCTGTGATGCTGTGATGCT 420  
820 GAAGAGAGAGAGGCTGTGATGCTGTGATGCTGTGATGCTGTGATGCTGTGATGCT 879  
421 AAGGCCATAGTAAAGGCTCATTTGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480  
880 AAGGCCATAGTAAAGGCTCATTTGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 939  
481 TTGCTCAGCTTTTCAACATACCTCAGATTGCTTACTCAGCAACCATCATGATGATG 540  
940 TTGCTCAGCTTTTCAACATACCTCAGATTGCTTACTCAGCAACCATCATGATGATG 999  
541 GACAAAGCTCTGTTCAAATATTTTCAATGAGGTTGTGCTTCAATGCTCAGCAGGCAAG 600  
1000 GACAAAGCTCTGTTCAAATATTTTCAATGAGGTTGTGCTTCAATGCTCAGCAGGCAAG 1059  
601 TCCATGTGACATATGAGAGAGGTACATGACCTATGATGATGACCTATGACAGAA 660  
1060 GCGATGTGACATATGAGAGAGGTACATGACCTATGATGATGACCTATGACAGAA 1119  
661 GCGAATCATGAGAGAGGTGAGAGGCTTCAAGATATGTCAGGAGAGAGGATTT 720  
1120 GCGAATCATGAGAGAGGTGAGAGGCTTCAAGATATGTCAGGAGAGAGGATTT 1179

721 TGCATGCCCACTCTTACAAATCTACATATGACAGGAGAGAGCTTTGATTAAGCTG 780  
1180 TGCATGCCCACTCTTACAAATCTACATATGACAGGAGAGAGCTTTGATTAAGCTG 1239  
781 CTGAAGAGCTCAAGATGATCTTCCCAAGGCGGAGTGTGCTTCTGTGAGGAGC 840  
1240 CTGAAGAGCTCAAGATGATCTTCCCAAGGCGGAGTGTGCTTCTGTGAGGAGC 1299  
841 ATGACGCTGAGAGGCTGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900  
1300 ATGACGCTGAGAGGCTGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1359  
901 CTTCTGGGACAGGA 914  
1360 CTTCTGGGACAGGA 1373

RESULT 5  
US-08-660-148-3  
Sequence 3, Application US/08660148  
Patent No. 6211353  
GENERAL INFORMATION:  
APPLICANT: Burnett, J. P.  
APPLICANT: Mayne, Nancy G.  
APPLICANT: Sharp, Robert L.  
APPLICANT: Snyder, Yvonne M.  
TITLE OF INVENTION: EXCITATORY AMINO RECEPTOR PROTEIN AND  
TITLE OF INVENTION: RELATED NUCLEIC ACID COMPOUNDS  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Eli Lilly and Company  
STREET: Lilly Corporate Center  
CITY: Indianapolis  
STATE: Indiana  
COUNTRY: United States of America  
ZIP: 46285  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/660,148  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/282,853  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Gaylo, Paul J.  
REGISTRATION NUMBER: 36,808  
REFERENCE/DOCKET NUMBER: X-9419  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (317) 276-0756  
TELEFAX: (317) 276-3861  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4207 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: mRNA  
US-08-660-148-3

Query Match 80.0%; Score 888.4; DB 3; Length 4207;  
Best Local Similarity 73.9%; Pred. No. 4,4e-269;  
Matches 675; Conservative 223; Mismatches 16; Indels 0; Gaps 0;

1 ATGGTCTTCTGTGATCCCTGCTGCTTCTTCTTGAAGAAGATGTCCTGGAGTGA 60  
460 ATGGTCTTCTGTGATCCCTGCTGCTTCTTCTTGAAGAAGATGTCCTGGAGTGA 519







Db 1360 CUUCUGGCGAGUGA 1373

## RESULT 8

US-08-072-574-11  
Sequence 11, Application US/08072574  
Patent No. 5521297  
GENERAL INFORMATION:  
APPLICANT: Daggett, Lorrie  
APPLICANT: Ellis, Steven B.  
APPLICANT: Liaw, Chen  
APPLICANT: Pontsler, Aaron  
TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,  
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME AND USES THEREOF  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
STREET: 444 South Flower Street, Suite 2000  
CITY: Los Angeles  
STATE: CA  
COUNTRY: USA  
ZIP: 00719  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/072,574  
FILING DATE: 19930604  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen E.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: P41 9383  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 213-622-7700  
TELEFAX: 213-489-4210  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3282 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 370..3003  
OTHER INFORMATION: /product= "HUMAN MGLUR5C"  
OTHER INFORMATION: /note= "Variant of MGLUR5A with truncated 3' end."  
US-08-072-574-11

Query Match 79.7%; Score 885.2; DB 1; Length 3282;  
Best local similarity 98.0%; Pred. No. 3.8e-268;  
Matches 896; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 1 ATGGCTCTTCTGTTGATCTGTCAGTCTTTGAAAGAGATGTCGGTGGAGTGA 60  
DB 370 ATGGCTCTTCTGTTGATCTGTCAGTCTTTGAAAGAGATGTCGGTGGAGTGA 429  
QY 61 CAGTCCAGGAG 120  
DB 430 CAGTCCAGGAG 489  
QY 121 TTTTCTGTTCAATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180  
DB 490 TTTTCTGTTCAATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 549  
QY 181 CCGAAG 240  
DB 550 CCGAAG 609

QY 241 TCAGACCCCACTCTTGCCCAATCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300  
DB 610 TCAGACCCCACTCTTGCCCAATCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 669  
QY 301 CATTGGCTGTGGCCCTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360  
DB 670 CATTGGCTGTGGCCCTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 729  
QY 361 GAAG 420  
DB 730 GAAG 789  
QY 421 AAGCCATAGTAG 480  
DB 790 AAGCCATAGTAG 849  
QY 481 TTGCTCAGCTTTTCAATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540  
DB 850 TTGCTCAGCTTTTCAATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 909  
QY 541 GACAG 600  
DB 910 GACAG 969  
QY 601 TCCAG 660  
DB 970 TCCAG 1029  
QY 661 GGCAG 720  
DB 1030 GGCAG 1089  
QY 721 TGCATGCCCACTCTTCAATCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780  
DB 1090 TGCATGCCCACTCTTCAATCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1149  
QY 781 CCGAAG 840  
DB 1150 CCGAAG 1209  
QY 841 ATGACGAG 900  
DB 1210 ATGACGAG 1269  
QY 901 CTTCTGGGAG 960  
DB 1270 CTTCTGGGAG 1020

## RESULT 9

US-08-486-270-11  
Sequence 11, Application US/08486270  
Patent No. 5807689  
GENERAL INFORMATION:  
APPLICANT: Daggett, Lorrie  
APPLICANT: Ellis, Steven B.  
APPLICANT: Liaw, Chen  
APPLICANT: Pontsler, Aaron  
APPLICANT: Johnson, Edwin C.  
APPLICANT: Hees, Stephen D.  
TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,  
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME AND USES THEREOF  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
STREET: 444 South Flower Street, Suite 2000  
CITY: Los Angeles  
STATE: CA  
COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,270  
FILING DATE: 02-JUN-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/072,574  
FILING DATE: 04-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen E.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: PP41 9772  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-546-4737  
TELEFAX: 619-546-9392  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3282 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 370..3003  
OTHER INFORMATION: /product= "HUMAN MGLUR5C"  
OTHER INFORMATION: /note= "Variant of MGLUR5A with truncated 3' end."  
US-08-486-270-11

Query Match 79.7%; Score 885.2; DB 1; Length 3282;  
Best Local Similarity 98.0%; Pred. No. 3,88-268;  
Matches 896; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 1 ATGGCTCTTCTGTTGATCTGTCAGTCTTATTTGAAGAAGATGCTCGGAGATGCA 60  
DB 370 ATGGCTCTTCTGTTGATCTGTCAGTCTTATTTGAAGAAGATGCTCGGAGATGCA 429  
QY 61 CAGTCCGATGAG 120  
DB 430 CAGTCCGATGAG 489  
QY 121 TTTTCTGTTATCCACGACCTACTGTGGAAGAGATTATGAGAGAGAGAGAGAGAGAG 180  
DB 490 TTTTCTGTTATCCACGACCTACTGTGGAAGAGATTATGAGAGAGAGAGAGAGAG 549  
QY 490 TTTTCTGTTATCCACGACCTACTGTGGAAGAGATTATGAGAGAGAGAGAGAGAG 549  
DB 181 CGTGAACAGTATGAGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 240  
DB 550 CGTGAACAGTATGAGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 609  
QY 241 TCAGACCCCACTCTTGGCCCAATCATCACTGGGCTGTGAGATTAAGAGAGATTCTG 300  
DB 610 TCAGACCCCACTCTTGGCCCAATCATCACTGGGCTGTGAGATTAAGAGAGATTCTG 669  
QY 301 CATTCGGCTGTGGCCCTAGAGACAGAGATTGATTAAGAGATTCCCTCATTTCTTGG 360  
DB 670 CATTCGGCTGTGGCCCTAGAGACAGAGATTGATTAAGAGATTCCCTCATTTCTTCA 729  
QY 361 GAAG 420  
DB 730 GAAG 789  
QY 421 AAGCCCATAG 480  
DB 790 AAGCCCATAG 849  
QY 481 TTGCTCAGCTTTCAACATACCTCAAGTTGCTTACAGAGAGAGAGAGAGAGAGAGAG 540  
DB 850 TTGCTCAGCTTTCAACATACCTCAAGTTGCTTACAGAGAGAGAGAGAGAGAGAG 909  
QY 541 GACAAAGACTCTGTTCAATATATTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600  
DB 910 GACAAAGACTCTGTTCAATATATTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 969

QY 601 TCATGATGAGACATAGTGAAGAGGTACAACTGACCTATGATACAGCCGTACACAGAA 650  
DB 970 GCGATGTGACATATATGAAAGAGTACAACTGACCTATGATACAGCCGTACACAGAA 1029  
QY 661 GCGACTATGAGAAAGTGGATGAGAGCTTCAAGATATGTCACGAGAGAGAGAGATT 720  
DB 1030 GCGACTATGAGAAAGTGGATGAGAGCTTCAAGATATGTCACGAGAGAGAGAGATT 1089  
QY 721 TGATGCCCCACTTTCACAAATCTACATTAATGACGGGAGAGAGAGCTTGAAGCTG 780  
DB 1090 TGATGCCCCACTTTCACAAATCTACATTAATGACGGGAGAGAGAGCTTGAAGCTG 1149  
QY 781 CTGAAGAAGCTCAACAGTCACTTCCCAAGGCCCGGGGTGGCTTACTTCTGTGAGGCG 840  
DB 1150 CTGAAGAAGCTCAACAGTCACTTCCCAAGGCCCGGGGTGGCTTACTTCTGTGAGGCG 1209  
QY 841 ATGACGGTGAAGAGTGTGATGAGCCATGAGGCGCTGGCTTACTGAGAGAAATTTCTG 900  
DB 1210 ATGACGGTGAAGAGTGTGATGAGCCATGAGGCGCTGGCTTACTGAGAGAAATTTCTG 1269  
QY 901 CTTCGTGGCAGGGA 914  
DB 1270 CTTCGTGGCAGGGA 1283

RESULT 10  
US-08-367-264-11  
Sequence 11, Application US/08367264  
GENERAL INFORMATION:  
APPLICANT: Daggett, Lorrie  
APPLICANT: Ellis, Steven B.  
APPLICANT: Liaw, Chen  
APPLICANT: Pontsler, Aaron  
APPLICANT: Johnson, Edwin C.  
TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,  
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME AND USES THEREOF  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESS: Pretty, Schroeder, Brueggemann & Clark  
STREET: 444 South Flower Street, Suite 2000  
CITY: Los Angeles  
STATE: CA  
COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/367,264  
FILING DATE: 02-JUN-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/072,574  
FILING DATE: 04-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen E.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: PP41 9772  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-546-4737  
TELEFAX: 619-546-9392  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3282 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: CDNA

FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 370..3003  
 OTHER INFORMATION: /product= "HUMAN MGLUR5C"  
 OTHER INFORMATION: /note= "Variant of MGLUR5A with truncated 3' end."  
 US-08-367-264-11

Query Match 79.7%; Score 885.2; DB 3; Length 3282;  
 Best Local Similarity 98.0%; Pred. No. 3.8e-268;  
 Matches 896; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

1 ATGGTCCTTCTGTGATCCTGTCAGTCTTAAAGAGATGTCGGTGGAGTGA 60  
 370 ATGGTCCTTCTGTGATCCTGTCAGTCTTAAAGAGATGTCGGTGGAGTGA 429  
 61 CAGTCCAGTGAAGAGAGGGGTGGTCTCACTGCTGGTGAATCTTATTTGAAGCTTC 120  
 430 CAGTCCAGTGAAGAGAGGGGTGGTCTCACTGCTGGTGAATCTTATTTGAAGCTTC 489  
 121 TTTTCTGTCATCAACAGCTTACTGTGAGAGAGTTCATGAGAGAGAGTGGGGAGTC 180  
 490 TTTTCTGTCATCAACAGCTTACTGTGAGAGAGTTCATGAGAGAGAGTGGGGAGTC 549  
 181 CGTGAACAGTATGAGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATCAAT 240  
 550 CGTGAACAGTATGAGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATCAAT 609  
 241 TGAAG 300  
 610 TGAAG 669  
 301 CATTGGGCTGTGGGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360  
 670 CATTGGGCTGTGGGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 729  
 361 GAAAG 420  
 730 GAAAG 789  
 421 AAGCCATATGAG 480  
 790 AAGCCATATGAG 849  
 481 TGGTCCAGCTTTTAAACATCTGATGCTTAACTGAGAGAGAGAGAGAGAGAGAGAGAG 540  
 850 TGGTCCAGCTTTTAAACATCTGATGCTTAACTGAGAGAGAGAGAGAGAGAGAGAGAG 909  
 541 GACAAGAGCTCTGTTCAATATTTTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600  
 910 GACAAGAGCTCTGTTCAATATTTTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 969  
 601 TGCATGAGTGAAG 660  
 970 GGCATGAGTGAAG 1029  
 661 GGCATGAGTGAAG 720  
 1030 GGCATGAGTGAAG 1089  
 721 TGCATGAGTGAAG 780  
 1090 TGCATGAGTGAAG 1149  
 781 CTGAAGAGAGTCAAGAGTCACTTGGCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840  
 1150 CTGAAGAGAGTCAAGAGTCACTTGGCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1209  
 841 ATGAG 900  
 1210 ATGAG 960  
 901 CTTCTGGGAGAGGA 914

DB 1270 CTTCTGGGAGAGGA 1283

RESULT 11  
 US-09-153-757-11

Sequence 11, Application US/09153757

Patent No. 6413764

GENERAL INFORMATION:

APPLICANT: Daggett, Lorrie

Ellis, Steven B.

Llao, Chen

Pontsler, Aaron

Johnson, Edwin C.

Hess, Stephen D.

TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,  
 NUCLEIC ACIDS ENCODING SAME AND USES THEREOF

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:  
 ADDRESS: Pretty, Schroeder, Brueggemann & Clark  
 STREET: 444 South Flower Street, Suite 2000  
 CITY: Los Angeles  
 STATE: CA

COUNTRY: USA

ZIP: 90071

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/153,757  
 FILING DATE: 15-Sep-1998

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/486,270  
 FILING DATE: 02-JUN-1994

APPLICATION NUMBER: US 08/072,574

FILING DATE: 04-JUN-1993

ATTORNEY/AGENT INFORMATION:  
 NAME: Reiter, Stephen B.  
 REGISTRATION NUMBER: 31,192

REFERENCE/DOCKET NUMBER: PP41 9772

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 619-546-4737  
 TELEFAX: 619-546-9392

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 3282 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: both  
 TOPOLOGY: both

MOLECULE TYPE: cDNA

FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 370..3003

OTHER INFORMATION: /product= "HUMAN MGLUR5C"  
 /note= "Variant of MGLUR5A with truncated 3' end."

SEQUENCE DESCRIPTION: SEQ ID NO: 11:

US-09-153-757-11

Query Match 79.7%; Score 885.2; DB 4; Length 3282;  
 Best Local Similarity 98.0%; Pred. No. 3.8e-268;  
 Matches 896; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

1 ATGGTCCTTCTGTGATCCTGTCAGTCTTAAAGAGATGTCGGTGGAGTGA 60  
 370 ATGGTCCTTCTGTGATCCTGTCAGTCTTAAAGAGATGTCGGTGGAGTGA 429  
 61 CAGTCCAGTGAAGAGAGGGGTGGTCTCACTGCTGGTGAATCTTATTTGAAGCTTC 120  
 430 CAGTCCAGTGAAGAGAGGGGTGGTCTCACTGCTGGTGAATCTTATTTGAAGCTTC 489  
 121 TTTTCTGTCATCAACAGCTTACTGTGAGAGAGTTCATGAGAGAGAGTGGGGAGTC 180

Db 490 TTTTCTGTTTCATACAGAGCTTCTGTGAGCAAAAGTTTCATAGAGAGAGTGGGGGCTC 549  
Qy 181 CGTGAACAGTATGGCATTCAGAGAGTGGAGGCAATGCTGATACCTCTGAAAGATCAAT 240  
Db 550 CGTGAACAGTATGGCATTCAGAGAGTGGAGGCAATGCTGATACCTCTGAAAGATCAAT 609  
Qy 241 TCAGAGCCCACTCTTGGCCCAATCACTGGGCTGTGAGATTAAGAGATTCCTGCTG 300  
Db 610 TCAGAGCCCACTCTTGGCCCAATCACTGGGCTGTGAGATTAAGAGATTCCTGCTG 669  
Qy 301 CATTGCGCTGTGGCCCTAGAGAGAGATTAAGATTCCTGCTGCTGCTGCTGCTGCTG 360  
Db 670 CATTGCGCTGTGGCCCTAGAGAGAGATTAAGATTCCTGCTGCTGCTGCTGCTGCTG 729  
Qy 361 GAAGAGAGAGAGGCTGTGTATGCTGTGAGATGCTGCTGCTGCTGCTGCTGCTGCTG 420  
Db 730 GAAGAGAGAGAGGCTGTGTATGCTGTGAGATGCTGCTGCTGCTGCTGCTGCTGCTG 789  
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Qy 661 GGCATGCTGACATAGTGAAGAGGTACATCTGACCTATATATAGCCGTACACACGAA 720  
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Db 1270 CTTCTGGGAGGGA 1283

RESULT 12

US-09-459-715-11

Sequence 11, Application US/09459715

Patent No. 6485919

GENERAL INFORMATION:

APPLICANT: Daggett, Lortie

Billis, Steven B.

Llaw, Chen

Pontelner, Aaron

Johnson, Edwin C.

Hess, Stephen D.

TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,

NUCLEIC ACIDS ENCODING SAME AND USES THEREOF

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESSES:

ADDRESSER: Pretty, Schroeder, Brueggemann &amp; Clark

STREET: 444 South Flower Street, Suite 2000

CITY: Los Angeles  
STATE: CA  
COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/459,715  
FILING DATE: 13-Dec-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/367,264  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen B.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: PP41 9772  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-546-4737  
TELEFAX: 619-546-9392  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3282 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 370..3003  
OTHER INFORMATION: /product= "HUMAN MEUR5C"  
/note= "Variant of MEUR5A with truncated 3' end."  
SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-09-459-715-11  
Query Match 79.7%; Score 885.2; DB 4; Length 3282;  
Best Local Similarity 98.0%; Pred. NO. 3.8e-268;  
Matches 896; Conservative 0; Mismatches 18; Indels 0; Gaps 0;  
Qy 1 ATGATCTTCTGTTGATCTCTGTCAGTCTTACTTTTGAAGAGATGCTGGAGTGA 60  
Db 370 ATGATCTTCTGTTGATCTCTGTCAGTCTTACTTTTGAAGAGATGCTGGAGTGA 429  
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Db 730 GAAGAGAGAGAGGCTGTGTATGCTGTGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 789  
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QY 541 GACAGACTCTGTTCAAAATATTTTCATGAGGTTGTGCTTCAGATGCTCAGACGCAAGG 609  
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QY 601 TCATGCTGACATGATGAGAGTACATGACCTGATGATGACCTGATGACCTGATGACCA 660  
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QY 901 CTTCGCGGAGGGA 914  
DB 1270 CTTCGCGGAGGGA 1283

RESULT 13  
US-08-072-574-7  
; Sequence 7, Application US/08072574  
; Patent No. 5521297  
; GENERAL INFORMATION:  
; APPLICANT: Daggett, Lortie  
; APPLICANT: Ellis, Steven B.  
; APPLICANT: Liaw, Chen  
; APPLICANT: Portisler, Aaron  
; TITLE OF INVENTION: HUMAN MATABOTROPIC GLUTAMATE RECEPTORS,  
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME AND USES THEREOF  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
; STREET: 444 South Flower Street, Suite 2000  
; CITY: Los Angeles  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 00719  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/072,574  
; FILING DATE: 19930604  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Reiter, Stephen E.  
; REGISTRATION NUMBER: 31,192  
; REFERENCE/DOCKET NUMBER: P41 9383  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 213-622-7700  
; TELEFAX: 213-489-4210  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4085 base pairs  
; TYPE: nucleic acid

STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 370..3912  
OTHER INFORMATION: /product= "HUMAN MGLUR5A"  
US-08-072-574-7  
Query Match 79.7%; Score 885.2; DB 1; Length 4085;  
Best Local Similarity 98.0%; Pred. No. 4.3e-268;  
Matches 896; Conservative 0; Mismatches 18; Indels 0; Gaps 0;  
QY 1 ATGCTCTTCTGTTGATTCCTGTCAGTCTTACTTTTGAAGAAGATGCTGGAGATGCA 60  
DB 370 ATGCTCTTCTGTTGATTCCTGTCAGTCTTACTTTTGAAGAAGATGCTGGAGATGCA 429  
QY 61 CAGTCCAGTGAAGAGAGGAGTGTGCTCACAATGCTGGTGAATCATTTATTTGAGCTCTC 120  
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DB 670 CATTCGCTGTGAGCCCTGAAGACAGACATTTAGATTAAGATTCCTCATTTCTTCG 729  
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DB 730 GAAGAGAGAGAGGCTTGTGATGCTGTGAGATGAGCTCTCTCTTCTTCCGCTCCAG 789  
QY 421 AAGCCATGATGAGGAGTCAATGGGCTGGTTCAGTCTTTAGCCATTCAGATCCAGAT 480  
DB 790 AAGCCATGATGAGGAGTCAATGGGCTGGTTCAGTCTTTAGCCATTCAGATCCAGAT 849  
QY 481 TTGCTCAGCTTTTCAACATACCTCAGATTGCTTACTCAGACCAACATCATGATCTGAGT 540  
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QY 541 GACAGACTCTGTTCAAAATATTTTCATGAGGTTGTGCTTCAGATGCTCAGACGCAAGG 600  
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DB 970 GCATGCTGACATGATGAGAGTACATGACCTGATGATGACCTGATGACCTGATGACCA 1029  
QY 661 GGCACATGAGAGAGTGGAGTGGAGAGCTTCAAAATATTTTCATGAGGAGAGAGATTT 720  
DB 1030 GGCACATGAGAGAGTGGAGTGGAGAGCTTCAAAATATTTTCATGAGGAGAGAGATTT 1089  
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QY 901 CTTCTGGGCGAGGA 914  
Db 1270 CTTCTGGGCGAGGA 1283

RESULT 14  
US-08-486-270-7  
Sequence 7, Application US/08486270  
Patent No. 5807689  
GENERAL INFORMATION:  
APPLICANT: Daggett, Lorie  
APPLICANT: Ellis, Steven B.  
APPLICANT: Liaw, Chen  
APPLICANT: Pontsler, Aaron  
APPLICANT: Johnson, Edwin C.  
APPLICANT: Hess, Stephen D.  
TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,  
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME AND USES THEREOF  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
STREET: 444 South Flower Street, Suite 2000  
CITY: Los Angeles  
STATE: CA  
COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,270  
FILING DATE: 02-JUN-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/072,574  
FILING DATE: 04-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen E.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: P41 9772  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-546-4737  
TELEFAX: 619-546-9392  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4085 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 370..3912  
OTHER INFORMATION: /product= "HUMAN MGLUR5A"  
US-08-486-270-7

Query Match 79.7%; Score 885.2; DB 1; Length 4085;  
Best Local Similarity 98.0%; Pred. No. 4.3e-268;  
Matches 896; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 1 ATGCTCTTCTGTTGATCTCTGCTGATCTTACTTTTGAAGAAGATGTCCTGGAGTGA 60  
Db 370 ATGCTCTTCTGTTGATCTCTGCTGATCTTACTTTGGAAGAAGATGTCCTGGAGTGA 429  
QY 61 CAGTCCAGTGAAGAGGAGGAGGAGTGCATCATGCTGGGTGACATCATATTAGAGCTCTC 120  
Db 430 CAGTCCAGTGAAGAGGAGGAGGAGTGCATCATGCTGGGTGACATCATATTAGAGCTCTC 489  
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QY 421 AAGCCCATAGTAGGGGCTATTGGGCTGTGCTTCACTTACCATTCAGATTCAGAT 480  
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QY 481 TTGCTCAGCTTTTCAACATCACTCAATTTGCTTACAGCAACCATAGATCTAGT 540  
Db 850 TTGCTCAGCTTTTCAACATCACTCAATTTGCTTACAGCAACCATAGATCTAGT 909  
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QY 661 GGCATCTATGAGAAAGTGGATGAGAAAGCTTTCAAGATTTGTCAGAGAGAGAGGAT 720  
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Db 1270 CTTCTGGGCGAGGA 1283

RESULT 15  
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Sequence 7, Application US/08367264  
Patent No. 6001581  
GENERAL INFORMATION:  
APPLICANT: Daggett, Lorie  
APPLICANT: Ellis, Steven B.  
APPLICANT: Liaw, Chen  
APPLICANT: Pontsler, Aaron  
APPLICANT: Johnson, Edwin C.  
APPLICANT: Hess, Stephen D.  
TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,  
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME AND USES THEREOF  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
STREET: 444 South Flower Street, Suite 2000  
CITY: Los Angeles  
STATE: CA



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COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/367,264
FILING DATE: 02-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/072,574
FILING DATE: 04-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: FP41 9772
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-4737
TELEFAX: 619-546-9392
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4085 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 370..3912
OTHER INFORMATION: /product= "HUMAN MGLUR5A"
US-08-367-264-7

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Query Match          79.7%; Score 885.2; DB 3; Length 4085;
Best Local Similarity 98.0%; Pred. No. 4.3e-268;
Matches 896; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

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QY 361 GAAGAGAGAGAGGCTTGTGATGCTGTGAGATGGCTCTCTCTTCCTCCGCTCAAG 420
DB 730 GAAGAGAGAGAGGCTTGTGATGCTGTGAGATGGCTCTCTCTTCCTCCGCTCAAG 789
QY 421 AAGCCCATAGTAGGGGTCATTGGGCTGTTCCAGTCTTTAGCATTTGAGTCCAGAAAT 480
DB 790 AAGCCCATAGTAGGGGTCATTGGGCTGTTCCAGTCTTTAGCATTTGAGTCCAGAAAT 849
QY 481 TTGCTCAGCTTTTCAACATACCTCAGATTGCTTACTCAGCAACCATCATGATCTGAGT 540
DB 850 TTGCTCAGCTTTTCAACATACCTCAGATTGCTTACTCAGCAACCATCATGATCTGAGT 909

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QY 541 GACAAGACTCTGTTCAAAATTTTCATGAGGTTTGTGCTTCAAGATGCTCAGACGCAAG 600
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DB 1270 CTTCTGGGCAAGTA 1283

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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## SUMMARIES

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6	417.4	37.6	667	29	AG046849 Pan trogl
7	400.6	36.1	414	10	BG150163 mad46D03
8	372.2	33.5	3879	11	AK032422 AK032422 Mus muscu
9	289.2	26.1	682	10	BG695213 NISC_IV13
10	287	25.9	664	12	B1826234 603075928
11	281.6	25.4	657	13	BU351729 603527561
12	281.6	25.4	669	13	BU393781 603803380
13	268.2	24.2	392	14	T78107 YC98A01.r1
14	257	23.2	515	13	BX280403 BX280403
15	252.2	22.7	673	13	BU390603 BU390603
16	246.8	22.2	471	14	CB730684 CB730684
17	228.8	20.6	439	14	CB750802 AMGNNUC:N
18	224.2	20.2	837	28	B2181748 B2181748
19	191.6	17.3	532	28	B2930457 CH240_36M
20	185	16.7	722	28	AZ815421 2M0083H07
21	174	15.7	744	29	CNS03K04 AL247981 Tetradon
22	173	15.6	681	29	CNS03K04 AL221636 Tetradon
23	159.2	14.3	657	28	B2164680 CH230-388
24	155.6	14.0	456	9	AI201184 AI201184 qf70d05.x
25	146	13.2	589	29	BX191055 BX191055 Dario rer
26	142.8	12.9	516	13	BX282658 BX282658
27	140	12.6	268	14	F05449 F05449 HSCOB111 n
28	135	12.2	673	28	B2101647 CH230-236
29	134.6	12.1	763	14	CA318495 UI-M-FW0-AL352309 Tetradon
30	129.6	11.7	1065	29	CNS05S04 AK038395 Mus muscu
31	125.6	11.3	3675	11	AK038395 BC051384 Mus muscu
32	125.6	11.3	3693	11	BC051384 BB625841 AK020963 Mus muscu
33	119	10.7	647	10	BB625841 B1514260 B160014B
34	118	10.6	1238	11	AK020963 CD355039 UI-M-GM0-AK047733 Mus muscu
35	111	10.0	455	12	B1514260 BY721282 BY721282
36	110.8	10.0	664	14	CD355039 BQ070358 AGENCOURT
37	110.6	10.0	1430	11	AK047733 BE275390 601122276
38	109	9.8	661	14	BY721282 BF125311 601762484
39	106.6	9.6	1013	13	BQ070358 B1093942 602857839
40	105.4	9.5	715	10	BE275390 BE125311 601762484
41	105.4	9.5	806	10	BF125311 B1093942 602857839
42	103.2	9.3	742	12	B1093942 BE893553 601438128
43	103.2	9.3	871	13	BE893553 BU154755 AGENCOURT
44	103.2	9.3	888	13	BU154755 BX410048 BX410048
45	101.8	9.2	916	13	BX410048

## ALIGNMENTS

RESULT 1  
BC031602  
LOCUS Homo sapiens, clone IMAGE:5167902, mRNA.  
DEFINITION BC031602  
ACCESSION BC031602  
VERSION BC031602.1 GI:21594893  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM  
REFERENCE  
AUTHORS Strausberg, R.  
TITLE Submitted (06-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2550, USA  
JOURNAL  
REMARK  
COMMENT NIH-MGC Project URL: <http://mgc.ncl.nih.gov>  
Contact: MGC help desk  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
Tissue Procurement: Life Technologies, Inc.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center  
Center code: BCM-HGSC

Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>  
 Contact: amegedcm.tmc.edu  
 Gunaratne, P.H., Garcia, A.M., Lu, X., Huiyk, S.W., Louised, H.,  
 Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavali,  
 A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Series: IRAC Plate: 51 Row: a Column: 11  
 This clone was selected for full length sequencing because it  
 passed the following selection criteria: matched mRNA gi: 4504142  
 This clone has the following problem: retained intron.  
 Location/Qualifiers

FEATURES  
 source  
 1..1297  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5167902"  
 /issue\_type="Brain, adult medulla"  
 /clone\_id="NH.MGC\_119"  
 /lab\_host="DH10B"  
 /note="Vector: pCMV-SPORT6"  
 BASE COUNT 343 a 301 c 325 g 328 t  
 ORIGIN

Query Match 57.7%; Score 640; DB 11; Length 1297;  
 Best Local Similarity 97.7%; Pred. No. 1.4e-179;  
 Matches 649; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

1 ATGCTCTTCTGTGATCTCTGATCTTACTTTTGAAGAAGATGTCCTGGAGATGCA 60  
 371 ATGCTCTTCTGTGATCTCTGATCTTACTTTTGAAGAAGATGTCCTGGAGATGCA 430  
 61 CAGTCCAGTGAAGAGAGGGTGTGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 120  
 431 CAGTCCAGTGAAGAGAGGGTGTGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 490  
 121 TTTTCTGTTCATCAACAGCTTCTGATGCTGATGCTGATGCTGATGCTGATGCTG 180  
 491 TTTTCTGTTCATCAACAGCTTCTGATGCTGATGCTGATGCTGATGCTGATGCTG 550  
 181 CGTGAACAGTATGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 240  
 551 CGTGAACAGTATGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 610  
 241 TCAGACCCACACACTTGTCCCAACATCACTGAGGCTGTGATGATGATGATGATGAT 300  
 611 TCAGACCCACACACTTGTCCCAACATCACTGAGGCTGTGATGATGATGATGATGAT 670  
 301 CATTGCGGTGTGCGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360  
 671 CATTGCGGTGTGCGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 730  
 361 GAAG 420  
 731 GAAG 790  
 421 AAGCCATAGTAGGGGCTGATGAGGCTGTGATGCTGATGCTGATGCTGATGCTGAT 480  
 791 AAGCCATAGTAGGGGCTGATGAGGCTGTGATGCTGATGCTGATGCTGATGCTGAT 850  
 481 TTGCTCCAGCTTTTCAACATCACTGATGCTTACTGATGATGATGATGATGATGAT 540  
 851 TTGCTCCAGCTTTTCAACATCACTGATGCTTACTGATGATGATGATGATGATGAT 910  
 541 GACAAGACTGTCTCAATATTTTCAATGAGGGTGTGATGCTGATGCTGATGCTGATG 600  
 911 GACAAGACTGTCTCAATATTTTCAATGAGGGTGTGATGCTGATGCTGATGCTGATG 970  
 601 TCATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660  
 971 GCATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1030

QY 661 GGCA 664  
 Db 1031 GGTG 1034

RESULT 2  
 LOCUS BE674422 519 bp mRNA linear EST 08-SEP-2000  
 DEFINITION 7601504.X1 NCI CGAP Lu24 Homo sapiens CDNA clone IMAGE:3281166 3'

PRECURSOR. 1, mRNA sequence.  
 ACCESION BE674422 GI:10034963

VERSION BE674422.1  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 519)  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgaps-remail.nih.gov  
 Tissue Procurement: Christopher Moshaluk, M.D., Ph.D., Michael R.  
 Emsert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: M. Bento Soares, Ph.D.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CCAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL, send email to:  
 info@image.llnl.gov

Seq primer: -40UP from Gibco  
 High quality sequence stop: 499.  
 Location/Qualifiers

FEATURES  
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 1..519  
 /organism="Homo sapiens"  
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 /clone="IMAGE:3281166"  
 /issue\_type="carcinoid"  
 /lab\_host="DH10B"  
 /clone\_id="NCI-CCAP Lu24"

/note="Organ: Lung; Vector: pT7TD-Pac (Pharmacia) with a  
 modified polylinker; Plasmid DNA from the normalized  
 library NCI CGAP Lu5 was prepared, and ss circles were  
 made in vitro. Following HAP purification, this DNA was  
 used as tracer in a subtractive hybridization reaction.  
 The driver was PCR-amplified cDNAs from a pool of 5,000  
 clones made from the same library (cloneids  
 1414920-1417991 and 1520904-1522439). Subtraction by Bento  
 Soares and M. Patricia Bernaldo."

BASE COUNT 143 a 114 c 143 g 119 t  
 ORIGIN

Query Match 45.9%; Score 509.8; DB 10; Length 519;  
 Best Local Similarity 99.6%; Pred. No. 6.6e-141;  
 Matches 511; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

484 CTCAGCTTTCAACATCACTGATGCTTACTGACGACCATGATGATGATGATGATGATG 543  
 7 CGCAGCTTTTCAACATCACTGATGCTTACTGACGACCATGATGATGATGATGATGATG 66  
 544 AAGACTGTCTCAATATTTTCAATGAGGGTGTGATGCTGATGCTGATGCTGATGCTG 603  
 67 AAGACTGTCTCAATATTTTCAATGAGGGTGTGATGCTGATGCTGATGCTGATGCTG 126  
 604 ATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 663  
 127 ATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 186  
 664 AACTATGATTGC 723

Db 187 AACATGAGAAAGTGGATGGAAGCTTCAGAAATATGTCAGGAAGGATTTGC 246  
 QY 724 ATGCCCACTCTTACAAATCTACATGATGACAGGGAGACAGCTTTGATTAAGCTG 783  
 Db 247 ATGGCCCACTCTTACAAATCTACATGATGACAGGGAGACAGCTTTGATTAAGCTG 306  
 QY 784 AAGAGCTCAAGATGCTTGGCCCAAGGCGCGGTGGTGGCTTACTTCTGAGGGGATG 843  
 Db 307 AAGAGCTCAAGATGCTTGGCCCAAGGCGCGGTGGTGGCTTACTTCTGAGGGGATG 366  
 QY 844 ACGGTGAGAGTCTGATGATGCGCATGAGCGCTGCGTCTAGTGGAGATTTCTGCTT 903  
 Db 367 ACGGTGAGAGTCTGATGATGCGCATGAGCGCTGCGTCTAGTGGAGATTTCTGCTT 426  
 QY 904 CTGGGCGAGGACCAAGATGCTTATTTAGATCTCAAGAAAGACAGATCTTATGAGAA 963  
 Db 427 CTGGGCGAGGACCAAGATGCTTATTTAGATCTCAAGAAAGACAGATCTTATGAGAA 486  
 QY 964 GACAGAGAAATGCGAAGGTGCTTCTTCAAG 996  
 Db 487 GACAGAGAAATGCGAAGGTGCTTCTTCAAG 519

RESULT 3  
 BE467477 499 bp mRNA linear EST 27-JUL-2000  
 LOCUS h26608.x1 NCI CGAP Lu24 Homo sapiens cDNA IMAGE:3212943 3,  
 DEFINITION similar to SW:MG95 HUMAN P41594 METABOTROPIC GLUTAMATE RECEPTOR 5  
 BE467477  
 BE467477.1 GI:9513252  
 EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 499)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished  
 Contact: Robert Strausberg, Ph.D.  
 Email: sgabbs-remail.nih.gov  
 Tissue Procurement: Christopher Moshalk, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: M. Bento Soares, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LINL, send email to:  
 info@image.lnl.gov  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 493.  
 Location/Qualifiers  
 1. 499  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3212943"  
 /tissue\_type="carcinoid"  
 /lab\_host="DH10B"  
 /clone\_id="NCI-CGAP Lu24"  
 /note="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a  
 modified polylinker; Plasmid DNA from the normalized  
 library NCI CGAP Lu24 was prepared, and ss circles  
 made in vitro. Following HAP purification, this DNA was  
 used as tracer in a subtractive hybridization reaction.  
 The driver was PCR-amplified cDNAs from a pool of 5,000  
 clones made from the same library (cloneids  
 1414920-1417991 and 1520904-1522439). Subtraction by Bento  
 Soares and M. Fatima Bonaldo."  
 BASE COUNT 141 a 107 c 138 g 113 t

ORIGIN  
 Query Match 45.0%; Score 499; DB 10; Length 499;  
 Best Local Similarity 100.0%; Pred.No. 1,1e-137;  
 Matches 499; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 497 ACATACCTGAGATGCTTACTGACCAACCATCTGATCTGATGACCAAGCTCTGTTCA 556  
 Db 1 ACATACCTGAGATGCTTACTGACCAACCATCTGATCTGATGACCAAGCTCTGTTCA 60  
 QY 557 AATATTTCAATGAGGGTTGCTTCAAGATGCTCAGACAGGAGGATTCATGAGCAATAG 616  
 Db 61 AATATTTCAATGAGGGTTGCTTCAAGATGCTCAGACAGGAGGATTCATGAGCAATAG 120  
 QY 617 TGAAGAGTACCACTGAGCTTATGATTCAGCCCTTACACAGAAAGCAATATAGAGAA 676  
 Db 121 TGAAGAGTACCACTGAGCTTATGATTCAGCCCTTACACAGAAAGCAATATAGAGAA 180  
 QY 677 GTGGATGGAAGGCTTCAAGATATGTCAGCAAGGAAGGATTTGATGAGGATCTT 736  
 Db 181 GTGGATGGAAGGCTTCAAGATATGTCAGCAAGGAAGGATTTGATGAGGATCTT 240  
 QY 737 ACAAATCTACAGTAATGACAGGGAGCAGAGCTTTGATTAAGCTGTAAGAGCTCA 796  
 Db 241 ACAAATCTACAGTAATGACAGGGAGCAGAGCTTTGATTAAGCTGTAAGAGCTCA 300  
 QY 797 GTACTTGGCCCAAGGCGCGGTGGTGGCTTCTTCTGAGGGCATGACGTGAGAGTGC 856  
 Db 301 GTACTTGGCCCAAGGCGCGGTGGTGGCTTCTTCTGAGGGCATGACGTGAGAGTGC 360  
 QY 857 TGGTATGAGCAATGAGAGCGCGGTGGTGGCTTCTTCTGAGGGCATGACGTGAGAGTGC 916  
 Db 361 TGGTATGAGCAATGAGAGCGCGGTGGTGGCTTCTTCTGAGGGCATGACGTGAGAGTGC 420  
 QY 917 CAGATCCATCTTATTTAGATCTCAAGAAAGCATCTTATGAGGAGACAGAAAGAAAT 976  
 Db 421 CAGATCCATCTTATTTAGATCTCAAGAAAGCATCTTATGAGGAGACAGAAAGAAAT 480  
 QY 977 GCCAAGTGGCTTCTTCAAG 995  
 Db 481 GCCAAGTGGCTTCTTCAAG 499

RESULT 4  
 CB153433 449 bp mRNA linear EST 29-JAN-2003  
 LOCUS K-EST0210877 BIT694954 Homo sapiens cDNA clone BIT694954-28-C09 5',  
 DEFINITION mRNA sequence.  
 CB153433  
 ACCESSION CB153433.1 GI:28138427  
 VERSION  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 449)  
 Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,  
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and.  
 Kim,Y.S.  
 21C Frontiers Korean EST Project 2001  
 Unpublished  
 Contact: Kim YS  
 Genome Research Center  
 Korea Research Institute of Bioscience & Biotechnology  
 52 Boseun-dong Yuseong-gu, Daejeon 305-333, South Korea  
 Tel: +82-42-860-4470  
 Fax: +82-42-860-4409  
 Email: yongsung@mail.kribb.re.kr  
 Plate: 28 row: C column: 09  
 High quality sequence stop: 449.  
 Location/Qualifiers  
 1. 449  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
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 /clone="IMAGE:3212943"  
 /tissue\_type="carcinoid"  
 /lab\_host="DH10B"  
 /clone\_id="NCI-CGAP Lu24"  
 /note="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a  
 modified polylinker; Plasmid DNA from the normalized  
 library NCI CGAP Lu24 was prepared, and ss circles  
 made in vitro. Following HAP purification, this DNA was  
 used as tracer in a subtractive hybridization reaction.  
 The driver was PCR-amplified cDNAs from a pool of 5,000  
 clones made from the same library (cloneids  
 1414920-1417991 and 1520904-1522439). Subtraction by Bento  
 Soares and M. Fatima Bonaldo."  
 BASE COUNT 141 a 107 c 138 g 113 t

/mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="BIT694954-28-C09"  
 /sex="M"  
 /lab\_host="Top10F"  
 /clone\_11b="BIT694954"  
 /note="Organ: Brain; Vector: PCNS-D2; Site 1: EcoRI; Site 2: NotI. The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then dephosphorylated with tobacco acid pyrophosphatase (TAP). The dephosphorylated intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

BASE COUNT 106 a 112 c 112 g 119 t

Query Match 40.2%; Score 445.8; DB 14; Length 449;  
 Best Local Similarity 99.6%; Pred. No. 8.6e-122;  
 Matches 447; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

120 CTTTTCCTGTCATCCAGCCCTACTGTCAGAGTTCATGAGAGAGTGTGGGAGT 179  
 1 CTTTTCCTGTCATCCAGCCCTACTGTCAGAGTTCATGAGAGAGTGTGGGAGT 60

180 CCGTGAACAGTATGCGATTCAGAGAGTGGAGGCCATGCTGCATACCTCGAAGATCAA 239  
 61 CCGTGAACAGTATGCGATTCAGAGAGTGGAGGCCATGCTGCATACCTCGAAGATCAA 120

240 TTTCAGACCCCACTCTTGGCCCAATCACTGCGGCTGGAGATTAAGAGATTCCTGCTG 299  
 121 TTTCAGACCCCACTCTTGGCCCAATCACTGCGGCTGGAGATTAAGAGATTCCTGCTG 180

300 GCATTCGGCTGTGGCCCTAGAGCAGACATTTAGATTAAGAGATTCCTCATTTCTTC 359  
 181 GCATTCGGCTGTGGCCCTAGAGCAGACATTTAGATTAAGAGATTCCTCATTTCTTC 240

360 GGAAGAGAGAGAGGCTTGTGATCTCTGTGATGCTCTCTCTCTCTCTCTCTCTCTCAA 419  
 241 GGAAGAGAGAGAGGCTTGTGATCTCTGTGATGCTCTCTCTCTCTCTCTCTCTCTCAA 300

420 GAAGCCCATGATGAGGGCTCATTTGGGCTGTTCCAGTCTTTTACCATTCAGATCCAGAA 479  
 301 GAAGCCCATGATGAGGGCTCATTTGGGCTGTTCCAGTCTTTTACCATTCAGATCCAGAA 360

480 TTTCCTCAGCTTTTCAACATCTCAGATTCCTTACTCAGCAACATTCAGATTCGAG 539  
 361 TTTCCTCAGCTTTTCAACATCTCAGATTCCTTACTCAGCAACATTCAGATTCGAG 420

540 TGACAGAGCTCTGTTCAATATTTCATGA 568  
 421 TGACAGAGCTCTGTTCAATATTTCATGA 449

RESULT 5  
 AMO15382  
 LOCUS  
 DEFINITION  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

AMO15382 442 bp mRNA linear EST 10-SEP-1999  
 IMAGE:2710331 3', mRNA sequence.  
 AMO15382  
 AMO15382.1 GI:5864139  
 EST.  
 Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 442)  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished  
 Contact: Robert Straube, Ph.D.  
 Email: cgaaps-remail.nih.gov  
 Oligo-dt track not found. Not 1 site shown in beginning of sequence  
 is likely internal to the message. cDNA library preparation: M.B.  
 Soares Lab cDNA distribution: NCI-CGAP clone distribution  
 information can be found through the I.M.A.G.E. Consortium/ILNLT at:  
 www-bio.illn.gov/bdrip/image/image.html  
 Seq primer: M13 forward  
 POLYA=No.

FEATURES  
 source

1. .442  
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 /lab\_host="DH10B (Life Technologies)"  
 /clone\_11b="NCI-CGAP Sub1"  
 /note="Vector: pT73D-Pac (Pharmacia) with a modified  
 polylinker; Site 1: Not I; Site 2: Eco RI; The  
 NCI-CGAP Sub1 library is a subcloned library derived from  
 B1. B1 constitutes a mixture of 21 normalized or  
 subcloned NCI-CGAP libraries: NCI-CGAP Co4, NCI-CGAP Co16,  
 NCI-CGAP Pr22, NCI-CGAP Pr28, NCI-CGAP Co10, NCI-CGAP Co16,  
 NCI-CGAP K1d5, NCI-CGAP K1d12, NCI-CGAP K1d3,  
 NCI-CGAP K1d11, NCI-CGAP Lym2, NCI-CGAP Br2, NCI-CGAP Co8,  
 NCI-CGAP C1d1, NCI-CGAP L1d2, NCI-CGAP Br23, NCI-CGAP Lu5,  
 NCI-CGAP Lu24, NCI-CGAP Lu19, NCI-CGAP GC4, NCI-CGAP GC6,  
 NCI-CGAP Brn25. These 21 libraries were pooled and a  
 single-stranded DNA preparation of the resulting mixture  
 was used as a tracer in a subtractive hybridization with a  
 driver whose composition is detailed below: NCI-CGAP K1d3  
 pool 1 L1AM 3334-3337, 3682-3683, 3798-3803 (IMAGE  
 cloneId: 132337c-1323911, 1456006-1456775, 1500552-1502555)  
 ) NCI-CGAP K1d5 pool 1 L1AM 3338-3342, 3722-3725,  
 3776-3778 (IMAGE cloneId: 1323912-1325831,  
 1471368-1472903, 1492104-1493255) NCI-CGAP Lu5 pool 1 L1AM  
 3575-3582, 3851-3854 (IMAGE cloneId: 1415920-1417991,  
 1520904-1522439) NCI-CGAP GC4 pool 1 L1AM 3164-3167,  
 3716-3720, 3733-3735 (IMAGE cloneId: 1257096-1258631,  
 1459064-1470983, 1475592-1476743) NCI-CGAP Pr22 pool 1  
 L1AM 2457-2459, 2758-2759, 3062-3068 (IMAGE cloneId  
 985608-986759, 1101192-1101959, 1217928-1220615)  
 NCI-CGAP Co10 pool 1 L1AM 2644-2653, 2871-2872 (IMAGE  
 cloneId: 1057416-1061255, 1144584-1145351) The resulting  
 subcloned library contained 530,000 recombinants.  
 Subtraction was performed as previously described [Bonaldo  
 Lennon & Soares (1996)]. Normalization and Subtraction:  
 Two Approaches To Facilitate Gene Discovery. Genome  
 Research 6, 791-806.  
 TAG L1B-NCI CGAP L1d2  
 TAG\_TISSUE=Ictomyoblastoma  
 TAG\_SEQ=ATTCG

BASE COUNT 118 a 97 c 127 g 100 t

Query Match 38.2%; Score 424.4; DB 9; Length 442;  
 Best Local Similarity 99.5%; Pred. No. 2.1e-115;  
 Matches 436; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

484 CTCACGCTTTTCAACATCTCAGATTCCTTACTCAGCAACATTCAGATTCGAGTAC 543  
 5 CGCAGCTTTTCAACATCTCAGATTCCTTACTCAGCAACATTCAGATTCGAGTAC 64

544 AAGACTCTGTTCAATATTTCATGAGGCTTGTGCTTCAGATCTCAGAGGAGTCC 603  
 65 AAGACTCTGTTCAATATTTCATGAGGCTTGTGCTTCAGATCTCAGAGGAGTCC 124







COMMENT CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Please visit our web site for further details.  
URL: <http://genome.gsc.riken.go.jp/>  
URL: <http://fantom.gsc.riken.go.jp/>  
Location/Qualifiers

FEATURES  
source  
1..3879  
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/mol\_type="mRNA"  
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/db\_xref="FANTOM:DB:6430542K11"  
/db\_xref="taxon:10090"  
/clone="6430542K11"  
/sex="male"  
/tissue\_type="olfactory brain"  
/clone\_lib="RIKEN full-length enriched mouse cDNA library"  
/dev\_stage="adult"  
misc\_feature  
1..3063  
/note="METABOTROPIC GLUTAMATE RECEPTOR MEUR5 PRECURSOR homolog [Rattus norvegicus] (SPT8|BAA01711, evidence: FASTV, 98.5%ID, 87%length, match=3058)  
putative"

BASE COUNT 1026 a 975 c 954 g 924 t

ORIGIN  
Query Match 33.5%; Score 372.2; DB 11; Length 3879;  
Best Local Similarity 88.4%; Pred. No. 3.2e-99;  
Matches 404; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 458 CTTTACCACTGAGTCCAGCAATTTGCTCCAGCTTTTCAACATACCTCAGATTGCTTACT 517  
DB 1 CTGTGCCATTCATCAAGTTCAGACTGCTCCAGCTTTTCAACATACCTCAGATTGCTTACT 60  
QY 518 CAGCAACATCATGATCTGATGACAGACTCTGTTCAATATTTTCATGAGGTTGTGC 577  
DB 61 CTGCAACTGACATGATTTGATGACAGACTCTTATTCAGATCTTCAATGAGGTTGTAC 120  
QY 578 CTTGAGATGCTCAGCAGGCAAGGTCCATGCTGATGACATGTAAGAGGTAACATGACCT 637  
DB 121 CTTCGATGCCCGCAGAGCCCGAGCCATGATGATGACATGTAAGAGGTAACATGACCT 180  
QY 638 ATGTATCAGCCCTGACACAGAGGCACTATGAGAAAGTGGATGGAAGCTTCAAG 697  
DB 181 ATGTCTCAGCTGACACAGAGGCACTATGAGAAAGTGGATGGAAGCTTCAAG 240  
QY 698 ATATGTCAGGAGAGGATTTGATGATGCCCACTCTTACAAATCTACATGATGAC 757  
DB 241 ATATGTCAGGAGAGGATTTGATGATGCCCACTCTTACAAATCTACATGATGAC 300  
QY 758 GGGAGCAGAGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 817  
DB 301 GGGAGCAGAGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360  
QY 818 TGGTGGCTTACTTCTGTGAGGAGGATGACGATGAGAGGCTGCTGATGAGGATGAGG 877  
DB 361 TGGTGGCTTACTTCTGTGAGGAGGATGACGATGAGAGGCTGCTGATGAGGATGAGG 940  
QY 878 TGGGCTTACGAGGAGGATTTCTGCTTCTGAGGAGGAG 914  
DB 421 TGGGCTTACGAGGAGGATTTCTGCTTCTGAGGAGGAG 957

RESULT 9  
BG695213 682 bp mRNA linear EST 04-MAY-2001  
LOCUS  
DEFINITION NISC\_i4v3g09.w1 Soares NMBP2 pleutitary Mus musculus cDNA clone  
IMAGE:4317880 5', mRNA sequence.  
ACCESSION BG695213  
VERSION BG695213.1 GI:13954900  
KEYWORDS EST.

SOURCE Mus musculus (house mouse)  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: [cgabbs-r@mail.nih.gov](mailto:cgabbs-r@mail.nih.gov)  
CDNA Library Preparation: M. Bento Soares Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium/HLNLT  
DNA Sequencing by: National Institutes of Health Intramural  
Sequencing Center (NISC)  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/HLNLT at: [infoimage.llnl.gov](http://infoimage.llnl.gov)  
MGI:1598648  
Plate: LLAM9922 row: M column: 17  
Seq primer: T7 primer.  
Location/Qualifiers  
1..682  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
/clone="IMAG:4317880"  
/tissue\_type="pituitary gland"  
/dev\_stage="embryo, 14 dpc"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="Soares NMBP2 pituitary"  
/note="Organ: brain; Vector: pRT3D-Pac; Site 1: NotI; Site 2: EcoRI; 1st strand cDNA was primed with a NotI - oligo(dT) primer  
5'-AACTGAGAGATTCGCGCGCGCGCGCTTTTCTTTTCTTTTCTTTT-3'; double-stranded cDNA was ligated to EcoRI adaptors 5'-AATTCGCGCAGG-3' AND 5'-CCTGTCGCG-3' (Pharmacia), digested with NotI and cloned into the NotI and EcoRI sites of the pRT3D-Pac vector. Library went through one round of normalization, and was constructed in the laboratory of M. Bento Soares (University of Iowa)."

BASE COUNT 190 a 121 c 162 g 209 t

ORIGIN  
Query Match 26.1%; Score 289.2; DB 10; Length 682;  
Best Local Similarity 88.0%; Pred. No. 7.5e-75;  
Matches 315; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

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DB 5 TTAAGTACTTCATGAGGCTTGTGCTTCAAGTCTCAGAGGCAAGCTTCATGCTGAC 64  
QY 614 TAGTGAAGAGTACCACTGACCTATGATGATGATGATGATGATGATGATGATGATGAT 673  
DB 65 TAGTGAAGAGTACCACTGACCTATGATGATGATGATGATGATGATGATGATGATGAT 124  
QY 674 AAGTGGAGTGAAGGCTTCAAGATATGTCAGGAGGAGGAGGATTTGATGCGCCACT 733  
DB 125 AAGTGGAGTGAAGGCTTCAAGATATGTCAGGAGGAGGAGGATTTGATGCGCCACT 184  
QY 734 CTTACAAATCTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 793  
DB 185 CTTACAAATCTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 244  
QY 794 CAAGTCACTTGCCTCAAGGCGCGGCTGCTGCTTCTGTGAGGAGGATGATGAGGAG 853  
DB 245 GAAGTCACTTGCCTCAAGGCGCGGCTGCTGCTTCTGTGAGGAGGATGATGAGGAG 904  
QY 854 GTCTGCTGATGCGCATGAGCGCGCTGCTGCTGATGAGGAGGATTTGCTTGGGCGAG 911  
DB 305 GTCTGCTGATGCGCATGAGCGCGCTGCTGCTGATGAGGAGGATTTGCTTGGGCGAG 962

RESULT 10  
BI826234 664 bp mRNA linear EST 04-OCT-2001  
LOCUS BI826234  
DEFINITION 603075928F1 NIH MGC\_119 Homo sapiens cDNA clone IMAGE:5167902 5', mRNA sequence.  
ACCESSION BI826234  
VERSION BI826234.1 GI:15937784  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE NIH-MGC <http://mgs.nci.nih.gov/>.  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished  
JOURNAL  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
Tissue Procurement: Life Technologies, Inc.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>  
Plate: LAM1417 row: g column: 07  
High quality sequence, stop: 662.  
Location/Qualifiers

## FEATURES

source

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/organism="Homo sapiens"  
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/db\_xref="taxon:9606"  
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/lab\_host="DH10B"  
/clone\_11b="NIH MGC\_119"  
/note="Organ: brain; Vector: pCMV-Sport6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH MGC Library."  
BASE COUNT 151 a 177 c 179 g 157 t  
ORIGIN

Query Match 25.9%; Score 287; DB 12; Length 664;  
Best Local Similarity 98.3%; Pred. No. 3.3e-74;  
Matches 290; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 1 ATGTCCTTCTGTGATCTGTCACTTACTTTGAAAGATGTCGGAGATGCA 60  
DB 370 ATGTCCTTCTGTGATCTGTCACTTACTTTGAAAGATGTCGGAGATGCA 429  
QY 61 CAGTTCAGTGAAGAGAGGAGGCTGCTCACTGCTGGTGCATCATTTATGAGCTTC 120  
DB 430 CAGTTCAGTGAAGAGAGGAGGCTGCTCACTGCTGGTGCATCATTTATGAGCTTC 489  
QY 121 TTTTCTGTATCAACGCTACTGTGAGCAAGTTCAATGAGGAAGTGGGGCAAGTC 180  
DB 490 TTTTCTGTATCAACGCTACTGTGAGCAAGTTCAATGAGGAAGTGGGGCAAGTC 549  
QY 181 CGTGAACAGTATGAGCTTCAAGAGAGTGAAGCCATGCTGATACCTTGAAGATCAAT 240  
DB 550 CGTGAACAGTATGAGCTTCAAGAGAGTGAAGCCATGCTGATACCTTGAAGATCAAT 609  
QY 241 TCAAGCCCACTCTTGTCCCAACATCACTGAGGCTGTGAGATPAGGATTCCT 295  
DB 610 TCAAGCCCACTCTTGTCCCAACATCACTGAGGCTGTGAGATPAGGATTCCT 664

RESULT 11  
BU51729 657 bp mRNA linear EST 28-NOV-2002  
LOCUS BU51729  
DEFINITION 603527561F1 CSEBCHN69 Gallus gallus cDNA clone CHEST47616 5', mRNA sequence.  
ACCESSION BU51729  
VERSION BU51729.1 GI:25859730  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.  
REFERENCE Boardman, P. B., Sanz-Bzquez, J., Overton, I. M., Burt, D. W., Bosch, E., Fong, W. T., Tickle, C., Brown, W. R. A., Wilson, S. A. and Hubbard, S. J.  
A Comprehensive Collection of Chicken cDNAs  
Curr. Biol. 12 (22), 1965-1969 (2002)  
JOURNAL MEDLINE  
PUBMED 22335534  
12445392  
COMMENT Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology (UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: [Simon.Hubbard@umist.ac.uk](mailto:Simon.Hubbard@umist.ac.uk).  
Location/Qualifiers

## FEATURES

source

1..657  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="Compton line 151"  
/db\_xref="taxon:9031"  
/clone="CHST47616"  
/sex="Female"  
/tissue\_type="cerebellum"  
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/clone\_11b="CSEBCHN69"  
/note="Organ: brain; Vector: pBluescript II KS(+); Site 1: EcoRI; Site 2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunt-ended, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996) 791, except that a significantly longer reannealing hybridization was used."  
BASE COUNT 161 a 168 c 178 g 150 t  
ORIGIN

Query Match 25.4%; Score 281.6; DB 13; Length 657;  
Best Local Similarity 72.4%; Pred. No. 1.4e-72;  
Matches 365; Conservative 0; Mismatches 139; Indels 0; Gaps 0;  
QY 411 CCGCTCAAGAGCCCATATGATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 470  
DB 10 CCGCTCAAGAGCCCATATGATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 69  
QY 471 GGTTCAGAAATTTCTCCAGCTTTTCAACATACCTCAGATTCTTACTCAGCAACATCAT 530  
DB 70 GTTCAGAACTCTGTGAGCTTTTGAATCCCAAAATGGCTTACTGTCAGCAGCAT 129  
QY 531 GGAATGAGTGAAGAAGCTGTGCAATATTTTCAATGAGGCTGTGCTTCAATGTCTCA 590  
DB 130 CGACTGAGTGAAGAAGCTCTTCAAAATTTTCTCCGTTGTGTCCCTCTGACACAT 189

Qy	591	GCAGGCAAGGTCATGAGTGAACATAGTGAAGAGTCAACCTGGACCTATGATCACCG	650
Db	190	CCAGCCCCGCGCATGCTCGATATGTCAAGCCTTACACTGGACTTACGTGCCCGT	249
Qy	651	AACACAGAGGCAACTATGAGAGAAAGTGGATGGAAGCTTCAAGATATGTCAGCGAA	710
Db	250	GCACACTGAAGGAATTACGGGGAAAGTGAATGAGAGCCTTCAAGAGCTGGCTGCCA	309
Qy	711	GGAGGGATTTCATGCCCCAAGCTTTACAAATCTACAGTAATGACAGGGAGCAGAGCTT	770
Db	310	AGAGGGCCCTCTGCATTTGCTCAATTCGACAAAGATCTATAGCAATGCTGGGAGAAAGCTT	369
Qy	771	TGATTAAGCTGTCGAAAGAACTCACAGTCACTTGTCGCCAAGCCCCGGGTGTGGCTACTT	830
Db	370	TGATGGCCTGCTCCGCAACCTCGAAGAAATTAACCCAAAGGCTGAGTGTGTTTGCTT	429
Qy	831	CTGTAGGGCATGACGGTGAAGGTGTGCTGATGGCCATGAGGCGCTGGGTCTTAATGGG	890
Db	430	CTGTAGGGCATGACGGTGAAGGGGATCTCATCTGTAATGACACGTCTGGAGATGCTTGG	489
Qy	891	AGAAATTCGTGCTTCTGGGCAAGGA	914
Db	490	GGAGTTCCTGCTAATTGGAAAGTGA	513

RESULT 12	
B0393781	
LOCUS	B0393781
DEFINITION	669 bp mRNA linear EST 27-NOV-2002 60380338001 CSEQCCH57 Gallus gallus CDNA clone ChnST778020 5', mRNA

ACCESSION	BU3933781	
VERSION	BU3933781.1	GI:257628200
KEYWORDS	EST.	
SOURCE	Gallus gallus	(chicken)
ORGANISM	Gallus gallus	

Bakaryota; Metazoa; Chordata; Craniata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phaasianidae; Phaesianinae; Gallus.

REFERENCE	AUTHORS	TITLE	JOURNAL	YEAR
1 (bases 1 to 669)	Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.	A Comprehensive Collection of Chicken cDNAs	Curr. Biol.	12 (22), 1965-1969 (2002)

**PUBMED  
COMMENT**

**COMMENT**

Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology (UMIST)

PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: [Simon.Hubbard@umist.ac.uk](mailto:Simon.Hubbard@umist.ac.uk)

## FEATURES

**Source**

```

/organism="Gallus gallus"
/mol_type="mRNA"
/strain="White Leghorn, Hlaex"
/db_xref="taxon:9031"
/clone="CHS1778c20"
/dev_stage="16 day embryo"
/lab_host="DH10B"
/clone_idb="CSEQCIN57"
/note="Organ: brain; Vector: pBluescript II KS(+); Site_1=
EcoRI; Site_2: NotI; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction,
following this first strand reaction, double-stranded cDNA
was bluntend, ligated to NotI adapters, digested with
EcoRI and NotI, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2

```

rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

Query Match	25.4%	Score 281.6;	DB 13;	Length 669;
Best Local Similarity	72.4%;	Pred. No. 1.4e-72;		
Matches 365;	Conservative 0;	Mismatches 139;	Indels 0;	Gaps 0;

411 CCGCTCCAGAGCCCATAGTAGGGGTCTTGGGCGCTGGTTCCAGTTCTTAGCCATTCA 470

471 GGCACGAAATTGCGCCAGCGTTTCAACATACCTCCAGATTGCTTACTCAGCAACCAATCAT 510

Db 82 GGTCAGAACTCTGCAGCTTTGACATCCACAATTGCTACTTGCACACAGCAT 141

531 GGATCTGATGACAGAAGCTCTGTTCAAATATTTCATGAGGGTGTGCGCTTCAGATGCTCA 590

[illegible]

Db 202 CCAAGCCCCGCCATGCTCGATATTGTCAAGCGTTACAACATGGAATTACGTGTCCGCCGT 261

651 ACAACAGAGGCAACTATGAGAGGAGTGGATGGAGCCCTCAAGATATGTCAAGCAA 710

DB 262 GCACACTGAAGGAAATACCGGGAAAGTCGAATGAGGCGCTCAAGAGCTGGCTGCCCA 321

Db 322 AGAGGGCCTCTGCAATGCTCAATTCTGACAGACATCTAATAGCAATGCTGGGGAAGAAAGCTT 381

771 TGATTAAGCTGCTGAAGAAGCTCAACAATTCATTGCCCAAGGCCGGGTGGTGGCTACTT 830

Db 382 TGATCGCCTGCTCCGCAAGCTGCGAAGATTACCAAGGCTAGAGTGTGTTGCTT 441

442 CTGTGAGGGCATGACGGTGAAGGGGATCTTCATTGGCTATGAGACGTCTGGGAGTGGCTTGG 501

891 AGAATTTCTGCTTCTGCGCAGGGA 914

Db 502 GGAGTTCTCTGCTAATTGGAAGTGA 525

**RESULT 13**  
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LOCUS	T78107	392 bp	mRNA	linear	EST 07-MAR-1995
DEFINITION	yc98a01.r1 Soares infant brain IN1B Homo sapiens CDNA clone				

RECEPTOR 5 A - ; mRNA sequence.  
T78107

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KEYWORDS
VERSION 1/810/1.1  GI:656616
EST.

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ORGANISM      Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

<b>REFERENCE</b>	
Mannila, A., Bucher, J., Fritzsche, C., Kallunki, M., Nieminen, R., Nuoli-	
1 (bases 1 to 392)	
Hiltner, L., Clay, N., Doherty, T., Ellstrom, K., Hawkins, M., Holman	

'M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaakis, E., Waterston

**TITLE**  
**JOURNAL**  
The WashU-Merck EST Project  
Unpublished

CONTACT: MILBORN RA  
Washington University School of Medicine  
444 Forest Park Drive Box 8001 St Louis MO 63108

**Tel: 314 286 1800**  
**Fax: 314 286 1810**



REFERENCE  
1 (bases 1 to 673)  
Phasianinae; Gallus.  
AUTHORS  
Boardman, P. E., Sanz-Baquero, J., Overton, I. M., Burt, D. W., Bosch, E.,  
Fong, W. T., Tickle, C., Brown, W. R. A., Wilson, S. A. and Hubbard, S. J.  
TITLE  
A Comprehensive Collection of Chicken CDNA  
JOURNAL  
Curr. Biol. 12 (22), 1965-1969 (2002)  
MEDLINE  
22335534  
PUBMED  
12445392  
COMMENT  
Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology (UMIST)

PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.  
Location/Qualifiers

## FEATURES

source  
1. 673  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="White Leghorn, Hisex"  
/db\_xref="taxon:9031"  
/clone="CHEST77411"  
/dev\_stage="16 day embryo"  
/lab\_host="DH10B"  
/clone\_lib="CSBCHN57"  
/note="Organ: brain; Vector: pBluescript II KS(+); Site\_1:  
EcoRI; Site\_2: NotI; This normalized library was  
constructed from 1 million independent clones. cDNA  
synthesis was initiated using an oligo(dT) primer, using  
methylated C in the first strand synthesis reaction.  
Following this first strand reaction, double-stranded cDNA  
was blunted, ligated to NotI adapters, digested with EcoRI  
, size-selected, and cloned into the NotI and EcoRI  
compatible sites of a custom modified MCS of the  
pBluescript (KS+) vector. The library was normalized in 2  
rounds using conditions adapted from Soares et al., PNAS  
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6  
(1996): 791, except that a significantly longer  
reannealing hybridization was used."

BASE COUNT 165 a 173 c 180 g 155 t  
ORIGIN

Query Match 22.7%; Score 252.2; DB 13; Length 673;  
Best Local Similarity 72.1%; Pred. No. 8.6e-64;  
Matches 341; Conservative 0; Mismatches 131; Indels 1; Gaps 1;

OY 443 GGCGTGGTCCAGTCTTTAGCCATTCAGGT-CCAGATTGCTCCAGCTTTCAACATA 501  
DB 56 GCCCTGGCTCCAGCTCAGTGGCATCAGGTGCTAGAACCTCTGCACTCTTTGACATC 115  
OY 502 CCTCAGATTGCTTACTCAGCAACCATCAGATCTGAGTACAAGACTCTGTTCAATAT 561  
DB 116 CCACAAATTGCCACTCTGCCACACATCGAAGTGAACAAGACTCTTCAAGTAT 175  
OY 562 TTCATGAGGTTGTGCTTCAAGTGTCTCAGCAGGCAAGTCCATGCTGAGCATAGTGAAG 621  
DB 176 TTTCCTCGTGTGCTCCCTCTGACACATCCAAAGCCCGCCCAAGTCTCATATTTGCAAG 235  
OY 622 AGGTACAATGCACTATGATATCAGCCGTACACACAGAAGCAACTATGAGAAAGTGGG 681  
DB 236 CGTTACAATGCACTTACGTGTCCGCCGTGCAACTGAAAGAAATTAACGGGAAAGTGA 295  
OY 682 ATGGAAGCTTCAAGATATGTCAGCGAAGAAAGGAAATTTGCAATGCCCCACTTTACAA 741  
DB 296 ATGGAAGCTTCAAGATATGTCAGCGAAGAAAGGAAATTTGCAATGCCCCACTTTACAA 741  
OY 742 ATCTAAGTAATGCAAGGAGCAGAGCTTTGATTAAGTGTGTAAGAAGCTCACAACTCAC 801  
DB 356 ATCTAAGTAATGCTGAGGAGAAAGCTTTGATGCTGCTCGCAAGCTGCGAAGAAAGA 415  
OY 802 TTGCCCAAGGCCCGGCTGTGCTCTACTTCTGTGAGGGCATGACGGTGAAGGTCTGCTG 861

DB 416 TTACCCAGCTAGAGTGTGTTTGTCTTGTGAGGGCATGACGCTGAGGGGATCTTC 475  
OY 862 ATGGCCATGAGGCGCTGGGTCTAGTGAAGAAATTTCTGCTTCTGGCAGGGA 914  
DB 476 ATGTATGAGACGTGTGGAGTCTTGGGAGTTCTCTTAATGGAAGTGA 528

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